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OM protein - protein search, using sw model

Run on: March 31, 2005, 11:42:18 ; Search time 38.75 Seconds
(without alignments)
49.905 Million cell updates/sec

Title: US-10-614-959-10

Perfect score: 29

Sequence: 1 TYAMH 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*\n2: Geneseqp1990s:*\n3: Geneseqp2000s:*\n4: Geneseqp2001s:*\n5: Geneseqp2002s:*\n6: Geneseqp2003as:*\n7: Geneseqp2003bs:*\n8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	5	3	AAV79068 Anti-fact
2	29	100.0	7	3	AAAB14789
3	29	100.0	12	3	AAAB14784
4	29	100.0	120	4	AAAG65570
5	29	100.0	121	5	ABG76537 HCV E1 an
6	29	100.0	128	5	ABG76559 HCV E1 an
7	29	100.0	206	6	ABU24807 Protein e
8	29	100.0	258	7	ABO77482 Pseudomon
9	29	100.0	278	8	ADN27332 Bacterial
10	29	100.0	307	4	AAAG72483
11	29	100.0	321	4	AAAG71475 Human OR-
12	29	100.0	531	8	ADRI10293 Human pro
13	29	100.0	690	3	AAAY50844 A. oryzae
14	29	100.0	690	3	AAAY50835 A. oryzae
15	29	100.0	703	3	AAAB14781
16	29	100.0	703	3	AAAB14782
17	29	88.7	46	4	AAAB82576 Human lmm
18	29	88.7	67	4	ABBA40299 Peptide #
19	29	88.7	67	4	AAAM33985 Peptide #
20	29	88.7	67	4	AAAW37398 Human bon
21	29	88.7	67	4	AAAM61093 Human liv
22	29	88.7	67	4	ABG55546 Human pep
23	29	88.7	67	5	ABG43685 Human pep
24	29	88.7	79	4	AAUI18208 Novel hum
25	29	88.7	79	5	ABG92629 Human DNA

26	26	89.7	79	7	ADC25346 Human ext
27	26	89.7	89	5	ABG68752 Cytochrom
28	26	89.7	162	5	ABP01422 Human ORF
29	26	89.7	173	5	ABG68756 Cytochrom
30	26	89.7	194	7	ADBO8218 Novel pro
31	26	89.7	205	7	ADBO8219 Novel pro
32	26	89.7	213	5	ABBB91152 Herdici
33	26	89.7	221	6	ADAA55412 Human pro
34	26	89.7	238	5	ABP46042 Human Bly
35	26	89.7	238	7	ADG96869 Single ch
36	26	89.7	242	5	ABBA49910 listeria
37	26	89.7	304	6	ABU17641 Protein e
38	26	89.7	370	4	AAAG91423 C glutam
39	26	89.7	370	4	AAAG90014 C glutam
40	26	89.7	454	7	ABO63767 Klebsie11
41	26	89.7	455	7	ADFO8003
42	26	89.7	501	8	ADCA7242 Rabbid cy
43	26	89.7	502	5	AAE26192 Human cyt
44	26	89.7	502	7	ADE57186 Human pro
45	26	89.7	502	7	ADE57190 Human pro

ALIGNMENTS

RESULT 1	AAV79068	standard; peptide; 5 AA.
ID	AAV79068	(first entry)
DT	12-JUN-2000	
DE	Anti-factor IX/IXa antibody H chain V domain CDRI amino acid sequence.	
XX	Complementarity determining region 1; CDRI; antibody; Gla domain;	
XX	factor IX/IXa; blood coagulation; deep venous thrombosis;	
XX	arterial thrombosis; unstable angina; post myocardial infarction;	
XX	coronary artery bypass graft; CABG; stroke; tumour growth; metastasis;	
XX	percutaneous transluminal coronary angioplasty; PTCA; inflammation;	
XX	septic shock; hypotension; adult respiratory distress syndrome; ARDS;	
XX	arterial fibrillation; disseminated intravascular coagulopathy; DIC.	
OS	Homo sapiens.	
XX	WO200012562-A1.	
PN	09-MAR-2000.	
PD	26-AUG-1999; 99WO-US019453.	
XX	28-AUG-1998; 98US-0098233P.	
PF	03-MAR-1999; 99US-0122767P.	
PR	(GETH) GENENTECH INC.	
XX	Adams CW, Devaux B, Eaton DL, Hase PE, Judice JK, Kirchhofer D,	
XX	Suggett S;	
XX	WPI; 2000-256595/22.	
XX	Novel human anti-Factor IX/IXa antibodies against IX/IXa gamma-	
XX	carboxyglutamic acid domains useful as anti-coagulant in thrombosis,	
XX	stroke, and post myocardial infarction.	
XX	Claim 2; Fig 2; 84pp; English.	
PS	This sequence represents a complementarity determining region 1 (CDRI) of	
CC	the heavy chain variable domain of a human anti-factor IX/IXa Gla domain	
CC	antibody. Factor IXa is a vitamin K dependent plasma serine protease that	
CC	participates in the blood coagulation pathways. The Gla domain of factor	
CC	IXa and its zymogen factor IX contains important structural determinants	
CC	for interaction with high affinity binding sites on vascular endothelial	

```
CC cells and platelets. Compositions comprising the antibodies are used for
CC the treatment or prophylaxis of thrombotic or coagulopathic diseases or
CC disorders in a mammal for which inhibiting a FIX/IXa mediated event is
CC indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable
CC angina, post myocardial infarction, post surgical thrombosis, coronary
CC artery bypass graft (CABG), percutaneous transluminal coronary
CC angioplasty (PTCA), stroke, tumour growth, invasion or metastasis,
CC inflammation, septic shock, hypotension, adult respiratory distress
CC syndrome (ARDS), arterial fibrillation and disseminated intravascular
CC coagulopathy (DIC)
CC
XX
SQ Sequence 5 AA;

Query Match          100.0%; Score 29; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TYAMH 5
Db      1 TYAMH 5

RESULT 2
AAB14789
ID AAB14789 standard; peptide; 7 AA.
XX
AC AAB14789;
XX
DT 06-DEC-2000 (first entry)
XX
DE Aspergillus oryzae KBN616 glutaminase peptide, SEQ ID NO:12.
XX
KW Glutaminase; Aspergillus oryzae KBN616; glutamic acid synthesis;
KW fermentation; foodstuff production; miso; soy sauce; peptide fragment;
KW PCR primer design.
XX
OS Aspergillus oryzae.
XX
PN JP200016547-A.
XX
PD 20-JUN-2000.
XX
PF 07-DEC-1998; 98JP-00347127.
XX
PR 07-DEC-1998; 98JP-00347127.
XX
PA (AICH-) AICHI KEN PREFECTURE.
XX
PA (ICHI-) ICHIBIKI KK.
XX
DR WPI; 2000-477931/42.
XX
PT A new glutaminase and its preparation.
XX
PS Example 2; Page 25; 27pp; Japanese.
XX
CC The invention relates to two novel glutaminases (AAB14781, AAB14782) from
CC Aspergillus oryzae KBN616 and Aspergillus sojae BA-104 respectively which
CC have molecular weights of approximately 73 kD (as determined by gel
CC filtration). The enzymes have an optimum temperature of approximately 50
CC degrees Celsius, and an optimum pH of about 8.5. The glutaminases
CC catalyse the conversion of L-glutamine to L-glutamic acid, and may be
CC used in the production of fermented foodstuffs such as soy sauce and
CC miso. Sequences AAB14787-B14789 represent fragments of Aspergillus oryzae
CC KBN616 glutaminase which were used as the basis for the design of
CC degenerate PCR primers AAA72206, AAA72207 and AAA72209. These primers
CC were used in the isolation of genomic DNA encoding Aspergillus oryzae
CC KBN616 (AAA72204)
CC
XX
SQ Sequence 7 AA;

Query Match          100.0%; Score 29; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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Qy      1 TYAMH 5
Db      3 TYAMH 7

RESULT 3
AAB14784
ID AAB14784 standard; peptide; 12 AA.
XX
AC AAB14784;
XX
DT 06-DEC-2000 (first entry)
XX
DE Aspergillus oryzae KBN616 glutaminase peptide fragment, SEQ ID NO:6.
XX
KW Glutaminase; Aspergillus oryzae KBN616; glutamic acid synthesis;
KW fermentation; foodstuff production; miso; soy sauce;
KW V8 protease digestion.
XX
OS Aspergillus oryzae.
XX
PN JP200016547-A.
XX
PD 20-JUN-2000.
XX
PF 07-DEC-1998; 98JP-00347127.
XX
PR 07-DEC-1998; 98JP-00347127.
XX
PA (AICH-) AICHI KEN PREFECTURE.
XX
PA (ICHI-) ICHIBIKI KK.
XX
DR WPI; 2000-477931/42.
XX
PT A new glutaminase and its preparation.
XX
PS Example 2; Page 9; 27pp; Japanese.
XX
CC The invention relates to two novel glutaminases (AAB14781, AAB14782) from
CC Aspergillus oryzae KBN616 and Aspergillus sojae BA-104 respectively which
CC have molecular weights of approximately 73 kD (as determined by gel
CC filtration). The enzymes have an optimum temperature of approximately 50
CC degrees Celsius, and an optimum pH of about 8.5. The glutaminases
CC catalyse the conversion of L-glutamine to L-glutamic acid, and may be
CC used in the production of fermented foodstuffs such as soy sauce and
CC miso. Sequences AAB14784-B14786 represent the N-terminal sequences
CC determined for three V8 protease fragments (P1-P3) of Aspergillus oryzae
CC KBN616 glutaminase in an exemplification of the invention
CC
XX
SQ Sequence 12 AA;

Query Match          100.0%; Score 29; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TYAMH 5
Db      7 TYAMH 11

RESULT 4
AAG65570
ID AAG65570 standard; protein; 120 AA.
XX
AC AAG65570;
XX
DT 30-NOV-2001 (first entry)
XX
DE Amino acid sequence of protein seq Id No. 95.
XX
KW Gene library; immunoglobulin; antibody library; human.
```

OS Homo sapiens.
 XX WO200162907-A1.
 PN
 XX
 PD 30-AUG-2001.
 XX
 PF 22-FEB-2001; 2001WO-JP001298.
 XX
 PR 22-FEB-2000; 2000JP-00050543.
 XX
 PA (MEDIC-) MEDICAL & BIOLOGICAL LAB CO LTD.
 XX
 PI Kurosawa Y, Akahori Y, Iba Y, Morino K, Shinohara M, Takahashi M,
 XX Okuno Y, Shiraki K;
 DR WPI; 2001-565420/63.
 DR N-P8DB; AAH47734.
 XX
 PT Producing gene libraries and antibody libraries, involves selecting a
 PT light chain that binds to a heavy chain product to produce a functional
 PT formation, and producing a gene library of the light chain variable
 PT regions.
 XX
 PS Examples; p 171; 181pp; Japanese.
 XX
 CC The invention relates to producing gene libraries, comprising
 CC immunoglobulin light and heavy variable region. The method involves
 CC selecting light chain that binds with the heavy chain product to produce
 CC a functional conformation, producing a gene library comprising a
 CC collection of these light chain variable genes, and combining with gene
 CC library of heavy chain variable genes. The method is used for production
 CC of gene and antibody libraries
 XX
 SQ Sequence 120 AA;

Query Match 100.0%; Score 29; DB 4; Length 120;
 Best Local Similarity 100.0%; Pred. No. 72;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
 |||||
 DB 31 TYAMH 35

RESULT 5
 ABG76537
 ID ABG76537 standard; protein; 121 AA.
 XX
 AC ABG76537;
 XX
 DT 05-NOV-2002 (first entry)
 XX
 DE HCV E1 antigen monoclonal antibody #25.
 XX
 KW Human; HCV; hepatitis C virus; E1 antigen; monoclonal antibody; vaccine;
 KW hepatotropic; Fab; hypervariable region; E2 antigen; antibody.
 XX
 OS Homo sapiens.
 XX
 PN WO200260954-A1.
 XX
 PD 08-AUG-2002.
 XX
 PF 14-JAN-2002; 2002WO-SE000044.
 XX
 PR 12-JAN-2001; 2001US-0260889P.
 XX
 PA (KARO-) KAROLINSKA INNOVATIONS AB.
 XX
 PI Drakenberg K, Persson MAA;
 XX
 DR WPI; 2002-608502/65.
 XX

PT Vaccine comprising a human monoclonal antibody against hepatitis C virus
 PT (HCV) E1 or E2 antigen, useful for treating or preventing HCV infection.
 XX
 PS Disclosure; Page 36; 64pp; English.
 XX

CC The invention relates to a human monoclonal antibody or its antigen
 CC binding fragments, which exhibit immunological binding affinity for a
 CC hepatitis C virus (HCV) E1 antigen, comprising an amino acid sequence
 CC homologous to the binding portion of a human antibody Fab molecule from a
 CC combinatorial antibody library. The vaccine composition comprising the
 CC antibodies or antigen binding fragments against HCV E1 or E2 antigen or
 CC its hypervariable region is useful in treating or preventing HCV
 CC infection in a subject. Sequences ABG76513-ABG76568 represent human
 CC monoclonal antibodies against HCV E1 antigen
 XX

SQ Sequence 121 AA;

Query Match 100.0%; Score 29; DB 5; Length 121;
 Best Local Similarity 100.0%; Pred. No. 73;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
 |||||
 DB 33 TYAMH 37

RESULT 6

ABG76559
 ID ABG76559 standard; protein; 128 AA.
 XX

AC ABG76559;
 XX

DT 05-NOV-2002 (first entry)
 XX

DE HCV E1 antigen monoclonal antibody #47.
 XX

KW Human; HCV; hepatitis C virus; E1 antigen; monoclonal antibody; vaccine;
 KW hepatotropic; Fab; hypervariable region; E2 antigen; antibody.
 XX

OS Homo sapiens.
 XX

PN WO200260954-A1.
 XX

PD 08-AUG-2002.
 XX

PF 14-JAN-2002; 2002WO-SE000044.
 XX

PR 12-JAN-2001; 2001US-0260889P.
 XX

PA (KARO-) KAROLINSKA INNOVATIONS AB.
 XX

PI Drakenberg K, Persson MAA;
 XX

DR WPI; 2002-608502/65.
 XX

PT Vaccine comprising a human monoclonal antibody against hepatitis C virus
 PT (HCV) E1 or E2 antigen, useful for treating or preventing HCV infection.
 XX

PS Disclosure; Page 52-53; 64pp; English.
 XX

CC The invention relates to a human monoclonal antibody or its antigen
 CC binding fragments, which exhibit immunological binding affinity for a
 CC hepatitis C virus (HCV) E1 antigen, comprising an amino acid sequence
 CC homologous to the binding portion of a human antibody Fab molecule from a
 CC combinatorial antibody library. The vaccine composition comprising the
 CC antibodies or antigen binding fragments against HCV E1 or E2 antigen or
 CC its hypervariable region is useful in treating or preventing HCV
 CC infection in a subject. Sequences ABG76513-ABG76568 represent human
 CC monoclonal antibodies against HCV E1 antigen
 XX

SQ Sequence 128 AA;

Query Match 100.0%; Score 29; DB 5; Length 128;

Best Local Similarity 100.0%; Pred. No. 77;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
|||
32 TYAMH 36

RESULT 7

ABU24807 ID ABU24807 standard; protein; 206 AA.

XX AC ABU24807;

XX DT 19-JUN-2003 (first entry)

XX DE Protein encoded by Prokaryotic essential gene #10334.

XX KM Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX OS Clostridium botulinum.

XX PN WO200277183-A2.

XX PD 03-OCT-2002.

XX PF 21-MAR-2002; 2002WO-US009107.

XX PR 21-MAR-2001; 2001US-00815242.

XX PR 06-SEP-2001; 2001US-00948993.

XX PR 25-OCT-2001; 2001US-0342923P.

XX PR 08-FEB-2002; 2002US-00072851.

XX PR 06-MAR-2002; 2002US-0362699P.

XX PA (ELIT-) ELITRA PHARM INC.

XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX DR WPI; 2003-029926/02.

XX DR N-PSDB; ACA28677.

XX PT New antisense nucleic acids, useful for identifying proteins or screening

XX PT for homologous nucleic acids required for cellular proliferation to

XX PT isolate candidate molecules for rational drug discovery programs.

XX PS Claim 25; SEQ ID NO 52731; 1766pp; English.

XX CC The invention relates to an isolated nucleic acid comprising any one of

XX CC the 6213 antisense sequences given in the specification where expression

XX CC of the nucleic acid inhibits proliferation of a cell. Also included are:

XX CC (1) a vector comprising a promoter operably linked to the nucleic acid

XX CC encoding a polypeptide whose expression is inhibited by the antisense

XX CC nucleic acid; (2) a host cell containing the vector; (3) an isolated

XX CC polypeptide or its fragment whose expression is inhibited by the

XX CC antisense nucleic acid; (4) an antibody capable of specifically binding

XX CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

XX CC proliferation or the activity of a gene in an operon required for

XX CC proliferation; (7) identifying a compound that influences the activity of

XX CC the gene product or that has an activity against a biological pathway

XX CC required for proliferation, or that inhibits cellular proliferation; (8)

XX CC identifying a gene required for cellular proliferation or the biological

XX CC pathway in which a proliferation-required gene or its gene product lies

XX CC or a gene on which the test compound that inhibits proliferation of an

XX CC organism acts; (9) manufacturing an antibiotic; (10) profiling a

XX CC compound's activity; (11) a culture comprising strains in which the gene

XX CC product is overexpressed or underexpressed; (12) determining the extent

XX CC to which each of the strains is present in a culture or collection of

XX CC strains; or (13) identifying the target of a compound that inhibits the

XX CC proliferation of an organism. The antisense nucleic acids are useful for

XX CC identifying proteins or screening for homologous nucleic acids required

XX CC for cellular proliferation to isolate candidate molecules for rational

XX CC drug discovery programs, or for screening homologous nucleic acids

CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

XX SQ Sequence 206 AA;

Query Match 100.0%; Score 29; DB 6; Length 206;

Best Local Similarity 100.0%; Pred. No. 1,3e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
|||
30 TYAMH 34

RESULT 8

ABO77482 ID ABO77482 standard; protein; 258 AA.

XX AC ABO77482;

XX DT 29-JUL-2004 (first entry)

XX DE Pseudomonas aeruginosa polypeptide #9657.

XX KM Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.

XX OS Pseudomonas aeruginosa.

XX PN US6551795-B1.

XX PD 22-APR-2003.

XX PF 18-FEB-1999; 99US-00252991.

XX PR 18-FEB-1998; 98US-0074788P.

XX PR 27-JUL-1998; 98US-0094190P.

XX PA (GENO-) GENOME THERAPEUTICS CORP.

XX PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;

XX PI WPI; 2003-615309/58.

XX DR N-PSDB; ABD11053.

XX PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,

XX PT useful as molecular targets for diagnostics, prophylaxis and treatment of

XX PT pathological conditions resulting from bacterial infection.

XX PS Disclosure; SEQ ID NO 26228; 455pp; English.

XX CC The invention relates to Pseudomonas aeruginosa polypeptides and the

XX CC polynucleotides encoding them. The sequences are useful in diagnosis and

XX CC therapy of pathological conditions, as molecular targets for diagnostics,

XX CC prophylaxis and treatment of pathological conditions resulting from a

XX CC bacterial infection, for evaluating a compound, such as a polypeptide,

XX CC for the ability to bind a P. aeruginosa nucleic acid, as components of

XX CC effective antibacterial targets, as targets for antibacterial drugs,

XX CC including anti-P. aeruginosa drugs, as templates for recombinant

XX CC production of P. aeruginosa-derived peptides or polypeptides, as target

XX CC components for diagnosis and/or treatment of P. aeruginosa-caused

XX CC infection, and in detection of P. aeruginosa sequences or other sequences

XX CC of Pseudomonas species using bioclip technology. Sequences ABO67826-

XX CC ABO84336 represent P. aeruginosa polypeptides of the invention. Note: The

XX CC sequence data for this patent did not form part of the printed

XX CC specification but was obtained in electronic format from USPTO at

XX CC segdata.uspto.gov/sequence.html

XX SQ Sequence 258 AA;

Query Match 100.0%; Score 29; DB 7; Length 258;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
 |||||
 DB 201 TYAMH 205

RESULT 9

ADN27332
 ID ADN27332 standard; protein; 278 AA.

AC ADN27332;
 XX

DT 02-DEC-2004 (first entry)
 XX

DE Bacterial polypeptide #985.
 XX

Recombinant DNA construct; transformed plant; improved plant property;
 cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 pathogen tolerance; pest tolerance; plant disease resistance;
 cell cycle pathway modification; plant growth regulator;
 homologous recombination; seed oil yield; protein yield; carbohydrate;
 nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 bacterial polypeptide.

OS Bacteria.
 XX

PN US200323675-A1.
 XX

PD 18-DEC-2003.
 XX

PP 20-FEB-2003; 2003US-00369493.
 XX

PR 21-FEB-2002; 2002US-0360039P.
 XX

PA (CAOY/) CAO Y.
 XX

PA (HINK/) HINKLE G J.
 XX

PA (SLAT/) SLATER S C.
 XX

PA (CHEN/) CHEN X.
 XX

PA (GOLD/) GOLDMAN B S.
 XX

PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
 XX

DR WPI; 2004-061375/06.
 XX

PT New recombinant DNA construct comprising a promoter positioned to provide
 XX for expression of a polynucleotide encoding a polypeptide from a
 XX microbial source, useful for producing plants with improved properties.
 XX

PS Claim 1; SEQ ID NO 9985; 122pp; English.
 XX

The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in a plant cell, where the promoter is positioned to
 CC provide for expression of a polynucleotide encoding a polypeptide from a
 CC microbial source. The invention also relates to a transformed plant
 CC comprising the recombinant DNA construct and a method of producing a
 CC transformed plant having an improved property. The plant is a crop plant
 CC such as maize or soybean. The method of producing a transformed plant
 CC having an improved property comprises transforming a plant with the
 CC recombinant DNA construct and growing the transformed plant, where the
 CC polynucleotide or polypeptide is useful for improving plant properties.
 CC The recombinant DNA construct is useful for producing plants with
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition, improved lignin production or improved galactomannan

CC production. This sequence represents a bacterial polypeptide used in the
 CC scope of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.

QY Sequence 278 AA;
 |||||

Query Match 100.0%; Score 29; DB 8; Length 278;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
 |||||
 DB 220 TYAMH 224

RESULT 10

AAG72483
 ID AAG72483 standard; protein; 307 AA.

AC AAG72483;
 XX

DT 31-JUL-2001 (first entry)
 XX

DE Human OR-like polypeptide query sequence, SEQ ID NO: 2164.
 XX

Human; olfactory receptor; OR; primary scent determination;
 secondary scent determination; polypeptide library; odour receptor;
 scent profile; scent fingerprint; scent representation.

OS Homo sapiens.
 XX

PN WO200127158-A2.
 XX

PD 19-APR-2001.
 XX

PP 06-OCT-2000; 2000WO-US027582.
 XX

PR 08-OCT-1999; 99US-0158615P.
 XX

PR 24-FEB-2000; 2000US-0184809P.
 XX

PA (DIGI-) DIGISCENTS.
 XX

PA (YEDA) YEDA RES & DEV CO LTD.
 XX

PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
 XX

DR WPI; 2001-290713/30.
 XX

PT New polynucleotides which encode polypeptides involved in olfactory
 XX sensation for identifying olfactory agonists and antagonists.
 XX

PS Example 6; Page 1455-1456; 1857pp; English.
 XX

The present sequence is a polypeptide encoded by one of 344 newly mined
 CC human genes. It was used as a query sequence in a database search of
 CC olfactory receptor (OR)-like sequences. The invention relates to isolated
 CC polynucleotides encoding polypeptides involved in olfactory sensation.
 CC The polynucleotides can be used in screening for olfactory agonists and
 CC antagonists. The methods allow for the determination of primary scents
 CC and the identification of the odour receptors used to detect these
 CC primary scents. The methods also enable determination of secondary scents
 CC and the identification of combinations of odour receptors that are
 CC involved in detecting such secondary scents. This enables the
 CC construction of a scent representation (also called a scent fingerprint
 CC or scent profile), which may be used to re-create and edit scents.
 CC Libraries of olfactory receptors are useful for determining the
 CC interaction pattern of a composition with the receptors, and can be used
 CC for determining differences in the olfactory faculties of different
 CC individuals
 XX
 SQ Sequence 307 AA;
 Query Match 100.0%; Score 29; DB 4; Length 307;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
DB 154 TYAMH 158

RESULT 11
AAG71475
ID AAG71475 standard; protein; 321 AA.

AC AAG71475;

DT 31-JUL-2001 (first entry)

DE Human olfactory receptor polypeptide, SEQ ID NO: 1156.

KM Human; olfactory receptor; OR; primary scent determination;
KW secondary scent determination; polypeptide library; odour receptor;
XX scent profile; scent fingerprint; scent representation.

OS Homo sapiens.

PN WO200127158-A2.

PD 19-APR-2001.

PF 06-OCT-2000; 2000WO-US027582.

PR 08-OCT-1999; 99US-0158615P.

PS 24-FEB-2000; 2000US-0184809P.

PA (DIGI-) DIGISCENTS.

PA (YEDA) YEDA RES & DEV CO LTD.

PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;

DR WPI; 2001-290713/30.

PT New polynucleotides which encode polypeptides involved in olfactory
PS sensation for identifying olfactory agonists and antagonists.

PS Claim 11; Page 674-675; 1857pp; English.

XX The present sequence is an olfactory receptor which is encoded by one of
CC a number of novel polynucleotides. The polynucleotides can be used in
CC screening for olfactory agonists and antagonists. The methods allow for
CC the determination of primary scents and the identification of the odour
CC receptors used to detect these primary scents. The methods also enable
CC determination of secondary scents and the identification of combinations
CC of odour receptors that are involved in detecting such secondary scents.
CC This enables the construction of a scent representation (also called a
CC scent fingerprint or scent profile), which may be used to re-create and
CC edit scents. Libraries of olfactory receptors are useful for determining
CC the interaction pattern of a composition with the receptors, and can be
CC used for determining differences in the olfactory faculties of different
XX individuals

XX Sequence 321 AA;

Query Match 100.0%; Score 29; DB 4; Length 321;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
DB 169 TYAMH 173

RESULT 12
ADRI0293
ID ADRI0293 standard; protein; 531 AA.

XX ADRI0293;
AC
XX
XX
DT 04-NOV-2004 (first entry)

DE Human protein useful for treating neurological disease Seq 3799.

KM human; oligo-capping method; diagnostic marker; gene therapy;
KW osteoporosis; neurological disease; Alzheimer's disease;
KW Parkinson's disease; dementia; short memory; cancer;
KW sense or motor function; emotional reaction; fear response; panic;
KW osteopathic; neuroprotective; nootropic; antiparkinsonian; cyostatic;
KW tranquilliser.

OS Homo sapiens.

PN EP1447413-A2.

PD 18-AUG-2004.

PF 12-FEB-2004; 2004EP-00003145.

PR 14-FEB-2003; 2003JP-00102207.

PS 09-MAY-2003; 2003JP-00131452.

PA (REAS-) RES ASSOC BIOTECHNOLOGY.

PI Isogai T, Yamamoto J, Nishikawa T, Isono Y, Sugiyama T, Otsuki T;

PI Wakamatsu A, Ishii S, Nagai K, Irie R;

DR WPI; 2004-583265/57.

PS N-PSDB; ADR08337.

PT New 1995 cDNA, useful for treating osteoporosis, neurological diseases,
XX Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.

PS Claim 1; SEQ ID NO 3799; 2686pp; English.

XX This invention relates to novel, isolated full length human cDNA
CC molecules and the encoded proteins thereof. Specifically, it refers to
CC cDNA clones obtained by an oligo-capping method, where none of these
CC clones are identical to any known human mRNAs. The present invention
CC describes an immunosay to identify agonists and antagonists, as well as
CC antibodies, antisense molecules and siRNAs that can all be used to bind
CC to and modulate expression of the cDNA molecules. As such, these
CC molecules are useful for diagnostic markers or therapeutic targets for
CC the various diseases or morbid states. In particular, they are useful in
CC gene therapy for treating osteoporosis, neurological disease, Alzheimer's
CC disease, Parkinson's disease, dementia, short memory and various cancers,
CC as well as for maintaining equilibrium of sense or motor function, and
CC for treating emotional reaction, fear response and panic. Accordingly,
CC they exhibit osteoprotective, neuroprotective, nootropic, antiparkinsonian,
CC cyostatic and tranquilliser activities. This polypeptide is a protein
CC encoded by a full length human cDNA sequence of the invention. NOTE: This
CC sequence is not given in the sequence listing of the specification but
CC can be obtained on CD-ROM from the European Patent Office, Vienna Sub-
XX office.

XX Sequence 531 AA;

Query Match 100.0%; Score 29; DB 8; Length 531;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
DB 50 TYAMH 54

RESULT 13
AA50844
ID AA50844 standard; protein; 690 AA.

```

AC  AA50844;
XX
XX  24-FEB-2000 (first entry)
XX
XX  A. oryzae glutaminase protein #2.
XX
XX  Glutaminase; decomposition; glutamine; glutamic acid; ammonia;
XX  taste enhancer; seasoning; sauce; paste.
XX
XX  Aspergillus oryzae.
XX
XX  Key      Location/Qualifiers
XX  Peptide  1..20
XX  Protein  /label= signal_peptide
XX              21..690
XX
XX  MO9960104-A1.
XX
XX  25-NOV-1999.
XX
XX  12-MAY-1999; 99WO-JP002455.
XX
XX  15-MAY-1998; 98JP-00134080.
XX  11-SEP-1998; 98JP-00258974.
XX  14-OCT-1998; 98JP-00292443.
XX  30-MAR-1999; 99JP-00089157.
XX
XX  (AJIN ) AJINOMOTO CO INC.
XX
XX  Koibuchi K, Nagasaki H, Yuasa A, Kataoka J, Kitamoto K;
XX
XX  WPI; 2000-053292/04.
XX  N-PSDB; AAZ43684.
XX
XX  Aspergillus oryzae-originated glutaminase and partial amino-acid
XX  sequences for enhancing taste particularly in glutamic acid-converting
XX  food processing to make e.g. seasoning sauces and pastes.
XX
XX  Example 3; Page 52-55; 74pp; Japanese.
XX
XX  This invention describes a novel glutaminase enzyme isolated from
XX  Aspergillus oryzae which catalyses the decomposition of glutamine to
XX  glutamic acid and ammonia. The purified glutaminase and determined
XX  partial amino-acid sequence can be used for enhancing taste particularly
XX  in glutamic acid-converting food processing to give e.g. seasoning sauces
XX  and pastes as well as other seasoning materials. The gene thus obtained
XX  can be applied as probe for hybridization providing the gene-containing
XX  DNA fragments from genome and cDNA libraries of A. oryzae and A.
XX  nidulans, and subsequently modified glutamine-producing breed. The
XX  novel strain of A. oryzae is a highly active because of its somatic
XX  secreting ability. This sequence represents the A. oryzae glutaminase
XX  enzyme described in the method of the invention
XX
XX  Sequence 690 AA;
XX
XX  Query Match      100.0%; Score 29; DB 3; Length 690;
XX  Best Local Similarity 100.0%; Pred. No. 4.5e+02;
XX  Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  1 TYAMH 5
XX  |||||
XX  423 TYAMH 427
XX
XX  RESULT 14
XX  ID AA50835 standard; protein; 690 AA.
XX  AC AA50835;
XX  DT 24-FEB-2000 (first entry)
XX  DE A. oryzae glutaminase protein #1.
XX

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XX  Glutaminase; decomposition; glutamine; glutamic acid; ammonia;
XX  taste enhancer; seasoning; sauce; paste.
XX
XX  Aspergillus oryzae.
XX
XX  Key      Location/Qualifiers
XX  Peptide  1..20
XX  Protein  /label= signal_peptide
XX              21..690
XX
XX  MO9960104-A1.
XX
XX  25-NOV-1999.
XX
XX  12-MAY-1999; 99WO-JP002455.
XX
XX  15-MAY-1998; 98JP-00134080.
XX  11-SEP-1998; 98JP-00258974.
XX  14-OCT-1998; 98JP-00292443.
XX  30-MAR-1999; 99JP-00089157.
XX
XX  (AJIN ) AJINOMOTO CO INC.
XX
XX  Koibuchi K, Nagasaki H, Yuasa A, Kataoka J, Kitamoto K;
XX
XX  WPI; 2000-053292/04.
XX  N-PSDB; AAZ43677.
XX
XX  Aspergillus oryzae-originated glutaminase and partial amino-acid
XX  sequences for enhancing taste particularly in glutamic acid-converting
XX  food processing to make e.g. seasoning sauces and pastes.
XX
XX  Claim 1a; Page 41-44; 74pp; Japanese.
XX
XX  This invention describes a novel glutaminase enzyme isolated from
XX  Aspergillus oryzae which catalyses the decomposition of glutamine to
XX  glutamic acid and ammonia. The purified glutaminase and determined
XX  partial amino-acid sequence can be used for enhancing taste particularly
XX  in glutamic acid-converting food processing to give e.g. seasoning sauces
XX  and pastes as well as other seasoning materials. The gene thus obtained
XX  can be applied as probe for hybridization providing the gene-containing
XX  DNA fragments from genome and cDNA libraries of A. oryzae and A.
XX  nidulans, and subsequently modified glutamine-producing breed. The
XX  novel strain of A. oryzae is a highly active because of its somatic
XX  secreting ability. This sequence represents the A. oryzae glutaminase
XX  enzyme described in the method of the invention
XX
XX  Sequence 690 AA;
XX
XX  Query Match      100.0%; Score 29; DB 3; Length 690;
XX  Best Local Similarity 100.0%; Pred. No. 4.5e+02;
XX  Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  1 TYAMH 5
XX  |||||
XX  423 TYAMH 427
XX
XX  RESULT 15
XX  ID AAB14781 standard; protein; 703 AA.
XX  AC AAB14781;
XX  DT 06-DEC-2000 (first entry)
XX  DE Aspergillus oryzae KBN616 glutaminase.
XX  XX  Aspergillus oryzae KBN616 glutaminase.
XX  XX  Glutaminase; Aspergillus oryzae KBN616; glutamic acid synthesis;
XX  XX  fermentation; foodstuff production; miso; soy sauce.
XX  OS Aspergillus oryzae.
XX

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XX FH Key Location/Qualifiers
FT Protein 34..703
XX /note="Mature glutaminase; specifically claimed"
XX JP200016547-A.
XX PD 20-JUN-2000.
XX XX
XX PF 07-DEC-1998; 98JP-00347127.
XX PR 07-DEC-1998; 98JP-00347127.
XX PA (AICH-) AICHI KEN PREFECTURE.
XX (ICHI-) ICHIBIKI KK.
XX WP1; 2000-477931/42.
XX DR N-PSDB; AAA72204.
XX PT A new glutaminase and its preparation.
XX PS Claim 2; Page 15-17; 27pp; Japanese.
XX CC This sequence represents a novel glutaminase from Aspergillus oryzae
CC KBN616. The invention relates to two novel glutaminases (AAB14781,
CC AAB14782) from Aspergillus oryzae KBN616 and Aspergillus sojae BA-104
CC respectively which have molecular weights of approximately 73 kD (as
CC determined by gel filtration). The enzymes have an optimum temperature of
CC approximately 50 degrees Celsius, and an optimum pH of about 8.5. The
CC glutaminases catalyse the conversion of L-glutamine to L-glutamic acid,
CC and may be used in the production of fermented foodstuffs such as soy
CC sauce and miso
XX SQ Sequence 703 AA;

Query Match 100.0%; Score 29; DB 3; Length 703;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TYAMH 5
DB 436 TYAMH 440

RESULT 16
AAB14782
ID AAB14782 standard; protein; 703 AA.
XX AC AAB14782;
XX DT 06-DEC-2000 (first entry)
XX DE Aspergillus sojae BA-104 glutaminase.
XX KW Glutaminase; Aspergillus sojae BA-104; glutamic acid synthesis;
XX fermentation; foodstuff production; miso; soy sauce.
XX OS Aspergillus sojae.
XX FT Key Location/Qualifiers
FT Protein 34..703
XX /note="Mature glutaminase; specifically claimed"
XX JP200016547-A.
XX PD 20-JUN-2000.
XX XX
XX PF 07-DEC-1998; 98JP-00347127.
XX PR 07-DEC-1998; 98JP-00347127.
XX PA (AICH-) AICHI KEN PREFECTURE.
XX (ICHI-) ICHIBIKI KK.
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XX DR WP1; 2000-477931/42.
XX DR N-PSDB; AAA72205.
XX PT A new glutaminase and its preparation.
XX PS Claim 6; Page 21-23; 27pp; Japanese.
XX CC This sequence represents a novel glutaminase from Aspergillus sojae BA-
CC 104. The invention relates to two novel glutaminases (AAB14781, AAB14782)
CC from Aspergillus oryzae KBN616 and Aspergillus sojae BA-104 respectively
CC which have molecular weights of approximately 73 kD (as determined by gel
CC filtration). The enzymes have an optimum temperature of approximately 50
CC degrees Celsius, and an optimum pH of about 8.5. The glutaminases
CC catalyse the conversion of L-glutamine to L-glutamic acid, and may be
CC used in the production of fermented foodstuffs such as soy sauce and miso
XX SQ Sequence 703 AA;

Query Match 100.0%; Score 29; DB 3; Length 703;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TYAMH 5
DB 436 TYAMH 440

RESULT 17
AAM82576
ID AAM82576 standard; protein; 46 AA.
XX AC AAM82576;
XX DT 07-NOV-2001 (first entry)
XX DE Human immune/haematopoietic antigen SEQ ID NO:10169.
XX KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX cyostatic; gene therapy; vaccine; metastasis.
XX OS Homo sapiens.
XX FN WO200157182-A2.
XX PD 09-AUG-2001.
XX PF 17-JAN-2001; 2001WO-US001354.
XX XX
XX PR 31-JAN-2000; 2000US-0179065P.
XX PR 04-FEB-2000; 2000US-0180628P.
XX PR 24-FEB-2000; 2000US-0184664P.
XX PR 02-MAR-2000; 2000US-0186350P.
XX PR 16-MAR-2000; 2000US-0189874P.
XX PR 17-MAR-2000; 2000US-0190076P.
XX PR 18-APR-2000; 2000US-0198123P.
XX PR 19-MAY-2000; 2000US-0205515P.
XX PR 07-JUN-2000; 2000US-0209467P.
XX PR 30-JUN-2000; 2000US-0214886P.
XX PR 07-JUL-2000; 2000US-0215135P.
XX PR 11-JUL-2000; 2000US-0216647P.
XX PR 11-JUL-2000; 2000US-0216880P.
XX PR 11-JUL-2000; 2000US-0217487P.
XX PR 14-JUL-2000; 2000US-0218290P.
XX PR 26-JUL-2000; 2000US-0220963P.
XX PR 26-JUL-2000; 2000US-0220964P.
XX PR 14-AUG-2000; 2000US-0224518P.
XX PR 14-AUG-2000; 2000US-0224519P.
XX PR 14-AUG-2000; 2000US-0225213P.
XX PR 14-AUG-2000; 2000US-0225214P.
XX PR 14-AUG-2000; 2000US-0225266P.
XX PR 14-AUG-2000; 2000US-0225267P.
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PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226881P.
PR 22-AUG-2000; 2000US-0226886P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0228287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0233397P.
PR 14-SEP-2000; 2000US-0233398P.
PR 14-SEP-2000; 2000US-0233398P.
PR 14-SEP-2000; 2000US-0233400P.
PR 14-SEP-2000; 2000US-0233400P.
PR 14-SEP-2000; 2000US-0233401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235835P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239335P.
PR 13-OCT-2000; 2000US-0239337P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241825P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.

PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249246P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251858P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.

(HUMA-) HUMAN GENOME SCT INC.
PA Rosen CA, Barash SC, Ruben SM;
XX MPI: 2001-483426/52.
XX N-PSDB; AAK53537.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and metastasis.
XX
XX Claim 11; SEQ ID NO 10169; 3071pp + Sequence Listing; English.
PS
CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytosolic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention
XX
XX Sequence 46 AA;
SQ
Query Match 89.7%; Score 26; DB 4; Length 46;

Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TYAMH 5
|||:
35 TYALH 39

RESULT 18

ABBA0299
ID ABB40299 standard; peptide; 67 AA.

AC ABB40299;

DT 04-FEB-2002 (first entry)

DE Peptide #7805 encoded by human foetal liver single exon probe.

KW Human; foetal liver; gene expression; single exon nucleic acid probe.

OS Homo sapiens.

PN WO200157277-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US000669.

PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

PA (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

DR WPI; 2001-483447/52.

XX Human genome-derived single exon nucleic acid probes useful for analyzing

PT gene expression in human foetal liver.

PS Claim 27; SEQ ID NO 32934; 639pp + Sequence Listing; English.

XX The invention relates to a single exon nucleic acid probe for measuring

CC human gene expression in a sample derived from human foetal liver. The

CC single exon nucleic acid probes may be used for predicting, measuring and

CC displaying gene expression in samples derived from human foetal liver. The

CC present sequence is a peptide encoded by a single exon nucleic acid probe

CC of the invention. Note: The sequence data for this patent did not form

CC part of the printed specification, but was obtained in electronic format

CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 67 AA;

Query Match 89.7%; Score 26; DB 4; Length 67;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TYAMH 5
|||:
48 TYALH 52

Db 48 TYALH 52

DT 17-OCT-2001 (first entry)

DE Peptide #8022 encoded by probe for measuring placental gene expression.

KW Probe; microarray; human; placenta; antenatal diagnosis;

KW genetic disorder.

OS Homo sapiens.

PN WO200157272-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US000663.

PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

PA (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

DR WPI; 2001-488897/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing

PT gene expression in human placenta.

PS Claim 27; SEQ ID NO 34254; 654pp; English.

XX The present invention relates to single exon nucleic acid probes (SENP:

CC see A13315-A157546). The present sequence is a peptide encoded by one

CC such probe. The probes are useful for producing a microarray for

CC predicting, measuring and displaying gene expression in samples derived

CC from human placenta. The probes are useful for antenatal diagnosis of

CC human genetic disorders

XX SQ Sequence 67 AA;

Query Match 89.7%; Score 26; DB 4; Length 67;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TYAMH 5
|||:
48 TYALH 52

Db 48 TYALH 52

RESULT 20
ID AAM73798 standard; protein; 67 AA.

AC AAM73798;

DT 06-NOV-2001 (first entry)

DE Human bone marrow expressed probe encoded protein SEQ ID NO: 34104.

KW Human; bone marrow expressed exon; gene expression analysis; probe;

KW microarray; cancer; leukaemia; lymphoma; myeloma.

OS Homo sapiens.

PN WO200157276-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US000668.

PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

PA (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

DR WPI; 2001-488897/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing

PT gene expression in human placenta.

PS Claim 27; SEQ ID NO 34254; 654pp; English.

XX The present invention relates to single exon nucleic acid probes (SENP:

CC see A13315-A157546). The present sequence is a peptide encoded by one

CC such probe. The probes are useful for producing a microarray for

CC predicting, measuring and displaying gene expression in samples derived

CC from human placenta. The probes are useful for antenatal diagnosis of

CC human genetic disorders

XX SQ Sequence 67 AA;

Query Match 89.7%; Score 26; DB 4; Length 67;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TYAMH 5
|||:
48 TYALH 52

Db 48 TYALH 52

RESULT 20
ID AAM73798 standard; protein; 67 AA.

AC AAM73798;

DT 06-NOV-2001 (first entry)

DE Human bone marrow expressed probe encoded protein SEQ ID NO: 34104.

KW Human; bone marrow expressed exon; gene expression analysis; probe;

KW microarray; cancer; leukaemia; lymphoma; myeloma.

OS Homo sapiens.

PN WO200157276-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US000668.

PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

PA (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

DR WPI; 2001-488897/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing

PT gene expression in human placenta.

PS Claim 27; SEQ ID NO 34254; 654pp; English.

XX The present invention relates to single exon nucleic acid probes (SENP:

CC see A13315-A157546). The present sequence is a peptide encoded by one

CC such probe. The probes are useful for producing a microarray for

CC predicting, measuring and displaying gene expression in samples derived

CC from human placenta. The probes are useful for antenatal diagnosis of

CC human genetic disorders

XX SQ Sequence 67 AA;

Query Match 89.7%; Score 26; DB 4; Length 67;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TYAMH 5
|||:
48 TYALH 52

Db 48 TYALH 52

RESULT 20
ID AAM73798 standard; protein; 67 AA.

AC AAM73798;

DT 06-NOV-2001 (first entry)

DE Human bone marrow expressed probe encoded protein SEQ ID NO: 34104.

KW Human; bone marrow expressed exon; gene expression analysis; probe;

KW microarray; cancer; leukaemia; lymphoma; myeloma.

OS Homo sapiens.

PN WO200157276-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US000668.

PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

PA (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

DR WPI; 2001-488897/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing

PT gene expression in human placenta.

PS Claim 27; SEQ ID NO 34254; 654pp; English.

XX The present invention relates to single exon nucleic acid probes (SENP:

CC see A13315-A157546). The present sequence is a peptide encoded by one

CC such probe. The probes are useful for producing a microarray for

CC predicting, measuring and displaying gene expression in samples derived

CC from human placenta. The probes are useful for antenatal diagnosis of

CC human genetic disorders

XX SQ Sequence 67 AA;

Query Match 89.7%; Score 26; DB 4; Length 67;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TYAMH 5
|||:
48 TYALH 52

Db 48 TYALH 52

RESULT 20
ID AAM73798 standard; protein; 67 AA.

AC AAM73798;

DT 06-NOV-2001 (first entry)

DE Human bone marrow expressed probe encoded protein SEQ ID NO: 34104.

KW Human; bone marrow expressed exon; gene expression analysis; probe;

KW microarray; cancer; leukaemia; lymphoma; myeloma.

OS Homo sapiens.

PN WO200157276-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US000668.

PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

PA (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

DR WPI; 2001-488897/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing

PT gene expression in human placenta.

PS Claim 27; SEQ ID NO 34254; 654pp; English.

XX The present invention relates to single exon nucleic acid probes (SENP:

CC see A13315-A157546). The present sequence is a peptide encoded by one

CC such probe. The probes are useful for producing a microarray for

CC predicting, measuring and displaying gene expression in samples derived

CC from human placenta. The probes are useful for antenatal diagnosis of

CC human genetic disorders

XX SQ Sequence 67 AA;

Query Match 89.7%; Score 26; DB 4; Length 67;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TYAMH 5
|||:
48 TYALH 52

Db 48 TYALH 52

RESULT 20
ID AAM73798 standard; protein; 67 AA.

AC AAM73798;

DT 06-NOV-2001 (first entry)

DE Human bone marrow expressed probe encoded protein SEQ ID NO: 34104.

KW Human; bone marrow expressed exon; gene expression analysis; probe;

KW microarray; cancer; leukaemia; lymphoma; myeloma.

OS Homo sapiens.

PN WO200157276-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US000668.

PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

PA (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

DR WPI; 2001-488897/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing

PT gene expression in human placenta.

PS Claim 27; SEQ ID NO 34254; 654pp; English.

XX The present invention relates to single exon nucleic acid probes (SENP:

CC see A13315-A157546). The present sequence is a peptide encoded by one

CC such probe. The probes are useful for producing a microarray for

CC predicting, measuring and displaying gene expression in samples derived

CC from human placenta. The probes are useful for antenatal diagnosis of

CC human genetic disorders

XX SQ Sequence 67 AA;

Query Match 89.7%; Score 26; DB 4; Length 67;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TYAMH 5
|||:
48 TYALH 52

Db 48 TYALH 52

RESULT 20
ID AAM73798 standard; protein; 67 AA.

AC AAM73798;

DT 06-NOV-2001 (first entry)

DE Human bone marrow expressed probe encoded protein SEQ ID NO: 34104.

KW Human; bone marrow expressed exon; gene expression analysis; probe;

KW microarray; cancer; leukaemia; lymphoma; myeloma.

OS Homo sapiens.

PN WO200157276-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US000668.

PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US

PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488900/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human bone marrow.
XX
XX Example 4; SEQ ID NO 34104; 658bp + Sequence Listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX bone marrow. They can be used to measure gene expression in bone marrow
XX samples, which may enable the improved diagnosis and treatment of cancers
XX such as lymphoma, leukemia and myeloma. The present sequence is a
XX protein encoded by one of the probes of the invention
XX
XX Sequence 67 AA;
XX

Query Match 89.7%; Score 26; DB 4; Length 67;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 TYAMH 5
Db 48 TYALH 52

RESULT 21
AAM61093
ID AAM61093 standard; protein; 67 AA.
XX
XX AAM61093;
XX
XX 05-NOV-2001 (first entry)
XX
XX Human brain expressed single exon probe encoded protein SEQ ID NO: 33198.
XX
XX Human; brain expressed exon; gene expression analysis; probe; microarray;
XX Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
XX
XX Homo sapiens.
XX
XX WO200157275-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000667.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483446/52.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human

PT brains.
XX
XX Example 4; SEQ ID NO 33198; 650bp + Sequence Listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX brain. They can be used to measure gene expression in brain cell samples,
XX which may enable the diagnosis and improved treatment of nervous system
XX diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX epilepsy and cancer. The present sequence is a protein encoded by one of
XX the probes of the invention
XX
XX Sequence 67 AA;
XX

Query Match 89.7%; Score 26; DB 4; Length 67;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 TYAMH 5
Db 48 TYALH 52

RESULT 22
ABG55546
ID ABG55546 standard; peptide; 67 AA.
XX
XX ABG55546;
XX
XX 25-FEB-2003 (first entry)
XX
XX Human liver peptide, SEQ ID No 34194.
XX
XX Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
XX hypercholesterolaemia; coronary heart disease.
XX
XX Homo sapiens.
XX
XX WO200157273-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000664.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488898/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human adult liver.
XX
XX Claim 27; SEQ ID NO 34194; 658bp; English.
XX
XX The invention relates to a single exon nucleic acid probe (SENP) (1) for
XX measuring human gene expression in a sample derived from human adult
XX liver, comprising one of 13109 defined nucleotide sequences given in the
XX specification (or complements/fragments). The probe hybridises at high
XX stringency to a nucleic acid molecule expressed in the human adult liver.
XX (1) may be used for predicting, measuring and displaying gene expression
XX in samples derived from human adult liver. The genes identified may be
XX involved in genetic liver diseases such as cirrhosis,
XX hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
XX associated with coronary heart disease. ABG47348-ABG59930 represent human

CC liver single exon encoded peptides of the invention. Note: The sequence
 CC information for this patent does not appear in the printed specification
 CC but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

SO Sequence 67 AA;

Query Match 89.7%; Score 26; DB 4; Length 67;
 Best Local Similarity 80.0%; Pred. No. 1.9e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Gy 1 TYAMH 5
 Db 48 TYALH 52

RESULT 23
 ABG43685
 ID ABG43685 standard; peptide; 67 AA.

AC ABG43685;

DT 19-AUG-2002 (first entry)

DE Human peptide encoded by genome-derived single exon probe SEQ ID 33350.

XX Human; single exon probe; asthma; lung cancer; COPD; ILD;
 KW chronic obstructive pulmonary disease; interstitial lung disease;
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
 KW tuberosus sclerosis; Gaucher's disease; Niemann-Pick disease;
 KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
 KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
 KW primary ciliary dyskinesia; pulmonary hypertension;
 KW hyaline membrane disease.

XX Homo sapiens.

XX WO200186003-A2.

XX 15-NOV-2001.

XX 30-JAN-2001; 2001WO-US000665.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2002-114183/15.

XX Claim 27; SEQ ID NO 33350; 634p; English.

XX The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human lung comprising single exon nucleic acid probes having one of
 CC 12614 nucleic acid sequences mentioned in the specification, or their
 CC complements or the 12387 open reading frames derived from the 12614
 CC probes. Also included are a microarray comprising the novel set of probes
 CC; the novel set of probes which hybridise at high stringency to a nucleic
 CC acid expressed in the human lung; measuring gene expression in a sample
 CC derived from human lung; comprising (a) contacting the array with a
 CC collection of detectably labeled nucleic acids derived from human lung

CC mRNA, and (b) measuring the label detectably bound to each probe of the
 CC array; identifying exons in a eukaryotic genome, comprising (a)
 CC algorithmically predicting at least one exon from genomic sequences of
 CC the eukaryote; and (b) detecting specific hybridisation of detectably
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
 CC having a fragment identical to the predicted exon, the probe is included
 CC in the above mentioned microarray; assigning exons to a single gene,
 CC comprising (a) identifying exons from genomic sequence by the method
 CC above and (b) measuring the expression of each of the exons in several
 CC tissues and/or cell types using hybridisation to a single exon
 CC microarrays having a probe with the exon, where a common pattern of
 CC expression of the exons in the tissues and/or cell types indicates that
 CC the exons should be assigned to a single gene; a peptide comprising one
 CC of 12011 sequences, mentioned in the specification, or encoded by the
 CC probes/open reading frames (ORF). The probes are used for gene expression
 CC analysis, and for identifying exons in a gene, particularly using human
 CC lung derived mRNA and for the study of lung diseases such as asthma, lung
 CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
 CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
 CC tuberosus sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
 CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
 CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
 CC Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
 CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The
 CC present sequence is a peptide/protein encoded by a single exon probe of
 CC the invention. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

SO Sequence 67 AA;

Query Match 89.7%; Score 26; DB 5; Length 67;
 Best Local Similarity 80.0%; Pred. No. 1.9e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Gy 1 TYAMH 5
 Db 48 TYALH 52

RESULT 24
 AAU18208
 ID AAU18208 standard; protein; 79 AA.

XX AAU18208;

XX 21-NOV-2001 (first entry)

XX Novel human DNA-binding protein #55.

XX Human; DNA-binding protein; histone; chromo domain protein;
 KW chromatin organisation modifier; Y-box binding protein; DNA organisation;
 KW gene transcription; malignant disease; autoimmune disorder;
 KW rheumatic disease; genetic abnormality; infectious disease;
 KW neurological disorder; gene therapy; immunomodulatory; anti-HIV;
 KW anti rheumatic; anti microbial; cytostatic.

XX Homo sapiens.

XX WO200155162-A1.

XX 02-AUG-2001.

XX 17-JAN-2001; 2001WO-US001305.

XX 31-JAN-2000; 2000US-0179065P.

XX 04-FEB-2000; 2000US-0180628P.

XX 24-FEB-2000; 2000US-0184664P.

XX 02-MAR-2000; 2000US-0186350P.

XX 16-MAR-2000; 2000US-0189874P.

XX 17-MAR-2000; 2000US-0190076P.

XX 18-APR-2000; 2000US-0198123P.

XX 19-MAY-2000; 2000US-0205515P.

PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-022547P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-022681P.
PR 22-AUG-2000; 2000US-0226868P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0228287P.
PR 01-SEP-2000; 2000US-0228343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-023497P.
PR 25-SEP-2000; 2000US-023498P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 13-OCT-2000; 2000US-0239335P.
PR 13-OCT-2000; 2000US-0239337P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.

PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI, 2001-465557/50.

N-PSDB; AAS29084.

Nucleic acid molecules encoding human secreted chromosomal binding proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers.

Claim 11; SEQ ID NO 193; 561pp; English.

The present invention relates to the isolation of novel DNA-binding proteins, and cDNA (AAS29010-AAS29157) and genomic sequences encoding for these proteins. DNA-binding proteins such as histones, chromo (chromatin organisation modifier) domain proteins, and Y-box binding proteins may

Query Match	Best Local Similarity	Score 26;	DB 4;	Length 79;
Matches	4;	Conservative	1;	Mismatches 0;
			Indels	Gaps
Qy	1 TYAMH 5			
Db	74 TYALH 78			
RESULT 25				
ABG92629				
ID	ABG92629 standard; protein; 79 AA.			
AC	ABG92629;			
XX				
DT	18-NOV-2002 (first entry)			
XX				
DE	Human DNA-binding protein #55.			
XX				
KM	Human; DNA-binding protein; B cell immunodeficiency; autoimmune disorder;			
KM	severe combined immunodeficiency; rheumatoid arthritis; Crohn's disease;			
KM	diabetes mellitus; allergy; asthma; inflammatory condition; thrombosis;			
KM	graft-versus-host disease; blood-related disorder; atherosclerosis;			
KM	hyperproliferative disorder; cancer; renal disorder; arrhythmia;			
KM	acute glomerulonephritis; cardiovascular disorder; respiratory disorder;			
KM	Goodpasture's syndrome; neurological disorder; Alzheimer's disease;			
KM	Parkinson's disease; endocrine disorder; Addison's disease;			
KM	reproductive system disorder; endometriosis; infectious disease;			
KM	viral infection; bacterial infection; fungal infection; vaccine;			
KM	gastrointestinal disorder; multiple sclerosis; gene therapy.			
XX				
OS	Homo sapiens.			
XX				
PN	US2002102638-A1.			
XX				
PD	01-AUG-2002.			
XX				
PF	17-JAN-2001; 2001US-00764846.			
XX				
PR	31-JAN-2000; 2000US-0179065P.			
PR	04-FEB-2000; 2000US-0180628P.			
PR	28-JUN-2000; 2000US-0214886P.			
PR	07-JUL-2000; 2000US-0216647P.			
PR	07-JUL-2000; 2000US-0216880P.			
PR	11-JUL-2000; 2000US-0217487P.			
PR	11-JUL-2000; 2000US-0217496P.			
PR	14-JUL-2000; 2000US-0218290P.			
PR	26-JUL-2000; 2000US-0220963P.			
PR	26-JUL-2000; 2000US-0220964P.			
PR	14-AUG-2000; 2000US-0224518P.			
PR	14-AUG-2000; 2000US-0225267P.			
PR	14-AUG-2000; 2000US-0225268P.			
PR	14-AUG-2000; 2000US-0225270P.			
PR	14-AUG-2000; 2000US-0225447P.			
PR	14-AUG-2000; 2000US-0225457P.			
PR	14-AUG-2000; 2000US-0225751P.			

Query Match 89.7%; Score 26; DB 5; Length 79;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
|||:
Db 74 TYALH 78

RESULT 26

ADC25346
ID ADC25346 standard; protein; 79 AA.

XX AC ADC25346;

XX DT 18-DEC-2003 (first entry)

XX DE Human extracellular matrix protein from gene 55.

XX Extracellular matrix protein; cytosolic; antibacterial; virucide;
XX neuroprotective; gynaecological; gastrointestinal; cardiac;
XX cardiovascular; nephrotoxic; antiinflammatory; muscular; Gen;
XX respiratory; immunosuppressive; cerebroprotective; vasotropic;
XX neotrophic; antiallergic; cancer; bacterial infection; viral infection;
XX muscular disorder; immune system disorder; blood disorder;
XX pulmonary disorder; reproductive disorder; gastrointestinal disorder;
XX inflammatory disorder; cardiovascular disorder; renal disorder;
XX inflammatory disorder; proliferative disorder; human; gene therapy.

XX Homo sapiens.

XX US2003049650-A1.

XX PD 13-MAR-2003.

XX PF 07-MAR-2002; 2002US-00091483.

XX PR 31-JAN-2000; 2000US-0179065P.

XX PR 04-FEB-2000; 2000US-0180628P.

XX PR 24-FEB-2000; 2000US-0184664P.

XX PR 02-MAR-2000; 2000US-0186350P.

XX PR 16-MAR-2000; 2000US-0189874P.

XX PR 17-MAR-2000; 2000US-0190076P.

XX PR 18-APR-2000; 2000US-0198123P.

XX PR 19-MAY-2000; 2000US-0205515P.

XX PR 07-JUN-2000; 2000US-0209467P.

XX PR 28-JUN-2000; 2000US-0214886P.

XX PR 30-JUN-2000; 2000US-0215135P.

XX PR 07-JUL-2000; 2000US-0216647P.

XX PR 07-JUL-2000; 2000US-0216880P.

XX PR 11-JUL-2000; 2000US-0217487P.

XX PR 14-JUL-2000; 2000US-0218290P.

XX PR 26-JUL-2000; 2000US-0220963P.

XX PR 26-JUL-2000; 2000US-0224518P.

XX PR 14-AUG-2000; 2000US-0224519P.

XX PR 14-AUG-2000; 2000US-0225213P.

XX PR 14-AUG-2000; 2000US-0225214P.

XX PR 14-AUG-2000; 2000US-0225267P.

XX PR 14-AUG-2000; 2000US-0225267P.

XX PR 14-AUG-2000; 2000US-0225268P.

XX PR 14-AUG-2000; 2000US-0225270P.

XX PR 14-AUG-2000; 2000US-0225447P.

XX PR 14-AUG-2000; 2000US-0225757P.

XX PR 14-AUG-2000; 2000US-0225757P.

XX PR 14-AUG-2000; 2000US-0225759P.

XX PR 18-AUG-2000; 2000US-0226279P.

XX PR 22-AUG-2000; 2000US-0226681P.

XX PR 22-AUG-2000; 2000US-0227182P.

XX PR 23-AUG-2000; 2000US-0227009P.

XX PR 30-AUG-2000; 2000US-0228924P.

PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235835P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0240967P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241222P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.

PR 17-NOV-2000; 2000US-0249212P.
 PR 17-NOV-2000; 2000US-0249213P.
 PR 17-NOV-2000; 2000US-0249214P.
 PR 17-NOV-2000; 2000US-0249215P.
 PR 17-NOV-2000; 2000US-0249216P.
 PR 17-NOV-2000; 2000US-0249217P.
 PR 17-NOV-2000; 2000US-0249218P.
 PR 17-NOV-2000; 2000US-0249219P.
 PR 17-NOV-2000; 2000US-0249220P.
 PR 17-NOV-2000; 2000US-0249221P.
 PR 17-NOV-2000; 2000US-0249222P.
 PR 17-NOV-2000; 2000US-0249223P.
 PR 17-NOV-2000; 2000US-0249224P.
 PR 17-NOV-2000; 2000US-0249225P.
 PR 17-NOV-2000; 2000US-0249226P.
 PR 17-NOV-2000; 2000US-0249227P.
 PR 17-NOV-2000; 2000US-0249228P.
 PR 17-NOV-2000; 2000US-0249229P.
 PR 17-NOV-2000; 2000US-0249230P.
 PR 01-DEC-2000; 2000US-0250160P.
 PR 01-DEC-2000; 2000US-0250391P.
 PR 05-DEC-2000; 2000US-0251030P.
 PR 05-DEC-2000; 2000US-0251988P.
 PR 05-DEC-2000; 2000US-0256719P.
 PR 06-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 PR 08-DEC-2000; 2000US-0251989P.
 PR 08-DEC-2000; 2000US-0251990P.
 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.
 PR 17-JAN-2001; 2001US-00764846.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Rosen CA, Ruben SM, Barash SC;
 DR WPI; 2003-605749/57.
 DR N-PSDB; ADC25218.
 XX
 PT New DNA-binding proteins and gene encoding them, useful for diagnosing,
 PT treating and/or preventing e.g. neurological, inflammatory, infectious,
 PT cardiovascular, autoimmune, respiratory, neoplastic or digestive
 PT diseases.
 XX
 PS Claim 1; SEQ ID NO 193; 226pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule (cDNA)
 CC encoding a human extracellular matrix protein, representing one of 161
 CC novel genes. Also included are recombinant vectors, host cells
 CC (expressing the protein), the extracellular matrix proteins (including
 CC their fragments, epitopes and homologues), an isolated antibody that
 CC binds specifically to the protein, diagnosing a pathological condition or
 CC susceptibility to a pathological condition (comprising determining the
 CC presence or absence of a mutation in the nucleic acid and diagnosing a
 CC condition based on the presence or absence of the mutation), diagnosing a
 CC pathological condition or susceptibility to a pathological condition
 CC (comprising determining the presence or amount of expression of the
 CC protein in a biological sample and diagnosing a condition based on the
 CC presence or amount of expression of the protein), preventing, treating or
 CC ameliorating a medical condition by administering the nucleic acid or
 CC protein to a mammalian subject, identifying a binding partner to the
 CC protein, the gene corresponding to the cDNA sequence, and identifying an
 CC activity in a biological assay (comprising expressing the nucleic acid in
 CC a cell, isolating the supernatant, detecting an activity in a biological
 CC assay and identifying the protein in the supernatant having the
 CC activity). The nucleic acids and proteins display the following
 CC activities Cytostatic, antibacterial, Virucide, Neuroprotective,
 CC Gynaecological, Gastrointestinal-Gen, Cardiant, Cardiovascular-Gen,

Query Match 89.7%; Score 26; DB 7; Length 79;
 Best Local Similarity 80.0%; Pred. No. 2.3e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 TYAMH 5
 |||:
 Db 74 TYALH 78

RESULT 27
 ABG68752
 ID ABG68752 standard; protein; 89 AA.
 XX
 AC ABG68752;
 XX
 DT 07-OCT-2002 (first entry)
 XX
 DE Cytochrome P450 3A5 exon 11-13 altern. 2 with CYP3A43 exon 1.
 XX
 KM Cytochrome P450; CYP3A1; CYP3A2; CYP3A3; CYP3A4; CYP3A5; CYP3A7;
 KM drug metabolism; drug design; drug screening.
 XX
 OS Homo sapiens.
 XX
 PN WO200244213-A1.
 XX
 PD 06-JUN-2002.
 XX
 PF 28-NOV-2001; 2001WO-SE002631.
 XX
 PR 28-NOV-2000; 2000SE-00004366.
 PR 11-JUN-2001; 2001SE-00002061.
 XX
 PA (ZAPH/) ZAPHIROPOULOS P. G.
 PA (FINT/) FINTA C.
 XX
 PI Zaphiropoulos PG, Finta C;
 XX
 DR WPI; 2002-557532/59.
 DR N-PSDB; ABK97691.
 XX
 PT Novel cytochrome P450 protein in which CYP3A3 exon 1 is joined to sets
 PT of CYP3A4 or CYP3A5 exons, useful as medicament, and in evaluating drug
 PT metabolism, in drug design and drug screening.
 XX
 PS Claim 1; Page 96-97; 131pp; English.
 XX
 CC The invention describes a cytochrome P450 protein (I) in which CYP3A43
 CC exon 1 is joined to sets of CYP3A4 or CYP3A5 exons, as well as sub
 CC fragments, variants and multiples of (I) having essentially the same
 CC characteristics. (I) is useful as a medicament, and for evaluating drug
 CC metabolism, in drug design, and drug screening, and in tests for
 CC adjusting the dose of drugs. This is the amino acid sequence of a novel
 CC cytochrome P450 protein
 XX
 SO Sequence 89 AA;

Query Match 89.7%; Score 26; DB 5; Length 89;
 Best Local Similarity 80.0%; Pred. No. 2.6e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 TYAMH 5
 |||:
 Db 69 TYALH 73

RESULT 28
 ABP01422
 ID ABP01422 standard; protein; 162 AA.
 XX
 AC ABP01422;
 XX
 DT 24-JUN-2002 (first entry)
 XX
 DE Human ORFX protein sequence SEQ ID NO:2826.
 XX
 XX Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
 KW hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;
 KW degenerative disorder; osteoarthritis; neurodegenerative disorder;
 KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;

KW hypertension; hypothyroidism; cholesterol ester storage disease;
 KW immune deficiency; immune disorder; infectious disease;
 KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
 KW myasthenia gravis.
 OS Homo sapiens.
 PN WO200192523-A2.
 XX
 PD 06-DEC-2001.
 XX
 PF 29-MAY-2001; 2001WO-US010836.
 XX
 PR 30-MAY-2000; 2000US-0206132P.
 PR 29-AUG-2000; 2000US-0228716P.
 XX
 PA (CUBA-) CUBAGEN CORP.
 PI Shimkels RA, Leach MD;
 DR N-PSDB; ABN17174.
 XX
 PT Novel human polypeptides and polynucleotides useful for diagnosing,
 PT preventing and treating cardiovascular disease, neurodegenerative,
 PT hyperproliferative disorders and autoimmune disorders.
 XX
 PS Disclosure; SEQ ID NO 2826; 10377P; English.
 XX
 CC The present invention describes substantially purified human proteins
 CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
 CC in the specification). ABN15762 to ABN27252 encode the human ORFX
 CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
 CC treating or preventing a pathology associated with an ORFX-associated
 CC disorder in humans, and in the manufacture of a medicament for treating a
 CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide
 CC sequences can be used in gene therapy. ORFX sequences can be used in the
 CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
 CC psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,
 CC osteoarthritis, neurodegenerative disorders, disorders related to organ
 CC transplantation, cardiovascular diseases, diabetes mellitus, systemic
 CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
 CC storage disease, various immune deficiencies and disorders, infectious
 CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
 CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
 CC disease and autoimmune inflammatory eye disease. ORFX proteins are also
 CC useful for treating burns, incisions, ulcers, for treating osteoporosis,
 CC bone degenerative disorders, or periodontal disease, and for gut
 CC protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues and conditions resulting from
 CC systemic cytokine damage. N.B. The sequence data for this patent did not
 CC form part of the printed specification, but was obtained in electronic
 CC format directly from WIPO at ftp.wipo.int/pub/published_pat_sequences
 XX
 SQ Sequence 162 AA;
 Query Match 89.7%; Score 26; DB 5; Length 162;
 Best Local Similarity 80.0%; Pred. No. 4.8e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TYAMH 5
 |||:
 Db 146 TYALH 150
 RESULT 29
 ABG68756
 ID ABG68756 standard; protein; 173 AA.
 XX
 AC ABG68756;
 XX
 XX 07-OCT-2002 (first entry)
 DT
 XX

DE Cytochrome P450 CYP3A43 exon 1-CYP3A4 exon 11-13 #1.
 XX
 XX Cytochrome P450; CYP3A1; CYP3AP2; CYP3A43; CYP3A4; CYP3A5; CYP3A7;
 KW drug metabolism; drug design; drug screening.
 KW
 OS Homo sapiens.
 PN WO200244213-A1.
 XX
 PD 06-JUN-2002.
 XX
 PF 28-NOV-2001; 2001WO-SE002631.
 XX
 PR 28-NOV-2000; 2000SE-00004366.
 PR 11-JUN-2001; 2001SE-00002061.
 XX
 PA (ZAPH/) ZAPHIROPOULOS P G.
 PA (FINY/) FINTA C.
 PI Zaphiropoulos PG, Finnta C;
 DR N-PSDB; ABR97695.
 DR
 DR WPI: 2002-557532/59.
 XX
 PT Novel cytochrome P450 protein in which CYP3A43 exon 1 is joined to sets
 PT of CYP3A4 or CYP3A5 exons, useful as medicament, and in evaluating drug
 PT metabolism, in drug design and drug screening.
 XX
 PS Claim 3; Fig 14; 131P; English.
 XX
 CC The invention describes a cytochrome P450 protein (I) in which CYP3A43
 CC exon 1 is joined to sets of CYP3A4 or CYP3A5 exons, as well as sub
 CC fragments, variants and multiples of (I) having essentially the same
 CC characteristics. (I) is useful as a medicament, and for evaluating drug
 CC metabolism, in drug design, and drug screening, and in tests for
 CC adjusting the dose of drugs. This is the amino acid sequence of a novel
 CC cytochrome P450 protein
 XX
 SQ Sequence 173 AA;
 Query Match 89.7%; Score 26; DB 5; Length 173;
 Best Local Similarity 80.0%; Pred. No. 5.2e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TYAMH 5
 |||:
 Db 69 TYALH 73
 RESULT 30
 ADE08218
 ID ADE08218 standard; protein; 194 AA.
 XX
 AC ADE08218;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 XX
 DE Novel protein (useful for identifying genetic disorders) #373.
 XX
 KW novel gene; novel protein; tissue marker; molecular weight marker;
 KW chromosome marker; genetic disorder.
 XX
 OS Unidentified.
 XX
 PN WO2003054152-A2.
 PN
 PD 03-JUL-2003.
 XX
 PD 10-DEC-2002; 2002WO-US039555.
 PF
 PF 10-DEC-2001; 2001US-0338739P.
 PR 11-DEC-2001; 2001US-0339453P.
 PR 14-MAR-2002; 2002US-0365091P.
 XX

PR 14-MAR-2002; 2002US-0365384P.
 PR 12-APR-2002; 2002US-0372381P.
 PR 12-APR-2002; 2002US-0372615P.
 PR 22-APR-2002; 2002US-00128558.
 PR 24-APR-2002; 2002US-0376045P.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang Z;
 PI Ghosh M, Xue AJ, Wehman T, Weng G, Zhou P, Drmanac RT, Wang Z;
 PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ,
 XX
 DR WPI: 2003-569235/53.
 DR N-PSDB; ADE07307.
 XX
 PT New polynucleotides, useful for expressing recombinant proteins for
 PT analysis, characterization or therapeutic use, or as markers for tissues
 PT in which the corresponding protein is preferentially expressed.
 XX
 PS Claim 20; SEQ ID NO 1284; 1177bp; English.
 XX
 CC The invention comprises the amino acid and coding sequences of novel
 CC proteins. The DNA and protein sequences of the invention are useful as:
 CC markers for tissues in which the corresponding protein is preferentially
 CC expressed; as molecular weight markers on gels; as chromosome markers or
 CC tags; to identify chromosomes or to map related gene positions; and to
 CC compare with endogenous DNA sequences in patients to identify potential
 CC genetic disorders. The present amino acid sequence represents a protein
 CC of the invention.
 XX
 SQ Sequence 194 AA;
 XX
 Query Match 89.7%; Score 26; DB 7; Length 194;
 Best Local Similarity 80.0%; Pred. No. 5.8e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TYAMH 5
 Db 20 TYSMH 24
 XX
 RESULT 31
 ADE08219
 ID ADE08219 standard; protein; 205 AA.
 XX
 AC ADE08219;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Novel protein (useful for identifying genetic disorders) #374.
 XX
 KW novel gene; novel protein; tissue marker; molecular weight marker;
 KW chromosome marker; genetic disorder.
 XX
 OS Undefined.
 XX
 PN WO2003054152-A2.
 XX
 PD 03-JUL-2003.
 XX
 PF 10-DEC-2002; 2002WO-US039555.
 XX
 PR 10-DEC-2001; 2001US-0339739P.
 PR 11-DEC-2001; 2001US-0339453P.
 PR 14-MAR-2002; 2002US-0365091P.
 PR 14-MAR-2002; 2002US-0365384P.
 PR 12-APR-2002; 2002US-0372381P.
 PR 12-APR-2002; 2002US-0372615P.
 PR 22-APR-2002; 2002US-00128558.
 PR 24-APR-2002; 2002US-0376045P.
 XX
 PA (HYSE-) HYSEQ INC.
 XX

PI Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang Z;
 PI Ghosh M, Xue AJ, Wehman T, Weng G, Zhou P, Drmanac RT, Wang Z;
 PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ,
 XX
 DR WPI: 2003-569235/53.
 DR N-PSDB; ADE07308.
 XX
 PT New polynucleotides, useful for expressing recombinant proteins for
 PT analysis, characterization or therapeutic use, or as markers for tissues
 PT in which the corresponding protein is preferentially expressed.
 XX
 PS Claim 20; SEQ ID NO 1285; 1177bp; English.
 XX
 CC The invention comprises the amino acid and coding sequences of novel
 CC proteins. The DNA and protein sequences of the invention are useful as:
 CC markers for tissues in which the corresponding protein is preferentially
 CC expressed; as molecular weight markers on gels; as chromosome markers or
 CC tags; to identify chromosomes or to map related gene positions; and to
 CC compare with endogenous DNA sequences in patients to identify potential
 CC genetic disorders. The present amino acid sequence represents a protein
 CC of the invention.
 XX
 SQ Sequence 205 AA;
 XX
 Query Match 89.7%; Score 26; DB 7; Length 205;
 Best Local Similarity 80.0%; Pred. No. 6.2e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TYAMH 5
 Db 20 TYSMH 24
 XX
 RESULT 32
 ABB91152
 ID ABB91152 standard; protein; 213 AA.
 XX
 AC ABB91152;
 XX
 DT 31-MAY-2002 (first entry)
 XX
 DE Herbicidally active polypeptide SEQ ID NO 363.
 XX
 KW Herbicidal; plant; agriculture; herbicide.
 XX
 OS Arabidopsis thaliana.
 XX
 PN WO200210210-A2.
 XX
 PD 07-FEB-2002.
 XX
 PF 28-AUG-2001; 2001WO-EP009892.
 XX
 PR 28-AUG-2001; 2001WO-EP009892.
 XX
 PA (FARB) BAYER AG.
 XX
 PI Tietjen K, Weidner M;
 XX
 DR WPI: 2002-269010/31.
 XX
 PT Identifying plant target proteins for herbicidally active compounds,
 PT comprising aligning and comparing nucleic acid or amino acid sequences
 PT from plant with nucleic acid or amino acid sequences from non-plant
 PT organisms.
 XX
 PS Claim 5; SEQ ID NO 363; 261pp + Sequence Listing; English.
 XX
 CC The invention relates to identifying target proteins (ABB90790-ABB94016)
 CC for herbicidally active compounds, comprising aligning and comparing
 CC nucleic acid or amino acid sequences from plant with nucleic acid or
 CC amino acid sequences from non-plant organisms using suitable search
 CC parameters, where plant sequences having an E-value greater by a factor

CC of 3 than the E-value of most similar non-plant sequences are selected.
CC The polypeptides or nucleic acids encoding them are useful for
CC identifying modulators. The identified modulators are useful as
CC herbicides

XX Sequence 213 AA;

Query Match 89.7%; Score 26; DB 5; Length 213;
Best Local Similarity 80.0%; Pred. No. 6.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
|||:
Db 202 TYALH 206

RESULT 33

ADA55412
ID ADA55412 standard; protein; 221 AA.

XX ADA55412;

XX 20-NOV-2003 (first entry)

XX Human protein, SEQ ID 2980.

XX Cytostatic; Anti-inflammatory; Osteoprotective; Neuroprotective; Nootropic;

XX Gene Therapy; human; secretory protein; membrane proteins; cancer;

XX Inflammatory disease; osteoporosis; neurological disease.

XX Homo sapiens.

XX EPI293569-A2.

XX 19-MAR-2003.

XX 21-MAR-2002; 2002EP-00006586.

XX 14-SEP-2001; 2001JP-00328381.

XX 24-JAN-2002; 2002US-0350435P.

XX (HELI-) HELIX RES INST.

XX (REAS-) RES ASSOC BIOTECHNOLOGY.

XX Isegai T, Sugiyama T, Otsuki T, Makamatsu A, Sato H, Ishii S;

XX Yamamoto U, Iseono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;

XX Seki N, Yoshikawa T, Otsuka M, Nagahara K, Masuno Y;

XX WPI; 2003-395539/38.

XX N-PSDB; ADA53773.

XX New polynucleotides encoding full-length polypeptides, e.g. secretory

XX and/or membrane proteins, useful for developing medicines for diseases in

XX which the gene is involved, or as target molecules for gene therapy.

XX Claim 14; SEQ ID NO 2980; 205pp; English.

XX The present invention relates to novel human secretory or membrane

XX proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-

XX ADA54071). The coding sequences are useful in the gene therapy of

XX diseases caused by abnormalities of the proteins, e.g. cancer,

XX inflammatory diseases, osteoporosis or neurological disease.

XX Sequence 221 AA;

QY 1 TYAMH 5
|||:
Db 162 TYALH 166

RESULT 34
ABP46042
ID ABP46042 standard; protein; 238 AA.

XX ABP46042;

Query Match 89.7%; Score 26; DB 5; Length 238;
Best Local Similarity 80.0%; Pred. No. 7.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
|||:
Db 31 TYSMH 35

RESULT 34

ABP46042
ID ABP46042 standard; protein; 238 AA.

XX ABP46042;

XX 19-AUG-2002 (first entry)

XX Human Blys binding scFv SEQ ID 2053.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;

XX tumour necrosis factor; B cell proliferation; B cell differentiation;

XX immunosuppressive; immunostimulant; immunomodulatory; antineumatic;

XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;

XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;

XX common variable immunodeficiency; acquired immunodeficiency syndrome.

XX Homo sapiens.

XX WO200202641-A1.

XX 10-JAN-2002.

XX 15-JUN-2001; 2001WO-US019110.

XX 16-JUN-2000; 2000US-0212210P.

XX 17-OCT-2000; 2000US-0240816P.

XX 16-MAR-2001; 2001US-0276248P.

XX 21-MAR-2001; 2001US-0277379P.

XX 25-MAY-2001; 2001US-0293499P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX WPI; 2002-114799/15.

XX Antibodies against B lymphocyte Stimulating polypeptides, useful for the

XX diagnosis and treatment of cancers and immune disorders.

XX Claim 1; Page 2847-2848; 3148pp; English.

XX This invention describes novel antibodies that immunospecifically bind to

XX B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the

XX tumour necrosis factor (TNF) super family and induces B cell

XX proliferation and differentiation. The antibodies of the invention have

XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,

XX antineumatic and antiAIDS activity and can be used in vaccines to

XX inhibit the expression and activity of Blys. The antibodies bind to Blys

XX and so may be used to detect and quantitate the presence of Blys in

XX biological samples and may be used in this way to diagnose disease

XX associated with aberrant expression of Blys. They may also be

XX administered to treat diseases associated with aberrant Blys expression

XX and activity such as cancer, immune, and autoimmune disorders and

XX diseases e.g. systemic lupus erythematosus, rheumatoid arthritis,

XX immunodeficiency (e.g. common variable immunodeficiency (CVID) and

XX acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent

XX the antibodies and fragments of the antibodies described in the method of

XX the invention

XX Sequence 238 AA;

QY 1 TYAMH 5
|||:
Db 31 TYSMH 35

ABU17641
ID ABU17641 standard; protein; 304 AA.
XX
AC ABU17641;
XX
XX 19-JUN-2003 (first entry)
XX
DE Protein encoded by Prokaryotic essential gene #3168.
XX
XX Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
OS Bacillus anthracis.
XX
PN MO20027183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002MO-US009107.
XX
XX 21-MAR-2001; 2001US-00815242.
XX 06-SEP-2001; 2001US-00948993.
XX 25-OCT-2001; 2001US-0342923P.
XX 08-FEB-2002; 2002US-00072851.
XX 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
PI
XX WPI; 2003-023926/02.
XX N-PSDB; ACA21511.
XX
XX New antisense nucleic acids, useful for identifying proteins or screening
XX for homologous nucleic acids required for cellular proliferation to
XX isolate candidate molecules for rational drug discovery programs.
XX
XX Claim 25; SEQ ID NO 45565; 1766pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising any one of
XX the 6213 antisense sequences given in the specification where expression
XX of the nucleic acid inhibits proliferation of a cell. Also included are:
XX (1) a vector comprising a promoter operably linked to the nucleic acid
XX encoding a polypeptide whose expression is inhibited by the antisense
XX nucleic acid; (2) a host cell containing the vector; (3) an isolated
XX polypeptide or its fragment whose expression is inhibited by the
XX antisense nucleic acid; (4) an antibody capable of specifically binding
XX the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
XX proliferation or the activity of a gene in an operon required for
XX proliferation; (7) identifying a compound that influences the activity of
XX the gene product or that has an activity against a biological pathway
XX required for proliferation, or that inhibits cellular proliferation; (8)
XX identifying a gene required for cellular proliferation or the biological
XX pathway in which a proliferation-required gene or its gene product lies
XX or a gene on which the test compound that inhibits proliferation of an
XX organism acts; (9) manufacturing an antibiotic; (10) profiling a
XX compound's activity; (11) a culture comprising strains in which the gene
XX product is overexpressed or underexpressed; (12) determining the extent
XX to which each of the strains is present in a culture or collection of
XX strains; or (13) identifying the target of a compound that inhibits the
XX proliferation of an organism. The antisense nucleic acids are useful for
XX identifying proteins or screening for homologous nucleic acids required
XX for cellular proliferation to isolate candidate molecules for rational
XX drug discovery programs; or for screening homologous nucleic acids
XX required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
XX *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
XX the target prokaryotic essential genes. Note: The sequence data for this
XX patent did not form part of the printed specification, but was obtained
XX in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 304 AA;
XX
XX

Query Match 89.7%; Score 26; DB 6; Length 304;
Best Local Similarity 80.0%; Pred. No. 9.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0;
Gaps 0;
QY 1 TYAMH 5
DB 299 TYALH 303
RESULT 38
AAG91423
ID AAG91423 standard; protein; 370 AA.
XX
XX AAG91423;
XX
AC AAG91423;
XX
XX 26-SEP-2001 (first entry)
XX
XX C glutamicum protein fragment SEQ ID NO: 5177.
XX
XX Corynebacterium; amino acid synthesis; vitamin; saccharide;
XX organic acid synthesis.
XX
XX Corynebacterium glutamicum.
XX
XX EP1108790-A2.
XX
XX 20-JUN-2001.
XX
XX 18-DEC-2000; 2000EP-00127688.
XX
XX 16-DEC-1999; 99JP-00377484.
XX 07-APR-2000; 2000JP-00159162.
XX 03-AUG-2000; 2000JP-00280988.
XX
XX (KYOW) KYOWA HAKKO KOGYO KK.
XX
XX Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
XX Tateishi N, Senoh A, Ikeda M, Ozaki A;
XX
XX WPI; 2001-376931/40.
XX N-PSDB; AAH66642.
XX
XX Novel polynucleotides derived from Corynebacterium bacteria, for identifying
XX mutation point of a gene, measuring expression of a gene, analyzing
XX expression profile or pattern of a gene and identifying homologous gene.
XX
XX Claim 17; SEQ ID NO 5177; 246pp + Sequence Listing; English.
XX
XX The present invention provides a number of nucleotide and protein
XX sequences from the Corynebacterium bacterium Corynebacterium glutamicum. These
XX are useful for identifying the mutation point of a gene derived from a
XX mutant of corynebacterium bacterium, measuring expression amount and analyzing
XX the expression profile or expression pattern of a gene derived from
XX Corynebacterium bacterium, and identifying a homologue of a gene derived from
XX corynebacterium bacterium. Corynebacterium bacteria are useful for producing amino
XX acids, nucleic acids, vitamins, saccharides and organic acids,
XX particularly L-lysine. The present sequence is a protein described in the
XX exemplification of the invention. Note: The sequence data for this patent
XX did not form part of the printed specification, but was obtained in
XX electronic format directly from the European Patent Office
XX
XX Sequence 370 AA;
XX
XX Query Match 89.7%; Score 26; DB 4; Length 370;
XX Best Local Similarity 80.0%; Pred. No. 1.1e+03;
XX Matches 4; Conservative 1; Mismatches 0; Indels 0;
XX Gaps 0;
QY 1 TYAMH 5
DB 172 TYALH 176
RESULT 39

xx	AAAG90014	standard; protein; 370 AA.
xx	AAAG90014;	
xx	AAAG90014;	
xx	26-SEP-2001	(first entry)
xx	C	glutamicum protein fragment SEQ ID NO: 3768.
xx	Corynebacterium	glutamicum.
xx	EP1108790-A2.	
xx	20-JUN-2001.	
xx	18-DEC-2000;	2000EP-00127688.
xx	16-DEC-1999;	99JP-00377484.
xx	07-APR-2000;	2000JP-00159162.
xx	03-AUG-2000;	2000JP-00280988.
xx	(KYOOW)	KYOOWA HAKKO KOGYO KK.
xx	Nakagawa S,	Mizoguchi H, Ando S, Hayaeshi M, Ochiai K, Yokoi H,
xx	Tateishi N,	Senoh A, Ikeda M, Ozaki A,
xx	WPI;	2001-376931/40.
xx	N-PSDB;	AAH65233.
xx	Novel polynucleotides	derived from Corynebacterium bacteria, for identifying
xx	mutation point of a gene,	measuring expression of a gene, analyzing
xx	expression profile or pattern	of a gene and identifying homologous gene.
xx	Claim 17;	SEQ ID NO 3768; 246pp + Sequence Listing; English.
xx	The present invention	provides a number of nucleotide and protein
xx	sequences from the	Corynebacterium glutamicum. These
xx	are useful for	identifying the mutation point of a gene derived from a
xx	mutant of corynebacterium	bacterium, measuring expression amount and analysing
xx	the expression profile	or expression pattern of a gene derived from
xx	Corynebacterium	bacterium, and identifying a homologue of a gene derived from
xx	corynebacterium	bacterium. Corynebacterium bacteria are useful for producing amino
xx	acids, nucleic acids,	vitamins, saccharides and organic acids,
xx	particularly L-lysine.	The present sequence is a protein described in the
xx	embodiment of the	invention. Note: The sequence data for this patent
xx	did not form part	of the printed specification, but was obtained in
xx	electronic format	directly from the European Patent Office
xx	Sequence 370 AA;	
xx	Query Match	89.7%; Score 26; DB 4; Length 370;
xx	Best Local Similarity	80.0%; Pred. No. 11e+03;
xx	Matches 4; Conservative	1; Mismatches 0; Indels 0; Gaps 0.
xx	1 TYAMH 5	
xx	172 TYALH 176	
xx	RESULT 40	
xx	ABO63767	
xx	ABO63767 standard;	protein; 454 AA.
xx	ABO63767;	
xx	29-JUN-2004	(first entry)
xx	Klebsiella pneumoniae	polypeptide seqid 10284.
xx	Recombinant expression	vector; transcription regulatory element;

```

KW Klebsiella pneumoniae protein; antibacterial; Vaccine.
XX
XX Klebsiella pneumoniae.
OS
XX US6610836-B1.
PN
XX 26-AUG-2003.
PD
XX
XX 27-JAN-2000; 2000US-00489039.
PF
XX 29-JAN-1999; 99US-0117747P.
FR
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
PA
XX
XX Breton GL, Osborne M;
PI
XX WPT; 2003-895346/82.
XX DR N-PSDB; ACH97318.
XX
XX New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for
PT preparing a vaccine composition against Klebsiella pneumoniae.
XX
XX Disclosure; SEQ ID NO 10284; 932P; English.
PS
XX
XX The invention describes a new isolated nucleic acid encoding a Klebsiella
XX pneumoniae polypeptide. Also described are: a recombinant expression
XX vector comprising the nucleic acid, operably linked to a transcription
XX regulatory element; and a cell comprising the recombinant expression
XX vector. The nucleic acid is useful for preparing a vaccine composition
XX against Klebsiella pneumoniae. This is the amino acid sequence of a
XX Klebsiella pneumoniae polypeptide of the invention
XX
XX Sequence 454 AA;
SQ
XX
XX Query Match 89.7%; Score 26; DB 7; Length 454;
XX Best Local Similarity 80.0%; Pred. No. 1.4e+03;
XX Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0
XX
XX 1 TYAMH 5
XX |||:|
XX 152 TYALH 156

```

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OM protein - protein search, using SW model

Run on: March 31, 2005, 11:51:44 ; Search time 9.76562 Seconds
(without alignments)
38.220 Million cell updates/sec

Title: US-10-614-959-10

Perfect score: 29

Sequence: 1 TYAMH 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents_Aa.*
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2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
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5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfill1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	5	US-09-383-667-10	Sequence 10, App1
2	29	100.0	118	US-09-232-290-45	Sequence 45, App1
3	29	100.0	258	US-09-252-991A-26228	Sequence 26228, A
4	29	100.0	690	US-10-262-083-2	Sequence 2, App1
5	29	100.0	690	US-10-262-083-18	Sequence 18, App1
6	26	89.7	108	US-09-270-767-35497	Sequence 35497, A
7	26	89.7	108	US-09-270-767-50714	Sequence 50714, A
8	26	89.7	454	US-09-489-039A-10284	Sequence 10284, A
9	26	89.7	455	US-09-543-681A-8288	Sequence 8288, Ap
10	26	89.7	502	US-09-949-016-5992	Sequence 5992, Ap
11	26	89.7	507	US-09-949-016-7091	Sequence 7091, Ap
12	26	89.7	544	US-09-975-594-699	Sequence 699, App
13	26	89.7	544	US-09-919-039-270	Sequence 270, App1
14	25	86.2	5	US-08-264-093-21	Sequence 21, App1
15	25	86.2	5	US-08-918-148-26	Sequence 26, App1
16	25	86.2	5	US-09-383-667-21	Sequence 21, App1
17	25	86.2	5	US-09-138-091A-26	Sequence 26, App1
18	25	86.2	5	US-09-424-840B-34	Sequence 34, App1
19	25	86.2	5	US-09-424-840B-91	Sequence 91, App1
20	25	86.2	5	US-09-830-748B-10	Sequence 10, App1
21	25	86.2	38	US-07-977-630-67	Sequence 67, App1
22	25	86.2	58	US-09-270-767-38850	Sequence 38850, A
23	25	86.2	58	US-09-270-767-54067	Sequence 54067, A
24	25	86.2	98	US-08-211-202-118	Sequence 118, App
25	25	86.2	114	US-09-726-219A-222	Sequence 222, App
26	25	86.2	116	US-08-211-202-141	Sequence 141, App
27	25	86.2	117	US-08-545-809A-91	Sequence 91, App1

28	25	86.2	117	3	US-09-025-769B-24	Sequence 24, App1
29	25	86.2	117	4	US-09-490-070A-24	Sequence 24, App1
30	25	86.2	117	4	US-09-490-153-24	Sequence 24, App1
31	25	86.2	117	4	US-09-490-324-24	Sequence 24, App1
32	25	86.2	118	3	US-08-545-809A-145	Sequence 145, App
33	25	86.2	118	4	US-09-248-796A-1439	Sequence 1439, A
34	25	86.2	119	1	US-08-331-388A-46	Sequence 46, App1
35	25	86.2	119	2	US-08-561-521-10	Sequence 10, App1
36	25	86.2	119	2	US-08-561-521-12	Sequence 12, App1
37	25	86.2	119	2	US-08-561-521-13	Sequence 13, App1
38	25	86.2	119	2	US-08-331-387B-46	Sequence 46, App1
39	25	86.2	119	2	US-08-759-804A-46	Sequence 46, App1
40	25	86.2	119	3	US-09-227-693-46	Sequence 46, App1
41	25	86.2	119	4	US-09-438-954-41	Sequence 41, App1
42	25	86.2	119	5	PCT-US95-01219-10	Sequence 10, App1
43	25	86.2	119	5	PCT-US95-01219-12	Sequence 12, App1
44	25	86.2	119	5	PCT-US95-01219-13	Sequence 13, App1
45	25	86.2	120	1	US-08-211-202-135	Sequence 135, App

ALIGNMENTS

```
RESULT 1
US-09-383-667-10
; Sequence 10, Application US/09383667
; Patent No. 6624295
; GENERAL INFORMATION:
; APPLICANT: Adams, Camelia W.
; APPLICANT: Devaux, Brigitte
; APPLICANT: Eaton, Dan L.
; APPLICANT: Hase, Philip E.
; APPLICANT: Judice, J. Kevin
; APPLICANT: Kirchhofer, Daniel
; APPLICANT: Suggest, Shelley
; TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
; FILE REFERENCE: P1661R2
; CURRENT APPLICATION NUMBER: US/09/383,667
; CURRENT FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098,233
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: US 60/122,767
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 10
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-383-667-10
Query Match      100.0%; Score 29; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 TYAMH 5
DB      1 TYAMH 5
RESULT 2
US-09-232-290-45
; Sequence 45, Application US/09232290A
; Patent No. 6815540
; GENERAL INFORMATION:
; APPLICANT: PLUCKTHUN, ANDREAS
; APPLICANT: NIEBA, LARS
; APPLICANT: HONEGGER, ANNEMARIE
; TITLE OF INVENTION: IMMUNOGLOBULIN SUPER FAMILY DOMAINS AND FRAGMENTS WITH
; FILE REFERENCE: MORPHO/7
; CURRENT APPLICATION NUMBER: US/09/232,290A
; CURRENT FILING DATE: 1999-01-15
; EARLIER APPLICATION NUMBER: PCT/EP96/02230
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;; EARLIER FILING DATE: 1996-05-23
;; NUMBER OF SEQ ID NOS: 60
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 45
;; LENGTH: 118
;; TYPE: PRT
;; ORGANISM: Murine
US-09-232-290-45

Query Match 100.0%; Score 29; DB 4; Length 118;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 31 TYAMH 35

RESULT 3
US-09-252-991A-26228
; Sequence 26228, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26228
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26228

Query Match 100.0%; Score 29; DB 4; Length 258;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 201 TYAMH 205

RESULT 4
US-10-262-083-2
; Sequence 2, Application US/10262083
; Patent No. 6830905
; GENERAL INFORMATION:
; APPLICANT: KOIBUCHI, Kyoko
; APPLICANT: NAGASAKI, Hiroaki
; APPLICANT: YUASA, Aki
; APPLICANT: KATOKA, Jiro
; APPLICANT: KITAMOTO, Katsuhiko
; TITLE OF INVENTION: A No. 6830905e1 Glutaminase, its Gene and a Method of Producing I
; FILE REFERENCE: 199438US-8222-10-0-PCT
; CURRENT APPLICATION NUMBER: US/10/262,083
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US/09/674,507
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: JP 10/134080
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: JP 10/258974
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: JP 10/292443
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: JP 11/89157
; PRIOR FILING DATE: 1999-03-30

;; PRIOR APPLICATION NUMBER: PCT/JP99/02455
;; PRIOR FILING DATE: 1999-05-12
;; NUMBER OF SEQ ID NOS: 26
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 2
;; LENGTH: 690
;; TYPE: PRT
;; ORGANISM: Aspergillus oryzae
US-10-262-083-2

Query Match 100.0%; Score 29; DB 4; Length 690;
Best Local Similarity 100.0%; Pred. No. 1,1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 423 TYAMH 427

RESULT 5
US-10-262-083-18
; Sequence 18, Application US/10262083
; Patent No. 6830905
; GENERAL INFORMATION:
; APPLICANT: KOIBUCHI, Kyoko
; APPLICANT: NAGASAKI, Hiroaki
; APPLICANT: YUASA, Aki
; APPLICANT: KATOKA, Jiro
; APPLICANT: KITAMOTO, Katsuhiko
; TITLE OF INVENTION: A No. 6830905e1 Glutaminase, its Gene and a Method of Producing I
; FILE REFERENCE: 199438US-8222-10-0-PCT
; CURRENT APPLICATION NUMBER: US/10/262,083
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US/09/674,507
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: JP 10/134080
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: JP 10/258974
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: JP 10/292443
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: JP 11/89157
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: PCT/JP99/02455
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Aspergillus oryzae
US-10-262-083-18

Query Match 100.0%; Score 29; DB 4; Length 690;
Best Local Similarity 100.0%; Pred. No. 1,1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 423 TYAMH 427

RESULT 6
US-09-270-767-35497
; Sequence 35497, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35497
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE: OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-35497

Query Match 89.7%; Score 26; DB 4; Length 108;
Best Local Similarity 80.0%; Pred. No. 85;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
|||:
64 TYALH 68

RESULT 7
US-09-270-767-50714
; Sequence 50714, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:

; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50714
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE: OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-50714

Query Match 89.7%; Score 26; DB 4; Length 108;
Best Local Similarity 80.0%; Pred. No. 85;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
|||:
64 TYALH 68

RESULT 8
US-09-489-039A-10284
; Sequence 10284, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:

; APPLICANT: Gary Bretton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709-2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 10284
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-10284

Query Match 89.7%; Score 26; DB 4; Length 454;
Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
|||:
64 TYALH 68

DB 152 TYALH 156

RESULT 9
US-09-543-681A-8288
; Sequence 8288, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:

; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709-1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 8288
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-8288

Query Match 89.7%; Score 26; DB 4; Length 455;
Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
|||:
225 TYALH 229

RESULT 10
US-09-949-016-5992
; Sequence 5992, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5992
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-5992

Query Match 89.7%; Score 26; DB 4; Length 502;
Best Local Similarity 80.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
|||:
398 TYALH 402

RESULT 11
US-09-949-016-7091
; Sequence 7091, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

```
;; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;; FILE REFERENCE: CLO01307
;; CURRENT APPLICATION NUMBER: US/09/949,016
;; CURRENT FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: 60/241,755
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO 7091
;; LENGTH: 507
;; TYPE: PRT
;; ORGANISM: Human
US-09-949-016-7091

Query Match      89.7%; Score 26; DB 4; Length 507;
Best Local Similarity 80.0%; Pred. No. 4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 TYAMH 5
        |||:-|
Db      403 TYALH 407

RESULT 12
US-09-976-594-699
; Sequence 699, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 699
; LENGTH: 544
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 4113161CD1
US-09-976-594-699

Query Match      89.7%; Score 26; DB 4; Length 544;
Best Local Similarity 80.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 TYAMH 5
        |||:-|
Db      485 TYALH 489

RESULT 13
US-09-919-039-270
; Sequence 270, Application US/09919039
; Patent No. 6727066
; GENERAL INFORMATION:
; APPLICANT: Kaseer, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
```

```
;; SOFTWARE: PERL Program
;; SEQ ID NO 270
;; LENGTH: 544
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc feature
;; OTHER INFORMATION: Incyte ID No. 6727066 4113161CD1
US-09-919-039-270

Query Match      89.7%; Score 26; DB 4; Length 544;
Best Local Similarity 80.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 TYAMH 5
        |||:-|
Db      485 TYALH 489

RESULT 14
US-08-264-093-21
; Sequence 21, Application US/08264093
; Patent No. 5639863
; GENERAL INFORMATION:
; APPLICANT: Michael D. Dan
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO
; TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE
; TITLE OF INVENTION: ANTIGEN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ridout & Maybee
; STREET: 2300 Richmond-Adelaide Centre
; STREET: 101 Richmond Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 2J7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.4 MB storage
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: MS-DOS 6.00
; SOFTWARE: ASCII Editor
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/264,093
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA: No. 5639863 applicable
; ATTORNEY/AGENT INFORMATION:
; NAME: Lake, James R.
; REGISTRATION NUMBER: 31081
; REFERENCE/DOCKET NUMBER: NOVOP/106A/7551
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 868-1482
; TELEFAX: (416) 362-0823
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: not applicable
; TOPOLOGY: linear
US-08-264-093-21

Query Match      86.2%; Score 25; DB 1; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 TYAMH 5
        :|||:-|
Db      1 SYAMH 5

RESULT 15
US-08-918-148-26
```

```
; Sequence 26, Application US/08918148A
; Patent No. 6342220
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia
; APPLICANT: W.
; APPLICANT: Carter, Paul J.
; APPLICANT: Fendly, Brian M.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Agonist Antibodies
; FILE REFERENCE: P0979
; CURRENT APPLICATION NUMBER: US/08/918,148A
; PRIOR FILING DATE: 1997-08-25
; NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 26
; LENGTH: 5
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; NAME/KEY: 10D10scFv, 12B5scFv VH CDR1
; LOCATION: 1-5
; OTHER INFORMATION:
US-08-918-148-26
```

```
Query Match      86.2% Score 25; DB 3; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 1 TYAMH 5
Db 1 TYGMH 5
```

```
RESULT 16
US-09-383-667-21
; Sequence 21, Application US/09383667
; Patent No. 6624295
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia W.
; APPLICANT: Devaux, Brigitte
; APPLICANT: Eaton, Dan L.
; APPLICANT: Hass, Philip E.
; APPLICANT: Judice, J. Kevin
; APPLICANT: Kirchofer, Daniel
; APPLICANT: Suggett, Shelley
; TITLE OF INVENTION: Human Anti-Factor IX/Xa Antibodies
; FILE REFERENCE: P1661R2
; CURRENT APPLICATION NUMBER: US/09/383,667
; PRIOR FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098,233
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: US 60/122,767
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 21
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-383-667-21
```

```
Query Match      86.2% Score 25; DB 4; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 TYAMH 5
Db 1 SYAMH 5
```

```
RESULT 17
US-09-138-091A-26
; Sequence 26, Application US/09138091A
; Patent No. 6737249
; GENERAL INFORMATION:
```

```
; APPLICANT: Adams, Camellia W.
; APPLICANT: Carter, Paul J.
; APPLICANT: Fendly, Brian M.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Agonist Antibodies
; FILE REFERENCE: 9491-013-27
; CURRENT APPLICATION NUMBER: US/09/138,091A
; PRIOR FILING DATE: 1998-08-21
; PRIOR APPLICATION NUMBER: US 60/056,736
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-138-091A-26
```

```
Query Match      86.2% Score 25; DB 4; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 1 TYAMH 5
Db 1 TYGMH 5
```

```
RESULT 18
US-09-424-840B-34
; Sequence 34, Application US/09424840B
; Patent No. 6790938
; GENERAL INFORMATION:
; APPLICANT: Berchtold, Peter
; APPLICANT: Escher, Robert F. A.
; TITLE OF INVENTION: ANTI-GPIIb/IIIa RECOMBINANT ANTIBODIES
; FILE REFERENCE: 100564-09049
; CURRENT APPLICATION NUMBER: US/09/424,840B
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: DE 19820663.1
; PRIOR FILING DATE: 1998-05-08
; PRIOR APPLICATION NUMBER: DE 19755227.7
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: DE 19723904.8
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-424-840B-34
```

```
Query Match      86.2% Score 25; DB 4; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 TYAMH 5
Db 1 SYAMH 5
```

```
RESULT 19
US-09-424-840B-91
; Sequence 91, Application US/09424840B
; Patent No. 6790938
; GENERAL INFORMATION:
; APPLICANT: Berchtold, Peter
; APPLICANT: Escher, Robert F. A.
; TITLE OF INVENTION: ANTI-GPIIb/IIIa RECOMBINANT ANTIBODIES
; FILE REFERENCE: 100564-09049
; CURRENT APPLICATION NUMBER: US/09/424,840B
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: DE 19820663.1
```

PRIOR FILING DATE: 1998-05-08
PRIOR APPLICATION NUMBER: DE 19755227.7
PRIOR FILING DATE: 1997-12-12
PRIOR APPLICATION NUMBER: DE 19723904.8
PRIOR FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 128
SOFTWARE: Patentin version 3.1
SEQ ID NO 91
LENGTH: 5
TYPE: PRT
ORGANISM: Homo sapiens
US-09-424-840B-91

Query Match 86.2%; Score 25; DB 4; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
DB 1 SYAMH 5

RESULT 20
US-09-830-748B-10
Sequence 10, Application US/09830748B
Patent No. 6818749
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as represented by The
APPLICANT: Secretary of the Department of Health and Human Services
APPLICANT: Kaushali Syed V.S.
APPLICANT: Padman, Eduardo A.
APPLICANT: Jeffery, Schilom
TITLE OF INVENTION: VARIANTS OF HUMANIZED ANTI-CARCINOMA MONOCLONAL ANTIBODY CC49
FILE REFERENCE: 4239-61725
CURRENT FILING DATE: 2001-04-30
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: PCT/US99/25552
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: US 60/106,757
PRIOR FILING DATE: 1998-11-02
PRIOR APPLICATION NUMBER: US 60/106,534
PRIOR FILING DATE: 1998-10-31
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin version 3.1
SEQ ID NO 10
LENGTH: 5
TYPE: PRT
ORGANISM: Homo sapiens
US-09-830-748B-10

Query Match 86.2%; Score 25; DB 4; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
DB 1 SYAMH 5

RESULT 21
US-07-977-630-67
Sequence 67, Application US/07977630
Patent No. 5583038
GENERAL INFORMATION:
APPLICANT: Stover, Charles K.
TITLE OF INVENTION: BACTERIAL EXPRESSION VECTORS CONTAINING
NUMBER OF SEQUENCES: 84
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
ADDRESSEE: Stewart & Olstein
STREET: 6 Becker Farm Road
CITY: Roseland

STATE: New Jersey
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/977,630
FILING DATE: No. 5583038member 17, 1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Heron, Charles J.
REGISTRATION NUMBER: 28,019
REFERENCE/DOCKET NUMBER: 469201-174
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-977-630-67

Query Match 86.2%; Score 25; DB 1; Length 38;
Best Local Similarity 80.0%; Pred. No. 51;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
DB 6 SYAMH 10

RESULT 22
US-09-270-767-38850
Sequence 38850, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 38850
LENGTH: 58
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-270-767-38850

Query Match 86.2%; Score 25; DB 4; Length 58;
Best Local Similarity 80.0%; Pred. No. 77;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TYAMH 5
DB 47 TYTWH 51

RESULT 23
US-09-270-767-54067
Sequence 54067, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 54067
 LENGTH: 58
 TYPE: PRT
 ORGANISM: Drosophila melanogaster
 US-09-270-767-54067

Query Match 86.2%; Score 25; DB 4; Length 58;
 Best Local Similarity 80.0%; Pred. No. 77;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TYAMH 5
 ||||
 47 TYTWH 51

RESULT 24
 US-08-211-202-118
 Sequence 118, Application US/08211202
 Patent No. 5565332

GENERAL INFORMATION:
 APPLICANT: HOOGENBOOM, Hendricus Reneerus Jacobus Matheus
 APPLICANT: BAIER, Michael
 APPLICANT: JESPER, Laurent Stephane Anne Therese
 APPLICANT: WINTER, Gregory Paul
 TITLE OF INVENTION: Production of chimeric antibodies - a
 TITLE OF INVENTION: combinatorial approach
 NUMBER OF SEQUENCES: 144
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
 ADDRESS: Borun
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60606-6402
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/211,202
 FILING DATE: 23-SEP-1992
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9120252.3
 FILING DATE: 23-SEP-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9120377.8
 FILING DATE: 25-SEP-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9206181.9
 FILING DATE: 24-MAR-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9206372.6
 FILING DATE: 24-MAR-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/GB92/00883
 FILING DATE: 15-MAY-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: David W. Clough
 REGISTRATION NUMBER: 36,107
 REFERENCE/DOCKET NUMBER: 28111/31960
 TELEPHONE: 312-474-6300
 TELEFAX: 312-474-0448
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 118:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 98 amino acids
 TYPE: amino acid

TOPOLOGY: linear
 MOLECULE TYPE: Protein
 US-08-211-202-118

Query Match 86.2%; Score 25; DB 1; Length 98;
 Best Local Similarity 80.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
 ||||
 31 SYAMH 35

RESULT 25
 US-09-726-219A-222
 Sequence 222, Application US/09726219A
 Patent No. 6806079

GENERAL INFORMATION:
 APPLICANT: Cambridge Antibody Technology
 APPLICANT: Cambridge Antibody Technology Limited
 APPLICANT: Medical Research Council
 APPLICANT: McCafferty, John
 APPLICANT: Pope, Anthony
 APPLICANT: Johnson, Kevin
 APPLICANT: Hooogenboom, Hendricus
 APPLICANT: Griffiths, Andrew
 APPLICANT: Jackson, Ronald
 APPLICANT: Holliger, Kasper
 APPLICANT: Marks, James
 APPLICANT: Jackson, Timothy
 APPLICANT: Clackson, David
 APPLICANT: Winter, Gregory
 APPLICANT: Bonert, Timothy

TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
 FILE REFERENCE: 213839-00013
 CURRENT APPLICATION NUMBER: US/09/726,219A
 FILING DATE: 2000-11-28
 PRIOR APPLICATION NUMBER: GB 9015198.6
 FILING DATE: 1990-07-10
 PRIOR APPLICATION NUMBER: GB 9022845.3
 FILING DATE: 1990-10-19
 PRIOR APPLICATION NUMBER: GB 9022845.3
 FILING DATE: 1990-10-19
 PRIOR APPLICATION NUMBER: GB 9024503.6
 FILING DATE: 1990-11-12
 PRIOR APPLICATION NUMBER: GB 9104744.9
 FILING DATE: 1991-03-06
 PRIOR APPLICATION NUMBER: GB 9110549.4
 FILING DATE: 1991-05-15
 PRIOR APPLICATION NUMBER: PCT/GB91/01134
 FILING DATE: 1991-07-10
 PRIOR APPLICATION NUMBER: US 07/971,857
 FILING DATE: 1993-01-08
 PRIOR APPLICATION NUMBER: US 08/484,893
 FILING DATE: 1995-06-07
 NUMBER OF SEQ ID NOS: 272
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 222
 LENGTH: 114
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: VH of scfv from mouse immunized with 2-phenyl-5-oxazolone
 US-09-726-219A-222

Query Match 86.2%; Score 25; DB 4; Length 114;
 Best Local Similarity 80.0%; Pred. No. 1.5e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
 ||||
 31 SYAMH 35

RESULT 26
US-08-211-202-141
Sequence 141, Application US/08211202
Patent No. 5565332
GENERAL INFORMATION:
APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Matheus
APPLICANT: BAIRER, Michael
APPLICANT: JESPEERS, Laurent Stephane Anne Therese
APPLICANT: WINTER, Gregory Paul
TITLE OF INVENTION: Production of chimeric antibodies - a
TITLE OF INVENTION: combinatorial approach
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211,202
FILING DATE: 23-SEP-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120252.3
FILING DATE: 23-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120377.8
FILING DATE: 25-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/31960
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 141:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-211-202-141

Query Match 86.2%; Score 25; DB 1; Length 116;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
:||||
Db 31 SYAMH 35

RESULT 27
US-08-545-809A-91
Sequence 91, Application US/08545809A

Patent No. 6096878
GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
APPLICANT: Matsuda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809A
FILING DATE: 27-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06501/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-545-809A-91

Query Match 86.2%; Score 25; DB 3; Length 117;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
:||||
Db 50 SYAMH 54

RESULT 28
US-09-025-769B-24
Sequence 24, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-24

Query Match 86.2% Score 25; DB 3; Length 117;
Best Local Similarity 80.0% Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
:||||
DB 31 SYAMH 35

RESULT 29
US-09-490-070A-24
Sequence 24, Application US/09490070A
Patent No. 6696248
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESSES:
ADDRESS: Colin G. Sandercock, Esq. c/o Heller Ehrman
White & McCulliffe
STREET: 1666 K Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-490-070A-24

Query Match 86.2% Score 25; DB 4; Length 117;
Best Local Similarity 80.0% Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
:||||
DB 31 SYAMH 35

RESULT 30
US-09-490-153-24
Sequence 24, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESSES:
ADDRESS: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-490-153-24

Query Match 86.2% Score 25; DB 4; Length 117;
Best Local Similarity 80.0% Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5

Db :|||
31 SYAMH 35

RESULT 31

US-09-490-324-24
Sequence 24, Application US/09490324

Patent No. 6828422

GENERAL INFORMATION:

APPLICANT: Knappik, Achim

Inag, Peter

Ge, Liming

Moroney, Simon

Flueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,324

FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769

FILING DATE: 18-FEB-1998

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 596-9000

TELEFAX: (212) 596-9090

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 117 amino acids

TYPE: amino acid

STRANDEDNESS: <unknown>

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 24:

US-09-490-324-24

Query Match 86.2%; Score 25; DB 4; Length 117;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
:|||
Db 31 SYAMH 35

RESULT 32

US-08-545-809A-145

Sequence 145, Application US/08545809A

Patent No. 6096878

GENERAL INFORMATION:

APPLICANT: Honjo, Tasuku

Applicant: Matsuda, Fumihiko

TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE

TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME

NUMBER OF SEQUENCES: 145

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson, P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: US

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows95

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/545,809A

FILING DATE: 27-MAR-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP93/00603

FILING DATE: 10-MAY-1993

ATTORNEY/AGENT INFORMATION:

NAME: Freeman, John W.

REGISTRATION NUMBER: 29,066

REFERENCE/DOCKET NUMBER: 06501/004001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-542-5070

TELEFAX: 617-542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 145:

SEQUENCE CHARACTERISTICS:

LENGTH: 118 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-545-809A-145

Query Match 86.2%; Score 25; DB 3; Length 118;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
:|||
Db 51 SYAMH 55

RESULT 33

US-09-248-796A-14399

Sequence 14399, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248,796A

PRIOR FILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR FILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 14399

LENGTH: 118

TYPE: PRT

ORGANISM: Candida albicans

US-09-248-796A-14399

Query Match 86.2%; Score 25; DB 4; Length 118;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
:|||
Db 57 SYAMH 61

RESULT 34
US-08-331-398A-46
Sequence 46, Application US/08331398A
Patent No. 5608039
GENERAL INFORMATION:
APPLICANT: Pastan, Ira
APPLICANT: Willingham, Mark
APPLICANT: Fitzgerald, David
APPLICANT: Brinkmann, Ulrich
APPLICANT: Pai, Lee
TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
TITLE OF INVENTION: and Their Uses (as amended)
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Plaza
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,398A
FILING DATE: 28-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-126110US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..119
OTHER INFORMATION: /note="Human fetal immunoglobulin
OTHER INFORMATION: 56P1/CL Variable Heavy chain (V-H)"
US-08-331-398A-46
Query Match 86.2%; Score 25; DB 1; Length 119;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 31 SYAMH 35

RESULT 35
US-08-561-521-10
Sequence 10, Application US/085615121
Patent No. 5840299
GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.

APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VIA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/186,269A
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-561-521-10
Query Match 86.2%; Score 25; DB 2; Length 119;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 31 SYAMH 35

RESULT 36
US-08-561-521-12
Sequence 12, Application US/085615121
Patent No. 5840299
GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
TITLE OF INVENTION: Adhesion Molecule VIA-4
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/186,269A
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-561-521-12

Query Match 86.2%; Score 25; DB 2; Length 119;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TYAMH 5
Db 31 SYAMH 35

RESULT 37
US-08-561-521-13
Sequence 13, Application US/08561521
Patent No. 5840299
GENERAL INFORMATION:
APPLICANT: Bendig, Mary M.
APPLICANT: Leger, Olivier J.
APPLICANT: Saldanha, Jose
APPLICANT: Jones, S. Tarran
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
ADHESION MOLECULE VLA-4
TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Hourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,521
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/186,269A
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William L.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15270-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-561-521-13

Query Match 86.2%; Score 25; DB 2; Length 119;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TYAMH 5
Db 31 SYAMH 35

RESULT 38
US-08-331-397B-46
Sequence 46, Application US/08331397B
Patent No. 5981726
GENERAL INFORMATION:
APPLICANT: Pastan, Ira
APPLICANT: Benhar, Itai
TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Plaza
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,397B
FILING DATE: 28-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-126120US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..119
OTHER INFORMATION: /note= "Human fetal immunoglobulin
OTHER INFORMATION: 56P1/CL Variable Heavy chain (V-H)"
US-08-331-397B-46

Query Match 86.2%; Score 25; DB 2; Length 119;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
:||||
Db 31 SYAMH 35

RESULT 39
US-08-759-804A-46
Sequence 46, Application US/08759804A
Patent No. 5990296
GENERAL INFORMATION:
APPLICANT: Pastan, Ira
APPLICANT: Willingham, Mark
APPLICANT: Fitzgerald, David J.
APPLICANT: Brinkmann, Ulrich
APPLICANT: Pai, Lee
TITLE OF INVENTION: Tumor-Specific Antibody Fragments,
TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/759,804A
FILING DATE: 03-DEC-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/331,398
FILING DATE: 28-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 015280-126140US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..119
OTHER INFORMATION: /note="Human fetal immunoglobulin
OTHER INFORMATION: 56Pl/CL Variable Heavy chain (V-H)"
US-08-759-804A-46
Query Match 86.2%; Score 25; DB 2; Length 119;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TYAMH 5
:||||
Db 31 SYAMH 35

RESULT 40
US-09-227-693-46
Sequence 46, Application US/09227693
Patent No. 6287562
GENERAL INFORMATION:
APPLICANT: PASTAN, Ira
APPLICANT: BENHAR, Itai
APPLICANT: PADILAN, Eduardo A.
APPLICANT: JUNG, Sun-Hee
APPLICANT: LEE, Byungkook
TITLE OF INVENTION: HUMANIZED TUMOR-SPECIFIC ANTIBODY
TITLE OF INVENTION: FRAGMENTS, FUSION PROTEINS, AND USES THEREOF
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: Stewart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/227,693
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/331,396
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 15280-126-1-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Protein
LOCATION: 1..119
OTHER INFORMATION:
OTHER INFORMATION: 56Pl/CL VH region"

US-09-227-693-46
Query Match 86.2%; Score 25; DB 3; Length 119;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TYAMH 5
:||||
Db 31 SYAMH 35
Search completed: March 31, 2005, 12:13:24
Job time : 10.7656 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 31, 2005, 12:10:00 ; Search time 27.9688 Seconds
(without alignments)
59.279 Million cell updates/sec

Title: US-10-614-959-10

Perfect score: 29

Sequence: 1 TYAMH 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1413372 seqs, 331592847 residues

Total number of hits satisfying chosen parameters: 1413372

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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20: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	11	US-10-468-543-91	Sequence 91, Appl
2	29	100.0	151	US-10-424-599-231272	Sequence 231272, A
3	29	100.0	206	US-10-282-122A-52731	Sequence 52731, A
4	29	100.0	278	US-10-369-493-9985	Sequence 9985, Ap
5	29	100.0	690	US-10-262-083-2	Sequence 2, Appl
6	29	100.0	690	US-10-262-083-18	Sequence 18, Appl
7	26	89.7	11	US-10-468-543-35	Sequence 35, Appl
8	26	89.7	59	US-10-424-599-217913	Sequence 217913, A
9	26	89.7	60	US-10-424-599-188252	Sequence 188252, A
10	26	89.7	61	US-10-437-963-109084	Sequence 109084, A
11	26	89.7	67	US-09-864-761-44407	Sequence 44407, A
12	26	89.7	67	US-10-424-599-190876	Sequence 190876, A
13	26	89.7	73	US-10-424-599-192746	Sequence 192746, A

14	26	89.7	73	US-10-424-599-205833	Sequence 205833, A
15	26	89.7	77	US-10-424-599-245586	Sequence 245586, A
16	26	89.7	79	US-09-764-846-193	Sequence 193, App
17	26	89.7	79	US-10-091-483-193	Sequence 193, App
18	26	89.7	85	US-10-767-701-48571	Sequence 48571, A
19	26	89.7	98	US-10-424-599-214193	Sequence 214193, A
20	26	89.7	137	US-10-424-599-227653	Sequence 227653, A
21	26	89.7	141	US-10-424-599-143644	Sequence 143644, A
22	26	89.7	168	US-10-767-701-39988	Sequence 39988, A
23	26	89.7	221	US-10-094-749-2980	Sequence 2980, Ap
24	26	89.7	238	US-09-880-748-2053	Sequence 2053, Ap
25	26	89.7	238	US-10-293-418-2053	Sequence 2053, Ap
26	26	89.7	304	US-10-282-122A-45565	Sequence 45565, A
27	26	89.7	370	US-09-738-626-3768	Sequence 3768, Ap
28	26	89.7	370	US-09-738-626-3768	Sequence 3768, Ap
29	26	89.7	420	US-10-425-114-54469	Sequence 54469, A
30	26	89.7	542	US-10-425-114-54414	Sequence 54114, A
31	26	89.7	544	US-09-919-039-270	Sequence 270, App
32	26	89.7	591	US-10-618-941-125	Sequence 125, App
33	26	89.7	619	US-10-424-599-155796	Sequence 155796, A
34	26	89.7	659	US-10-369-493-8287	Sequence 8287, Ap
35	26	89.7	678	US-10-369-493-19452	Sequence 19452, A
36	26	89.7	801	US-10-282-122A-58937	Sequence 58937, A
37	26	89.7	886	US-10-424-599-165676	Sequence 165676, A
38	26	89.7	929	US-10-060-841-3	Sequence 3, Appl
39	26	89.7	929	US-10-288-798-11	Sequence 11, Appl
40	26	89.7	929	US-10-362-892-11	Sequence 11, Appl
41	26	89.7	929	US-10-618-941-105	Sequence 105, App
42	26	89.7	929	US-09-972-656-38	Sequence 38, Appl
43	26	86.2	5	US-10-320-094-5	Sequence 5, Appl
44	26	86.2	5	US-10-399-701-4	Sequence 4, Appl
45	26	86.2	9	US-10-884-830-308	Sequence 308, App

ALIGNMENTS

RESULT 1
US-10-468-543-91
Sequence 91, Application US/10468543
Publication No. US20040091938A1
GENERAL INFORMATION:
APPLICANT: Irimura, Tatsuro
APPLICANT: Matsumoto, Mariko
APPLICANT: Yim, Mijung
APPLICANT: Ono, Takashi
TITLE OF INVENTION: Lectins for Analyzing Sugar Chains and Method of Using the Same
FILE REFERENCE: 03-786
CURRENT APPLICATION NUMBER: US/10/468, 543
CURRENT FILING DATE: 2003-08-20
PRIOR APPLICATION NUMBER: JP 2001-044221
PRIOR FILING DATE: 2001-02-20
NUMBER OF SEQ ID NOS: 95
SOFTWARE: PatentIn version 3.1
SEQ ID NO 91
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Generated from randomly recombinant DNA part of MAH.
US-10-468-543-91

Query Match 100.0%; Score 29; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.5; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

Cy 1 TYAMH 5
DB 2 TYAMH 6

RESULT 2
US-10-424-599-231272

Sequence 231272, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 231272
LENGTH: 151
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(151)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_50860C.1.pep
US-10-424-599-231272

Query Match 100.0%; Score 29; DB 15; Length 151;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TYAMH 5
Db 120 TYAMH 124

RESULT 3
US-10-282-122A-52731
Sequence 52731, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zykkind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 52731
LENGTH: 206
TYPE: PRT
ORGANISM: Clostridium botulinum
US-10-282-122A-52731

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Best Local Similarity 100.0%; Pred. No. 92;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TYAMH 5
Db 30 TYAMH 34

RESULT 4
US-10-369-493-9985
Sequence 9985, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 9985
LENGTH: 278
TYPE: PRT
ORGANISM: magnetite-containing magnetic coccus
US-10-369-493-9985

Query Match 100.0%; Score 29; DB 15; Length 278;
Best Local Similarity 100.0%; Pred. No. 1,2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TYAMH 5
Db 220 TYAMH 224

RESULT 5
US-10-262-083-2
Sequence 2, Application US/10262083
Publication No. US20030170670A1
GENERAL INFORMATION:
APPLICANT: KOIBUCHI, Kyoko
APPLICANT: MAGASAKI, Hiroaki
APPLICANT: YUNASA, Aki
APPLICANT: KATAMOKA, Jiro
APPLICANT: KITAMOTO, Katsuhiko
TITLE OF INVENTION: A No. US20030170670A1el Glutaminase, its Gene and a Method of Pro
FILE REFERENCE: 199438US-8222-10-0-PCF
CURRENT APPLICATION NUMBER: US/10/262,083
CURRENT FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: US/09/674,507
PRIOR FILING DATE: 2000-11-15
PRIOR APPLICATION NUMBER: JP 10/134080
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: JP 10/258974
PRIOR FILING DATE: 1998-09-11

; PRIOR APPLICATION NUMBER: JP 10/292443
 ; PRIOR FILING DATE: 1998-10-14
 ; PRIOR APPLICATION NUMBER: JP 11/89157
 ; PRIOR FILING DATE: 1999-03-30
 ; PRIOR APPLICATION NUMBER: PCT/JP99/02455
 ; PRIOR FILING DATE: 1999-05-12
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 690
 ; TYPE: PRT
 ; ORGANISM: Aspergillus oryzae
 ; US-10-262-083-2

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 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
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 Db 423 TYAMH 427

RESULT 6
 ; Sequence 18, Application US/10262083
 ; Publication No. US20030170670A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KOIBUCHI, Kyoto
 ; APPLICANT: NAGASAKI, Hiroaki
 ; APPLICANT: YUASA, Aki
 ; APPLICANT: KATAOKA, Jiro
 ; APPLICANT: KITAMOTO, Katsuhiko
 ; TITLE OF INVENTION: A NO. US20030170670A1 Glutaminase, its Gene and a Method of Pro
 ; FILE REFERENCE: 19943805-8222-10-0-PCT
 ; CURRENT FILING DATE: 2002-10-02
 ; PRIOR APPLICATION NUMBER: US/10/262,083
 ; PRIOR FILING DATE: 2000-11-15
 ; PRIOR APPLICATION NUMBER: JP 10/134080
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: JP 10/258974
 ; PRIOR FILING DATE: 1998-09-11
 ; PRIOR APPLICATION NUMBER: JP 10/292443
 ; PRIOR FILING DATE: 1998-10-14
 ; PRIOR APPLICATION NUMBER: JP 11/89157
 ; PRIOR FILING DATE: 1999-03-30
 ; PRIOR APPLICATION NUMBER: PCT/JP99/02455
 ; PRIOR FILING DATE: 1999-05-12
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 18
 ; LENGTH: 690
 ; TYPE: PRT
 ; ORGANISM: Aspergillus oryzae
 ; US-10-262-083-18

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 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 423 TYAMH 427

RESULT 7
 ; Sequence 35, Application US/10468543
 ; Publication No. US20040091938A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Iitamura, Tatsuro
 ; APPLICANT: Matsumoto, Mariko

; APPLICANT: Yim, Mijung
 ; APPLICANT: Ono, Takashi
 ; TITLE OF INVENTION: Lectins for Analyzing Sugar Chains and Method of Using the Same
 ; FILE REFERENCE: 03-786
 ; CURRENT APPLICATION NUMBER: US/10/468,543
 ; PRIOR FILING DATE: 2003-08-20
 ; PRIOR APPLICATION NUMBER: JP 2001-044221
 ; PRIOR FILING DATE: 2001-02-20
 ; NUMBER OF SEQ ID NOS: 95
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 35
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Generated from randomly recombinant DNA part of MAH.
 ; US-10-468-543-35

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 Db 2 TYALH 6

RESULT 8
 ; Sequence 217913, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kovalic David K
 ; APPLICANT: Zhou Yihua
 ; APPLICANT: Cao Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(53223)B
 ; CURRENT APPLICATION NUMBER: US/10/424,599
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 285684
 ; SEQ ID NO 217913
 ; LENGTH: 59
 ; TYPE: PRT
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_38802C.1.pcp
 ; US-10-424-599-217913

Query Match 89.7%; Score 26; DB 15; Length 59;
 Best Local Similarity 80.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
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 Db 10 TYSMH 14

RESULT 9
 ; Sequence 188252, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa Thomas J
 ; APPLICANT: Kovalic David K
 ; APPLICANT: Zhou Yihua
 ; APPLICANT: Cao Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(53223)B
 ; CURRENT APPLICATION NUMBER: US/10/424,599
 ; CURRENT FILING DATE: 2003-04-28

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; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 186252
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_141004C.1.pep
US-10-424-599-188252

Query Match      89.7%; Score 26; DB 15; Length 60;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 TYAMH 5
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Db      46 TYSMH 50

RESULT 10
US-10-437-963-109084
; Sequence 109084, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 109084
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_13276C.1.pap
US-10-437-963-109084

Query Match      89.7%; Score 26; DB 16; Length 61;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 TYAMH 5
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Db      43 TYALH 47

RESULT 11
US-09-864-761-44407
; Sequence 44407, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wenheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
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; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
; SEQ ID NO 44407
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC005020.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.83
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.58
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 13
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.7
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.5
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.62
; OTHER INFORMATION: SWISSPROT HIT: P20815, EVALUATE 3.00e-35
; OTHER INFORMATION: EST_HUMAN HIT: A1861809.1, EVALUATE 2.00e-34
US-09-864-761-44407

Query Match      89.7%; Score 26; DB 9; Length 67;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 TYAMH 5
        |||:|
Db      48 TYALH 52

RESULT 12
US-10-424-599-190876
; Sequence 190876, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
```

SEQ ID NO 190876
LENGTH: 67
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_14380C.1.pep
US-10-424-599-190876

Query Match 89.7%; Score 26; DB 15; Length 67;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TYAMH 5
|||:|
Db 25 TYALH 29

RESULT 13
US-10-424-599-192746
Sequence 192746, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 192746
LENGTH: 73
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_16071C.1.pep
US-10-424-599-192746

Query Match 89.7%; Score 26; DB 15; Length 73;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TYAMH 5
|||:|
Db 12 TYSMH 16

RESULT 14
US-10-424-599-205833
Sequence 205833, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 205833
LENGTH: 73
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_27896C.1.pep
US-10-424-599-205833

Query Match 89.7%; Score 26; DB 15; Length 73;

Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TYAMH 5
|||:|
Db 22 TYSMH 26

RESULT 15
US-10-424-599-245586
Sequence 245586, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 245586
LENGTH: 77
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_63796C.1.pep
US-10-424-599-245586

Query Match 89.7%; Score 26; DB 15; Length 77;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TYAMH 5
|||:|
Db 12 TYALH 16

RESULT 16
US-09-764-846-193
Sequence 193, Application US/09764846
Patent No. US20020102638A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT12
CURRENT APPLICATION NUMBER: US/09/764,846
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 348
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 193
LENGTH: 79
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (8)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-846-193

Query Match 89.7%; Score 26; DB 9; Length 79;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TYAMH 5
|||:|
Db 74 TYALH 78

RESULT 17

US-10-091-483-193
; Sequence 193, Application US/10091483
; Publication No. US20030049650A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT212C1
; CURRENT APPLICATION NUMBER: US/10/091,483
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 348
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 193
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (8)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-091-483-193

Query Match 89.7%; Score 26; DB 14; Length 79;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
|||:
Db 74 TYALH 78

RESULT 18
US-10-767-701-48571
; Sequence 48571, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(5353)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 48571
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3481-046-Q6-K1-A9.pep
US-10-767-701-48571

Query Match 89.7%; Score 26; DB 16; Length 85;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
|||:
Db 1 TYALH 5

RESULT 19
US-10-424-599-214193
; Sequence 214193, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 214193
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_35443C.1.pep
US-10-424-599-214193

Query Match 89.7%; Score 26; DB 15; Length 98;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
|||:
Db 57 TYALH 61

RESULT 20
US-10-424-599-227653
; Sequence 227653, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 227653
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_4759C.1.pep
US-10-424-599-227653

Query Match 89.7%; Score 26; DB 15; Length 137;
Best Local Similarity 80.0%; Pred. No. 3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
|||:
Db 16 TYALH 20

RESULT 21
US-10-424-599-143644
; Sequence 143644, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 143644
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:

NAME/KEY: unsure
LOCATION: (1)..(141)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_100724C.1.pep
US-10-424-599-143644

Query Match 89.7%; Score 26; DB 15; Length 141;
Best Local Similarity 80.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 83 TYALH 87

RESULT 22
US-10-767-701-39988
Sequence 39988, Application US/10767701
Publication No. US20040172684A1
GENERAL INFORMATION:
APPLICANT: Kovacic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 39988
LENGTH: 168
TYPE: PRT
ORGANISM: Sorghum bicolor
FEATURE:
OTHER INFORMATION: Clone ID: SORBI-28WAY03-C3913_1.pep
US-10-767-701-39988

Query Match 89.7%; Score 26; DB 16; Length 168;
Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 77 TYALH 81

RESULT 23
US-10-094-749-2980
Sequence 2980, Application US/10094749
Publication No. US20030219741A1
GENERAL INFORMATION:
APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YURI
APPLICANT: OTSUKA, KAORU
APPLICANT: NAGAI, KEIICHI
APPLICANT: IRIE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHICO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOKYUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749

CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2980
LENGTH: 221
TYPE: PRT
ORGANISM: Homo sapiens
US-10-094-749-2980

Query Match 89.7%; Score 26; DB 15; Length 221;
Best Local Similarity 80.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 162 TYALH 166

RESULT 24
US-09-880-748-2053
Sequence 2053, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2053
LENGTH: 238
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-2053

Query Match 89.7%; Score 26; DB 10; Length 238;
Best Local Similarity 80.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 31 TYSMH 35

RESULT 25
US-10-293-418-2053
Sequence 2053, Application US/10293418
Publication No. US20030223996A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523P2
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 2053
LENGTH: 238
TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-418-2053

Query Match 89.7%; Score 26; DB 15; Length 238;
Best Local Similarity 80.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TYAMH 5
Db 31 TYAMH 35

RESULT 26
US-10-282-122A-45565
Sequence 45565, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Hagelbeck, Robert
APPLICANT: Ohlsen, Karl
APPLICANT: Zykied, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 45565

LENGTH: 304
TYPE: PRT
ORGANISM: Bacillus anthracis
US-10-282-122A-45565

Query Match 89.7%; Score 26; DB 15; Length 304;
Best Local Similarity 80.0%; Pred. No. 6.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TYAMH 5
Db 299 TYAMH 303

RESULT 27
US-09-738-626-3768
Sequence 3768, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 3768
LENGTH: 370
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-09-738-626-3768

Query Match 89.7%; Score 26; DB 9; Length 370;
Best Local Similarity 80.0%; Pred. No. 7.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TYAMH 5
Db 172 TYAMH 176

RESULT 28
US-09-738-626-5177
Sequence 5177, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125

;; CURRENT APPLICATION NUMBER: US/09/738,626
;; CURRENT FILING DATE: 2000-12-18
;; PRIOR APPLICATION NUMBER: JP 99/377484
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: JP 00/159162
;; PRIOR FILING DATE: 2000-04-07
;; PRIOR APPLICATION NUMBER: JP 00/280988
;; PRIOR FILING DATE: 2000-08-03
;; NUMBER OF SEQ ID NOS: 7059
;; SOFTWARE: PatentIn ver. 3.0
;; SEQ ID NO 5177
;; LENGTH: 370
;; TYPE: PRT
;; ORGANISM: Corynebacterium glutamicum
US-09-738-626-5177

Query Match 89.7%; Score 26; DB 9; Length 370;
Best Local Similarity 80.0%; Pred. No. 7.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 172 TYALH 176

RESULT 29
US-10-425-114-54469
; Sequence 54469, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 54469
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4651-038-H5_F11.pep
US-10-425-114-54469

Query Match 89.7%; Score 26; DB 15; Length 420;
Best Local Similarity 80.0%; Pred. No. 8.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 361 TYALH 365

RESULT 30
US-10-425-114-54114
; Sequence 54114, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53313)B

;; CURRENT APPLICATION NUMBER: US/10/425,114
;; CURRENT FILING DATE: 2003-04-28
;; NUMBER OF SEQ ID NOS: 73128
;; SEQ ID NO 54114
;; LENGTH: 542
;; TYPE: PRT
;; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4119-111-F11_F11.pep
US-10-425-114-54114

Query Match 89.7%; Score 26; DB 15; Length 542;
Best Local Similarity 80.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 483 TYALH 487

RESULT 31
US-09-919-039-270
; Sequence 270, Application US/09919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 270
; LENGTH: 544
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 4113161CD1
US-09-919-039-270

Query Match 89.7%; Score 26; DB 10; Length 544;
Best Local Similarity 80.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 485 TYALH 489

RESULT 32
US-10-618-941-125
; Sequence 125, Application US/10618941
; Publication No. US2004019792A1
; GENERAL INFORMATION:
; APPLICANT: WHITE, DAVID
; APPLICANT: MANNING, GERARD
; APPLICANT: CAENEPEEL, SEAN
; TITLE OF INVENTION: NOVEL KINASES
; FILE REFERENCE: 034536-0321
; CURRENT APPLICATION NUMBER: US/10/618,941
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: 60/395,632
; PRIOR FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 125
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-618-941-125

Query Match 89.7%; Score 26; DB 16; Length 591;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 TYAMH 5
DB 532 TYALH 536

RESULT 33
US-10-424-599-155796
; Sequence 155796, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 155796
; LENGTH: 619
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_111703C.1.pep
US-10-424-599-155796

Query Match 89.7%; Score 26; DB 15; Length 619;
Best Local Similarity 80.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 TYAMH 5
DB 242 TYSMH 246

RESULT 34
US-10-369-493-8287
; Sequence 8287, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 8287
; LENGTH: 659
; TYPE: PRT
; ORGANISM: Thermobifida fusca
US-10-369-493-8287

Query Match 89.7%; Score 26; DB 15; Length 659;
Best Local Similarity 80.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 TYAMH 5
DB 354 TYALH 358

RESULT 35
US-10-369-493-19452
; Sequence 19452, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 19452
; LENGTH: 678
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-10-369-493-19452

Query Match 89.7%; Score 26; DB 15; Length 678;
Best Local Similarity 80.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 TYAMH 5
DB 515 TYALH 519

RESULT 36
US-10-282-122A-58937
; Sequence 58937, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zvekind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: EITRA 034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636

;; PRIOR FILING DATE: 2001-02-09
;; PRIOR APPLICATION NUMBER: 60/269,308
;; PRIOR FILING DATE: 2001-02-16
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 78614
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO: 58937
;; LENGTH: 801
;; TYPE: PRT
;; ORGANISM: Helicobacter pylori
US-10-282-122A-58937

Query Match 89.7%; Score 26; DB 15; Length 801;
Best Local Similarity 80.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
|||:
Db 95 TYSMH 99

RESULT 37
US-10-424-599-165676
;; Sequence 165676, Application US/10424599
;; Publication No. US20040031072A1
;; GENERAL INFORMATION:
;; APPLICANT: La Rosa Thomas J
;; APPLICANT: Kovalic David K
;; APPLICANT: Zhou Yihua
;; APPLICANT: Cao Yongwei
;; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
;; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
;; FILE REFERENCE: 38-21(53223)B
;; CURRENT FILING DATE: 2003-04-28
;; NUMBER OF SEQ ID NOS: 285684
;; SEQ ID NO 165676
;; LENGTH: 886
;; TYPE: PRT
;; ORGANISM: Glycine max
;; FEATURE:
;; NAME/KEY: unsure
;; LOCATION: (1)..(886)
;; OTHER INFORMATION: unsure at all Xaa locations
;; FEATURE:
;; OTHER INFORMATION: Clone ID: PAT_MFT3847_120620C.1.pep
US-10-424-599-165676

Query Match 89.7%; Score 26; DB 15; Length 886;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
|||:
Db 158 TYALH 162

RESULT 38
US-10-060-841-3
;; Sequence 3, Application US/10060841
;; Publication No. US20020162127A1
;; GENERAL INFORMATION:
;; APPLICANT: Gu, Yizhong
;; APPLICANT: Nguyen, Chung-Thong
;; TITLE OF INVENTION: A HUMAN PROTEIN KINASE DOMAIN-CONTAINING PROTEIN
;; FILE REFERENCE: PB0179
;; CURRENT FILING DATE: 2002-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668

;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 09/864,761
;; PRIOR FILING DATE: 2001-05-23
;; PRIOR APPLICATION NUMBER: US 60/335,941
;; PRIOR FILING DATE: 2001-10-24
;; NUMBER OF SEQ ID NOS: 37
;; SOFTWARE: Aecmca Sequence Listing Engine
;; SEQ ID NO: 3
;; LENGTH: 929
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-060-841-3

Query Match 89.7%; Score 26; DB 13; Length 929;
Best Local Similarity 80.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
|||:
Db 249 TYALH 253

RESULT 39
US-10-288-798-11
;; Sequence 11, Application US/10288798
;; Publication No. US20030207299A1
;; GENERAL INFORMATION:
;; APPLICANT: BANDMAN, Olga; NGUYEN, Daniel B;
;; APPLICANT: WALIA, Nartinder K.; HARLITA, April J.A.;
;; APPLICANT: YAO, Monique G.; GANDHI, Ameena R.;
;; APPLICANT: GURURAJAN, Rajagopal; DING, Li;
;; APPLICANT: PATTERSON, Chandra; YUE, Henry;
;; APPLICANT: BAUGHN, Mariah R.; TRIBOULEY, Catherine M.;
;; APPLICANT: THORNTON, Michael; ELLIOTT, Vicki S.;
;; APPLICANT: LU, Yan; TSON, Craig H.;
;; APPLICANT: AU-YOUNG, Janice; TRANG, Y. Tom;
;; APPLICANT: AZIMZAI, Yalda; BURRILL, John D.;
;; APPLICANT: MARCUS, Gregory A.; ZINGLER, Kurt A.;
;; APPLICANT: LU, Dzung Alina M.; LAL, Preeti G.;
;; APPLICANT: RAMKUMAR, Jayalaxmi; WARREN, Bridget A.;
;; APPLICANT: KEARNEY, Liam; POLICKY, Jennifer L.;
;; APPLICANT: THANGAVELOU, Kavitha; BURFORD, Neil
;; TITLE OF INVENTION: HUMAN KINASES
;; FILE REFERENCE: PI-0209 USA
;; CURRENT APPLICATION NUMBER: US/10/288,798
;; CURRENT FILING DATE: 2002-11-01
;; PRIOR APPLICATION NUMBER: PCT/US01/27219
;; PRIOR FILING DATE: 2001-08-31
;; PRIOR APPLICATION NUMBER: US 60/240,542
;; PRIOR FILING DATE: 2000-10-13
;; PRIOR APPLICATION NUMBER: US 60/236,389
;; PRIOR FILING DATE: 2000-10-06
;; PRIOR APPLICATION NUMBER: US 60/236,499
;; PRIOR FILING DATE: 2000-09-29
;; PRIOR APPLICATION NUMBER: US 60/234,902
;; PRIOR FILING DATE: 2000-09-22
;; PRIOR APPLICATION NUMBER: US 60/232,654
;; PRIOR FILING DATE: 2000-09-14
;; PRIOR APPLICATION NUMBER: US 60/231,357
;; PRIOR FILING DATE: 2000-09-08
;; PRIOR APPLICATION NUMBER: US 60/229,873
;; PRIOR FILING DATE: 2000-08-31
;; NUMBER OF SEQ ID NOS: 48
;; SOFTWARE: PERL Program
;; SEQ ID NO 11
;; LENGTH: 929
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc feature
;; OTHER INFORMATION: Incyte ID No. US20030207299A1 7481989CD1
US-10-288-798-11

Query Match 89.7%; Score 26; DB 15; Length 929;
Best Local Similarity 80.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
|||:
249 TYALH 253

RESULT 40
US-10-362-892-11
; Sequence 11, Application US/10362892
; Publication No. US20040038881A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; BANDMAN, Olga
; APPLICANT: NGUYEN, Danielle B.; WALIA, Nardinder K.
; APPLICANT: HAPALIA, April J.A.; YAO, Monique G.
; APPLICANT: GANDHI, Ameena R.; GURURAJAN, Rajagopal
; APPLICANT: DING, Li; PATTERSON, Chandra S.
; APPLICANT: YUE, Henry; BAUGHN, Mariah R.
; APPLICANT: TRIBOULET, Catherine M.; THORNTON, Michael B.
; APPLICANT: ELIOTT, Vicki S.; LU, Yan
; APPLICANT: ISON, Craig H.; AU-YOUNG, Janice K.
; APPLICANT: TANG, Y. Tom; AZIMZAI, Yalda
; APPLICANT: BURRILL, John D.; MARCUS, Gregory A.
; APPLICANT: ZINGLER, Kurt A.; LU, Dyung Aina M.
; APPLICANT: LAI, Preeti G.; RAMKUMAR, Jayalaxmi
; APPLICANT: WARREN, Bridget A.; KEARNEY, Liam
; APPLICANT: POLICKY, Jennifer L.; THANGAVERLU, Kavitha
; APPLICANT: BUREFORD, Neil
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PF-0209 USN
; CURRENT APPLICATION NUMBER: US/10/362, 892
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: PCT/US01/27219
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229, 873
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US 60/231, 357
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: US 60/232, 654
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US 60/234, 902
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US 60/236, 499
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 60/238, 389
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 60/240, 542
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PERL Program
; SEQ ID NO 11
; LENGTH: 929
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID NO. US20040038881A1 7481989CD1
US-10-362-892-11

Query Match 89.7%; Score 26; DB 15; Length 929;
Best Local Similarity 80.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
|||:
249 TYALH 253

Search completed: March 31, 2005, 12:46:06
Job time : 28.9688 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: March 31, 2005, 11:51:19 ; Search time 7.10938 Seconds
(without alignments)
67.669 Million cell updates/sec

Title: US-10-614-959-10

Perfect score: 29

Sequence: 1 TYAMH 5

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR_79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	100.0	122	1 M3HUGA	Ig heavy chain V-I
2	29	100.0	138	2 A35676	Ig heavy chain pre
3	29	100.0	196	2 D71184	adenylate kinase (
4	29	100.0	249	2 B83290	conserved hypotet
5	29	100.0	1151	2 H71347	hypothetical prote
6	29	100.0	1377	2 I54632	tsh protein - Esch
7	26	89.7	95	2 T34500	hypothetical prote
8	26	89.7	196	2 I50675	retinol-binding pr
9	26	89.7	213	2 H86403	hypothetical prote
10	26	89.7	228	2 E90215	conserved hypotet
11	26	89.7	228	2 T22924	hypothetical prote
12	26	89.7	242	2 AD1165	B. subtilis YVPB p
13	26	89.7	242	2 AD1524	B. subtilis YVPB p
14	26	89.7	501	2 A29487	cytochrome P450 3A
15	26	89.7	501	2 A34236	cytochrome P450 3A
16	26	89.7	502	1 A34101	cytochrome P450 3A
17	26	89.7	504	2 A25222	cytochrome P450 3A
18	26	89.7	609	2 B82423	hypothetical prote
19	26	89.7	723	2 A84425	hypothetical prote
20	26	89.7	801	2 B64679	paralysed flagella
21	26	89.7	852	1 GNLJGA	pol polyprotein -
22	26	89.7	852	1 GNLJGB	pol polyprotein -
23	26	89.7	852	2 S29358	fix23-3 protein -
24	26	89.7	966	2 S18955	probable helicase
25	26	89.7	1265	2 T84517	hypothetical prote
26	26	89.7	1385	2 T21706	integumentary muc
27	26	89.7	1506	2 T30886	polypeptide syntha
28	26	89.7	6260	2 T30228	Ig heavy chain V r
29	25	86.2	35	2 S26887	Ig heavy chain V r

30	25	86.2	35	2 S46473	Ig heavy chain V r
31	25	86.2	94	2 P10120	Ig heavy chain V-I
32	25	86.2	96	2 S17609	Ig heavy chain V r
33	25	86.2	97	2 S10385	Ig heavy chain V r
34	25	86.2	97	2 S26885	Ig heavy chain V r
35	25	86.2	97	2 S26886	Ig heavy chain V r
36	25	86.2	98	2 S29546	Ig heavy chain V r
37	25	86.2	102	2 S53076	probable membrane
38	25	86.2	104	2 P11653	Ig heavy chain V r
39	25	86.2	109	2 P11653	Ig heavy chain V r
40	25	86.2	109	2 P11646	Ig heavy chain V r
41	25	86.2	109	2 P11644	Ig heavy chain V r
42	25	86.2	111	2 P11645	Ig heavy chain V r
43	25	86.2	113	2 E33936	Ig heavy chain V r
44	25	86.2	114	2 P11667	Ig heavy chain V r
45	25	86.2	114	2 S46390	Ig heavy chain V r

ALIGNMENTS

RESULT 1

M3HUGA
Ig heavy chain V-III region (Ga) - human (tentative sequence)

C:Species: Homo sapiens (man)

C:Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 09-Jul-2004

C:Accession: A02052

R:Florent, G., Lehman, D., Putnam, F.W.

Biochemistry 13, 2482-2498, 1974

A:Title: The switch point in mu heavy chains of human IgM immunoglobulins.

F:15-98/Domain: immunoglobulin homology <IMM>

A:Accession: A02052

A:Molecule type: protein

A:Residues: 1-122 <F10>

A:Cross-references: UNIPROT:P01769

C:Comment: This chain was isolated from a Waldenström's macroglobulin.

C:Genetics:

A:Gene: GDB:IGHV@

A:Cross-references: GDB:128528; OMIM:147070

A:Map position: 14q32.33-14q32.33

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin; pyroglyutamic acid

F:1/Modified site: pyroglutamic acid (Gln) #status experimental

F:22-96/Disulfide bonds: #status predicted

Query Match Score 29; DB 1; Length 122;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
DB 31 TYAMH 35

RESULT 2

A35676
Ig heavy chain precursor V-D-J region - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 28-Sep-1990 #sequence_revision 28-Sep-1990 #text_change 23-Jul-1999

C:Accession: A35676

Mol: Cell. Biol. 10, 3690-3699, 1980

A:Title: Immunoglobulin D switching can occur through homologous recombination in human

A:Reference number: A35676; MUID:90287160; PMID:2113175

A:Accession: A35676

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-138 <WHI>

A:Cross-references: GB:M38066; NID:g185466; PIDN:AA52974.1; PID:g553407

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 29; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 50 TYAMH 54

RESULT 3

D11184
adenylate kinase (EC 2.7.4.3) PH1753 [similarity] - Pyrococcus horikoshii
C/Species: Pyrococcus horikoshii
C/Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C/Accession: D11184
R/Kawarayashi, Y.; Sawada, M.; Horikawa, H.; Halkawa, Y.; Hino, Y.; Yamamoto, S.; Sekit
M.; Ohtuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5: 55-76, 1998
A/Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
A/Reference number: A7100; MUID:98344137; PMID:9679194
A/Accession: D11184
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-196 <KAM>
A/Cross-references: UNIPROT:O59443; GB:AF000007; NID:g3236134; PIDN:BAA30867.1; PID:g325
A/Experimental source: strain 073
A/Note: this accession replaces an interim accession for a sequence replaced by GenBank
C/Genetics:
A/Gene: PH1753
C/Keywords: phosphotransferase

Query Match 100.0%; Score 29; DB 2; Length 196;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 157 TYAMH 161

RESULT 4

B83290
conserved hypothetical protein PA2847 [imported] - Pseudomonas aeruginosa (strain PA01)
C/Species: Pseudomonas aeruginosa
C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C/Accession: B83290
R/Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lim,
J.; Lory, S.; Olson, M.V.
Nature 406: 959-964, 2000
A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A/Reference number: A82950; MUID:20437337; PMID:10984043
A/Accession: B83290
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-249 <STD>
A/Cross-references: UNIPROT:Q9HZZ6; GB:AE004711; GB:AE004091; NID:g9948927; PIDN:AA60623
A/Experimental source: strain PA01
C/Genetics:
A/Gene: PA2847

Query Match 100.0%; Score 29; DB 2; Length 249;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 192 TYAMH 196

RESULT 5

H71347

hypothetical protein TP0245 - syphilis spirochete
C/Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C/Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C/Accession: H71347
R/Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uetzerack, T.; McDo
rthey, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281: 375-388, 1998
A/Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A/Reference number: A71250; MUID:98332770; PMID:9665876
A/Accession: H71347
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-1151 <COL>
A/Cross-references: UNIPROT:O83273; GB:AE001206; GB:AE000520; NID:g3322514; PIDN:AA6523;
A/Experimental source: strain Nichols
C/Genetics:
A/Gene: TP0245
C/Superfamily: syphilis spirochete hypothetical protein TP0245

Query Match 100.0%; Score 29; DB 2; Length 1151;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 700 TYAMH 704

RESULT 6

I54632
tsh protein - Escherichia coli
C/Species: Escherichia coli
C/Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
C/Accession: I54632
R/Providence, D.L.; Curtiss, R.
Infect. Immun. 62: 1369-1380, 1994
A/Title: Isolation and characterization of a gene involved in hemagglutination by an avi
A/Reference number: I54632; MUID:94178945; PMID:8132344
A/Accession: I54632
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1377 <RES>
A/Cross-references: UNIPROT:Q47692; GB:I27423; NID:g469235; PIDN:AAA24698.1; PID:g469236
C/Superfamily: IGA-specific metalloendopeptidase

Query Match 100.0%; Score 29; DB 2; Length 1377;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 TYAMH 5

RESULT 7

T34500
hypothetical protein ZK1248.17 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C/Accession: T34500
R/Latrelle, P.
submitted to the EMBL Data Library, June 1995
A/Description: The sequence of C. elegans cosmid ZK1248.
A/Reference number: Z21534
A/Accession: T34500
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-95 <LAT>
A/Cross-references: UNIPROT:Q23428; EMBL:U29244; PIDN:AACT1098.1; GSPDB:GNO0020; CESP:ZK
A/Experimental source: strain Bristol N2; clone ZK1248
C/Genetics:
A/Gene: CESP:ZK1248.17

A:Map position: 2
C:Superfamily: Caenorhabditis elegans major sperm protein

Query Match 89.7%; Score 26; DB 2; Length 95;
Best Local Similarity 80.0%; Pred. No. 32;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 12 TYSMH 16

RESULT 8

150675
retinol-binding protein precursor - chicken

C:Species: Gallus gallus (chicken)

C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004

C:Accession: 150675; S42887

R:Vieira, A.V.; Kuchler, K.; Schneider, W.J.

DNA Cell Biol. 14, 403-410, 1995

A:Title: Retinol in avian oogenesis: molecular properties of the carrier protein.

A:Reference number: 150675; PMID:95267350; PMID:7748490

A:Accession: 150675

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Residues: 1-196 <VIR>

A:Cross-references: UNIPROT:P41263; EMBL:X77960; NID:g457778; PIDN:CAA54922.1; PID:g4577

C:Genetics:

A:Gene: RBP

C:Superfamily: lipocalin; lipocalin homology

F:1-21/Domain: signal sequence #status predicted <SIG>

F:36-195/Domain: lipocalin homology <LIP>

F:25-181,91-195,141-150/Disulfide bonds: #status predicted

Query Match 89.7%; Score 26; DB 2; Length 196;

Best Local Similarity 80.0%; Pred. No. 67;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 134 TYALH 138

RESULT 9

H86403
hypothetical protein F28U5.12 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C:Accession: H86403

R:Theologis, A.; Becker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewart, K.;

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luoro, J.S.; Malt, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Xu, G.; Frazer, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A66141; PMID:21016719; PMID:11130712

A:Accession: H86403

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-213 <STO>

A:Cross-references: UNIPROT:Q9CGN1; GB:AE005172; NID:g10999924; PIDN:AA626064.1; GSPDB:G

A:Genetics:

A:Map position: 1

Query Match 89.7%; Score 26; DB 2; Length 213;
Best Local Similarity 80.0%; Pred. No. 73;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5

Db 202 TYALH 206

RESULT 10

E30215
conserved hypothetical protein [imported] - Sulfolobus solfataricus

C:Species: Sulfolobus solfataricus

C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004

C:Accession: E90215

R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aweez, M.J.; Chan-

Jong, I.; Jeffries, A.C.; Kozera, C.D.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.

aret, R.A.; Ragan, M.A.; Sengen, C.W.; Van der Oost, J.

submitted to GenBank, April 2001

A:Description: Sulfolobus solfataricus complete genome.

A:Reference number: A99139

A:Accession: E90215

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-222 <KUR>

A:Cross-references: UNIPROT:Q9UX67; GB:AE006641; NID:g13813846; PIDN:AAK40980.1; GSPDB:G

C:Genetics:

A:Gene: SS00678

C:Superfamily: hypothetical protein M0570

Query Match 89.7%; Score 26; DB 2; Length 222;
Best Local Similarity 80.0%; Pred. No. 76;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 14 TYALH 18

RESULT 11

T22924
hypothetical protein F58B6.8 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T22924

R:McMurray, A.

submitted to the EMBL Data Library, April 1996

A:Reference number: T22924

A:Accession: T22924

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-228 <WIL>

A:Cross-references: UNIPROT:Q20984; EMBL:Z70754; PIDN:CAA94778.1; GSPDB:GN00023; CESP:F5

A:Experimental source: clone F58B6

C:Genetics:

A:Gene: CESP:F58B6.8

A:Map position: 5

A:Introns: 153/2

C:Superfamily: Caenorhabditis elegans hypothetical protein Y75B12A.2

Query Match 89.7%; Score 26; DB 2; Length 228;
Best Local Similarity 80.0%; Pred. No. 78;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 177 TYALH 181

RESULT 12

AD1165
B. subtilis YvpB protein homolog lmo0724 [imported] - Listeria monocytogenes (strain EGD

C:Species: Listeria monocytogenes

C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

C:Accession: AD1165

R:Glaeser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker,

; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurge, O.; Entian, K.D.; Fahn, H.

D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001
 A:Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
 ok, C.; Schlueder, T.; Simoes, N.; Tietze, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,
 A:Title: Comparative genomics of *Listeria* species.
 A:Reference number: AB1077; MUID:21537279; PMID:11679669
 A:Accession: AD1524
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-242 <GLA>
 A:Cross-references: UNIPROT:Q8Y918; GB:NC_003210; PIDN:CAC98802.1; PID:g16410113; GSPDB:
 A:Experimental source: strain ESD-e
 C:Genetics:
 A:Gene: lmo0724
 C:Superfamily: Bacillus subtilis hypothetical protein yvpB

Query Match 89.7%; Score 26; DB 2; Length 242;
 Best Local Similarity 80.0%; Pred. No. 83;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 TYAMH 5
 |||:
 Db 191 TYSMH 195

RESULT 13
 AD1524
 B. subtilis yvpB protein homolog lmo732 [imported] - *Listeria innocua* (strain C11p11262
 C:Species: *Listeria innocua*
 C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
 C:Accession: AD1524
 R:Glaser, P.; Franke, L.; Buchreiser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
 .; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fehrl, H.
 Science 294, 849-852, 2001
 D.; Jones, L.M.; Karet, U.
 A:Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
 ok, C.; Schlueder, T.; Simoes, N.; Tietze, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,
 A:Title: Comparative genomics of *Listeria* species.
 A:Reference number: AB1077; MUID:21537279; PMID:11679669
 A:Accession: AD1524
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-242 <GLA>
 A:Cross-references: UNIPROT:Q92PT0; GB:AL592022; PIDN:CAC95964.1; PID:g16413184; GSPDB:C
 A:Experimental source: strain C11p11262
 C:Genetics:
 A:Gene: lmo732
 C:Superfamily: Bacillus subtilis hypothetical protein yvpB

Query Match 89.7%; Score 26; DB 2; Length 242;
 Best Local Similarity 80.0%; Pred. No. 83;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 TYAMH 5
 |||:
 Db 191 TYSMH 195

RESULT 14
 A29487
 Cytochrome P450 3A6 (version 1) - rabbit
 N:Alternate names: cytochrome P450 3C
 N:Contains: oxidoreductase (EC 1.-.-.-)
 C:Species: *Oryctolagus cuniculus* (domestic rabbit)
 C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
 C:Accession: A29487
 R:Delet, C.; Clair, P.; Dautat, M.; Fort, P.; Blanchard, J.M.; Meurel, P.
 DNA 7, 39-46, 1988
 A:Title: Complete sequence of cytochrome P450 3C cDNA and presence of two mRNA species
 A:Reference number: A29487; MUID:88166352; PMID:3349903
 A:Accession: A29487
 A:Molecule type: mRNA
 A:Residues: 1-501 <DAL>
 A:Cross-references: UNIPROT:P11707; GB:M19139; NID:g165573; PIDN:AAA31430.1; PID:g165574

C:Genetics:
 A:Gene: CYP3A6
 C:Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
 C:Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; monooxygenase;
 F:301-462/Domains: cytochrome P450 homology <P45>
 F:440/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 89.7%; Score 26; DB 2; Length 501;
 Best Local Similarity 80.0%; Pred. No. 17e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 TYAMH 5
 |||:
 Db 396 TYALH 400

RESULT 15
 A34236
 Cytochrome P450 3A6 (version 2) - rabbit
 N:Alternate names: cytochrome P450 3C
 N:Contains: oxidoreductase (EC 1.-.-.-)
 C:Species: *Oryctolagus cuniculus* (domestic rabbit)
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
 C:Accession: A34236
 R:Potenza, C.L.; Pendurthi, U.R.; Strom, D.K.; Tukey, R.H.; Griffin, K.J.; Schwab, G.E.;
 J. Biol. Chem. 264, 16222-16228, 1989
 A:Title: Regulation of the rabbit cytochrome P-450 3C gene. Age-dependent expression and
 A:Reference number: A34236; MUID:89380226; PMID:2777787
 A:Accession: A34236
 A:Molecule type: mRNA
 A:Residues: 1-501 <POT>
 A:Cross-references: UNIPROT:P11707; GB:J05034; NID:g164829; PIDN:AAA31178.1; PID:g164830
 C:Genetics:
 A:Gene: CYP3A6
 C:Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
 C:Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; monooxygenase;
 F:300-462/Domains: cytochrome P450 homology <P45>
 F:440/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 89.7%; Score 26; DB 2; Length 501;
 Best Local Similarity 80.0%; Pred. No. 1.7e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 TYAMH 5
 |||:
 Db 396 TYALH 400

RESULT 16
 A34101
 Cytochrome P450 3A5 - human
 N:Alternate names: cytochrome P450 H1p2
 N:Contains: oxidoreductase (EC 1.-.-.-)
 C:Species: *Homo sapiens* (man)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C:Accession: A34101; S06491; I52302
 R:Aoyama, T.; Yamano, S.; Waxman, D.J.; Lapenson, D.P.; Meyer, U.A.; Fischer, V.; Tyndal
 J. Biol. Chem. 264, 10388-10395, 1989
 A:Title: Cytochrome P-450 hPCN3, a novel cytochrome P-450 IIA gene product that is diff
 DNA-expressed hPCN1 and hPCN3 for the metabolism of steroid hormones and cyclosporine.
 A:Reference number: A34101; MUID:89278095; PMID:2732228
 A:Accession: A34101
 A:Molecule type: mRNA
 A:Residues: 1-502 <AOY>
 A:Cross-references: UNIPROT:P20815; GB:J04813; NID:g181345; PIDN:AAA02993.1; PID:g181346
 R:Schuetz, J.D.; Molowa, D.T.; Guelzian, P.S.
 Arch. Biochem. Biophys. 274, 355-365, 1989
 A:Title: Characterization of a cDNA encoding a new member of the glucocorticoid-responsi
 A:Reference number: S06491; MUID:90025114; PMID:2802615
 A:Accession: S06491
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-304, 'P', 306-317, 'F', 319-323, 'D', 325-376, 'G', 378-502 <SCH>

R;Jounaidi, Y.; Guzelian, P.S.; Maurel, P.; Vilarem, M.J.
Biochem. Biophys. Res. Commun. 205, 1741-1747, 1994
A;Title: Sequence of the 5'-flanking region of CYP3A5: comparative analysis with CYP3A4
A;Reference number: 152302; MUID:95110318; PMID:811260
A;Accession: 152302
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-24 <RES>
A;Cross-references: GB:S74639; NID:9786472; PIDN:RAD14157.1; PID:94261857
C;Genetics:
A;Gene: GDB:CYP3A5
A;Cross-references: GDB:118783
A;Map position: 7q22.1-7q22.1
C;Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
C;Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; monooxygenase;
F:303-463/Domain: cytochrome P450 homology <P45>
F:441/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 89.7%; Score 26; DB 1; Length 502;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 398 TYALH 402

RESULT 17
A25222
Cytochrome P450 3a2 - rat
N;Alternate names: cytochrome P450C2, pregnenolone 16-alpha-carbonitrile-inducible; tes
N;Contents: oxidoreductase (EC 1.-.-.-)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 05-Oct-1988 #sequence revision 05-Oct-1988 #text change 09-Jul-2004
C;Accession: A25222; S27108; S46938; EX0032; EX0034; S30379
R;Gonzalez, F.J.; Song, B.J.; Hardwick, J.P.
Mol. Cell. Biol. 6, 2969-2976, 1986
A;Title: Pregnenolone 16-alpha-carbonitrile-inducible P-450 gene family: gene conversion
A;Reference number: A25222; MUID:87064606; PMID:3785219
A;Accession: A25222
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-504 <GON>
A;Cross-references: UNIPROT:P05183; GB:M13646; NID:9203827; PIDN:AAA1051.1; PID:9203828
A;Note: the authors translated the codon GAC for residue 445 as Gly
R;Telhada, M.B.; Pereira, T.M.; Lechner, M.C.
Arch. Biochem. Biophys. 298, 715-725, 1992
A;Title: Effect of dexamethasone and phenobarbital on run-on transcription rate and CYP3
A;Reference number: S27107; MUID:93037516; PMID:1417000
A;Accession: S27108
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-36 <TEL>
A;Cross-references: EMBL:X62087
R;Miyata, M.; Nagata, K.; Shimada, M.; Yamazoe, Y.; Kato, R.
submitted to the EMBL Data Library, May 1994
A;Description: Structure of a gene and cDNA of a major constitutive form of testosterone
A;Reference number: S46938
A;Accession: S46938
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-428, 'D', '430-444', 'G', '446-504 <MIY>
A;Cross-references: EMBL:X79920; NID:9515381; PIDN:CAA55888.1; PID:9515382
R;Nagata, K.; Gonzalez, F.J.; Yamazoe, Y.; Kato, R.
Biochem. 107, 718-725, 1990
A;Title: Purification and characterization of four catalytically active testosterone 6be
nally related forms.
A;Reference number: EX0032; MUID:90375438; PMID:2398038
A;Accession: EX0032
A;Molecule type: protein
A;Residues: 1-21, 'X', '23-26', 'X', '28-29', 'X', '31-33 <NAG>
A;Experimental source: liver, Sprague-Dawley male rat
A;Accession: EX0034
A;Molecule type: protein

A;Residues: 1-27, 'X', '29', 'X', '31-33 <NA2>
R;Cooper, K.O.; Reik, L.M.; Jayoshi, Z.; Bandiera, S.; Kelley, M.; Ryan, D.E.; Daniel, R.
Arch. Biochem. Biophys. 301, 345-354, 1993
A;Title: Regulation of two members of the steroid-inducible cytochrome P450 subfamily (3
A;Reference number: S30378; MUID:93213168; PMID:7681660
A;Accession: S30379
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-25 <COO>
C;Genetics:
A;Gene: CYP3A2
A;Introns: 24/2
A;Note: this list of introns is incomplete
C;Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
C;Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; monooxygenase;
F:303-465/Domain: cytochrome P450 homology <P45>
F:443/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 89.7%; Score 26; DB 2; Length 504;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 399 TYALH 403

RESULT 18
B82423
Hypochemical protein VCA0730 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence revision 20-Aug-2000 #text change 09-Jul-2004
C;Accession: B82423
R;Heldelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;
Charlson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: B82423
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-609 <HEL>
A;Cross-references: UNIPROT:O9KLL3; GB:AE004402; GB:AE003853; NID:99658148; PIDN:AAF9662
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VCA0730
A;Map position: 2

Query Match 89.7%; Score 26; DB 2; Length 609;
Best Local Similarity 80.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 321 TYALH 325

RESULT 19
A84425
Hypochemical protein At2g01460 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence revision 02-Feb-2001 #text change 09-Jul-2004
C;Accession: A84425
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vankken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Merriam, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617137
A;Accession: A84425
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-723 <STO>

A:Cross-references: UNIPROT:Q9ZVF8; GB:AE002093; NID:93785975; PIDN:AA067322.1; GSPDB:GN
C:Genetics:
A:Gene: AT2901460
A:Map position: 2

Query Match 89.7%; Score 26; DB 2; Length 723;
Best Local Similarity 80.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 173 TYALH 177

RESULT 20
B64679
paralysed flagella protein - Helicobacter pylori (strain 26695)

C:Species: Helicobacter pylori
C>Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C:Accession: B64679

R:Comb, J.F.; White, O.; Kervavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khaliq, H.G.; Glodek, A.; McKenney, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Wathey, L.; Nature 388, 539-547, 1997

A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; MUID:97394467; PMID:9252185

A:Accession: B64679

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-801 <TOM>

A:Cross-references: UNIPROT:O25864; GB:AE000631; GB:AE000511; NID:92314421; PIDN:AA00831

C:Genetics:

A:Start codon: TTG

Query Match 89.7%; Score 26; DB 2; Length 801;
Best Local Similarity 80.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 95 TYSMH 99

RESULT 21
GNLJGA

pol polyprotein - bovine leukemia virus (strain Australia)

N:Contains: endonuclease (EC 3.1.1.-); RNA-directed DNA polymerase (EC 2.7.7.49)

C:Species: bovine leukemia virus, BLV

A:Note: host Bos sp. (cattle)

C>Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004

C:Accession: JQ0555

R:Collection: J. Nelf, H. Brandon, R. Kumar, S. Khan, S. Daniel, R.C.W. Lavin, M.F.

J. Gen. Virol. 71, 1737-1746, 1990

A:Title: Molecular cloning and sequencing of an Australian isolate of proviral bovine le

A:Reference number: JQ0554; MUID:90362060; PMID:2167927

A:Accession: JQ0555

A:Molecule type: DNA

A:Residues: 1-852 <COU>

A:Cross-references: UNIPROT:P25059; DDBJ:D00647; NID:92920795; PIDN:BA00544.1; PID:9221

A:Note: this reading frame extends between two stop codons and does not begin with a sta

A:Note: the authors translated the codon CCC for residue 514 as Gln

C:Comment: The precise boundary between RNA-directed DNA polymerase and endonuclease has

C:Genetics:

A:Gene: pol

C:Superfamily: pol polyprotein

C:Keywords: endonuclease; hydrolase; nucleotidyltransferase; polyprotein; reverse trans

Query Match 89.7%; Score 26; DB 1; Length 852;
Best Local Similarity 80.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5

Db 636 TYALH 640

RESULT 22

GNLJGB

pol polyprotein - bovine leukemia virus

N:Contains: endonuclease (EC 3.1.1.-); RNA-directed DNA polymerase (EC 2.7.7.49)

C:Species: bovine leukemia virus, BLV

A:Note: host Bos sp. (cattle)

C>Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 09-Jul-2004

C:Accession: A03960

R:Sagata, N.; Yasunaga, T.; Tsubuku-Kawamura, T.; Ohishi, K.; Ogawa, Y.; Ikawa, Y.

Proc. Natl. Acad. Sci. U.S.A. 82, 677-681, 1985

A:Title: Complete nucleotide sequence of the genome of bovine leukemia virus: its evolu

A:Reference number: A94063; MUID:85140159; PMID:2983308

A:Accession: A03960

A:Molecule type: DNA

A:Residues: 1-852 <SAG>

A:Cross-references: UNIPROT:P03361

A:Note: the authors translated the codon TTC for residue 104 as Ser and CTA for residue

C:Comment: Specific enzymatic cleavages may yield mature proteins including reverse tran

C:Genetics:

A:Superfamily: pol polyprotein

C:Keywords: endonuclease; hydrolase; nucleotidyltransferase; polyprotein; reverse trans

Query Match 89.7%; Score 26; DB 1; Length 852;
Best Local Similarity 80.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 636 TYALH 640

RESULT 23

S29358

pol protein - bovine leukemia virus

C:Species: bovine leukemia virus, BLV

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C:Accession: S29358

R:Rice, N.R.; Stephens, R.M.; Burny, A.; Gilden, R.V.

Virolgy 142, 357-377, 1985

A:Title: The gag and pol genes of bovine leukemia virus: nucleotide sequence and analysis

A:Reference number: S29356; MUID:86045859; PMID:2997990

A:Accession: S29358

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-852 <RIC>

A:Cross-references: UNIPROT:Q85491; EMBL:M10987

C:Superfamily: pol polyprotein

Query Match 89.7%; Score 26; DB 2; Length 852;
Best Local Similarity 80.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 636 TYALH 640

RESULT 24

S18955

fix23-3 protein - Rhizobium meliloti

C:Species: Rhizobium meliloti

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C:Accession: S18955

R:Petrovics, G.; Putnoky, P.; Kondorosi, A.

submitted to the EMBL Data Library, January 1992

A:Description: A fatty acid synthase like gene cluster of Rhizobium meliloti is involved

A:Reference number: S18955

A:Accession: S18955

A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-966 <P&T>
A/Cross-references: UNIPROT:Q52932; EMBL:X64131; NID:g1235585; PIDN:CAA45485.1; PID:g462

Query Match
Best Local Similarity 89.7%; Score 26; DB 2; Length 966;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TYAMH 5
Db 198 TYALH 202

RESULT 25

Probable helicase [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C/Accession: F84517
R/Lin: X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanhaken, S.E.; Umayam, L.; Tallon, L.;
Euse, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A/Reference number: A84420; MUID:20083487; PMID:10617197
A/Accession: F84517
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1265 <STO>
A/Cross-references: UNIPROT:Q9ZOR0; GB:AE002093; NID:g4263825; PIDN:AAD15468.1; GSPDB:GN

C/Genetics:
A/Map position: 2
Query Match
Best Local Similarity 89.7%; Score 26; DB 2; Length 1265;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TYAMH 5
Db 195 TYSMH 199

RESULT 26

T21706
hypochemical protein F33H1.4 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T21706
R/Wilkinson, J.
submitted to the EMBL Data Library, March 1995
A/Reference number: Z19462
A/Accession: T21706
A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA
A/Residues: 1-1385 <WTL>
A/Cross-references: UNIPROT:Q19991; EMBL:Z48783; PIDN:CAA86699.1; GSPDB:GN00020; CESP:F3

A/Experimental source: clone F33H1
C/Genetics:
A/Map position: 2
A/Introns: 88/2; 699/1; 1021/3; 1330/3; 1350/3
Query Match
Best Local Similarity 89.7%; Score 26; DB 2; Length 1385;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TYAMH 5
Db 1131 TYALH 1135

RESULT 27

T30886
Integumentary mucin B.1 - African clawed frog (fragment)
C/Species: Xenopus laevis (African clawed frog)
C/Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C/Accession: T30886
R/Joda, W.; Hoffmann, W.
J. Biol. Chem. 272, 1805-1810, 1997
A/Title: Similarities of integumentary mucin B.1 (FIM-B.1) from Xenopus laevis and prepr

A/Reference number: Z20920; MUID:97153143; PMID:899864
A/Accession: T30886
A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA
A/Residues: 1-1506 <JOB>
A/Cross-references: UNIPROT:P79927; EMBL:X08296; NID:g1839051; PIDN:CAA69604.1; PID:g183
C/Genetics:
A/Note: FIM-B.1
A/Superfamily: pig submaxillary mucin
Query Match
Best Local Similarity 89.7%; Score 26; DB 2; Length 1506;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TYAMH 5
Db 527 TYSMH 531

RESULT 28

T30228
polyketide synthase - Streptomyces hygroscopicus
C/Species: Streptomyces hygroscopicus
C/Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C/Accession: T30228
R/Aparicio, J.F.; Molnar, I.; Schwecke, T.; Koenig, A.; Haydock, S.F.; Khaw, L.E.; Staun

Gene 169, 9-16, 1996
A/Title: Organization of the biosynthetic gene cluster for rapamycin in Streptomyces hyg
A/Reference number: Z20782; MUID:96186896; PMID:8635756
A/Accession: T30228
A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA
A/Residues: 1-6260 <APA>
A/Cross-references: UNIPROT:Q54299; EMBL:X86780; NID:g987088; PID:g987102; PIDN:CAA60462
C/Genetics:
A/Genes: rapC

C/Keywords: carrier protein
F/55-451/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS1>
F/1556-1607/Domain: acyl carrier protein homology <ACP1>
F/1651-2042/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS2>
F/3123-3194/Domain: acyl carrier protein homology <ACP2>
F/3228-3632/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS3>
F/3725-3999/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT1>
F/5114-5185/Domain: acyl carrier protein homology <ACP3>
F/5242-5638/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS4>
F/5759-6044/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT2>
F/6135-6206/Domain: acyl carrier protein homology <ACP4>

Query Match
Best Local Similarity 89.7%; Score 26; DB 2; Length 6260;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TYAMH 5
Db 2611 TYALH 2615

RESULT 29

S26887
Ig heavy chain V region (DP-61) - human
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S26887
R/Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.

J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26887
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-35 <TOM>
A:Cross-references: EMBL:Z12361; NID:932941; PIDN:CAA76231.1; PID:932942
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 86.2%; Score 25; DB 2; Length 35;
Best Local Similarity 80.0%; Pred. No. 21;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TYAMH 5
:||||
Db 4 SYAMH 8

RESULT 30
S46473
Ig heavy chain V region (YAC-6) - human
C:Species: Homo sapiens (man)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C:Accession: S46473
R:Cook, G.P.; Tomlinson, I.M.; Walter, G.; Rietman, H.; Carter, N.P.; Bulwela, L.; Win
Nature Gene. 7, 162-168, 1994
A:Title: A map of the human immunoglobulin V(H) locus completed by analysis of the telom
A:Reference number: S46460; MUID:95004581; PMID:7920635
A:Accession: S46473
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-35 <COO>
A:Cross-references: EMBL:Z27505; NID:9505447; PIDN:CAA81825.1; PID:9505448
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 86.2%; Score 25; DB 2; Length 35;
Best Local Similarity 80.0%; Pred. No. 21;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TYAMH 5
:||||
Db 4 SYAMH 8

RESULT 31
P10120
Ig heavy chain V-III region (TD-Vo) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C:Accession: P10120
R:Bird, J.; Galili, N.; Link, M.; Stites, D.; Sklar, J.
J. Exp. Med. 168, 229-245, 1988
A:Title: Continuing rearrangement but absence of somatic hypermutation in immunoglobulin
A:Reference number: P10116; MUID:88286083; PMID:2840480
A:Accession: P10120
A:Molecule type: mRNA
A:Residues: 1-94 <5'>
A:Cross-references: UNIPROT:O8WTK1; UNIPROT:O9UJ93
A:Experimental source: B cells from patient TD with acute lymphoblastic leukemia, ALL
A:Note: the sequence shows the V region (TD-Vo) from a nonproductive DNA rearrangement
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: acute lymphoblastic leukemia; heterotetramer; immunoglobulin
F:31-35/Region: complementarity-determining 1
F:49-65/Region: complementarity-determining 2

Query Match 86.2%; Score 25; DB 2; Length 94;
Best Local Similarity 80.0%; Pred. No. 55;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TYAMH 5

Db 31 SYAMH 35
:||||

RESULT 32
S17609
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S17609
R:Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A:Title: Making antibody fragments using phage display libraries.
A:Reference number: S17230; MUID:91326098; PMID:1907718
A:Accession: S17609
A:Status: Preliminary
A:Molecule type: nucleic acid
A:Residues: 1-96 <CTA>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:8-91/Domain: immunoglobulin homology <IMM>

Query Match 86.2%; Score 25; DB 2; Length 96;
Best Local Similarity 80.0%; Pred. No. 57;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TYAMH 5
:||||
Db 24 SYAMH 28

RESULT 33
S10385
Ig heavy chain V region (clone Re107) - little skate (fragment)
C:Species: Raja erinacea (little skate)
C:Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 20-Jun-2000
C:Accession: S10385
R:Harding, F.A.; Cohen, N.; Litman, G.W.
Nucleic Acids Res. 18, 1015-1020, 1990
A:Title: Immunoglobulin heavy chain gene organization and complexity in the skate, Raja e
A:Reference number: S08462; MUID:90192082; PMID:2107524
A:Accession: S10385
A:Molecule type: DNA
A:Residues: 1-97 <HAR>
A:Cross-references: EMBL:X15124; NID:964278; PIDN:CAA33218.1; PID:91334768
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 86.2%; Score 25; DB 2; Length 97;
Best Local Similarity 80.0%; Pred. No. 57;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TYAMH 5
:||||
Db 31 SYAMH 35

RESULT 34
S26885
Ig heavy chain V region (DP-44) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 23-Jul-1999
C:Accession: S26885; S36596
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26885
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-97 <TOM1>
A:Cross-references: EMBL:Z12344

R/Tomlinson, M.
submitted to the EMBL Data Library, June 1992
A:Reference number: S36536
A:Accession: S36536
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-5, 'Q', 7-12, 'H', 14-97 <TOM2>
A:Cross-references: EMBL:Z12344; NID:G32908; PIDN:CAA78214.1; PID:G32909
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 86.2%; Score 25; DB 2; Length 97;
Best Local Similarity 80.0%; Pred. No. 57;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 31 SYAMH 35

RESULT 35
S26886
Ig heavy chain V region (DP-45) - human
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
A:Accession: S26886
R/Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26886
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-97 <TOM>
A:Cross-references: EMBL:Z12345; NID:G32910; PIDN:CAA78215.1; PID:G32911
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 86.2%; Score 25; DB 2; Length 97;
Best Local Similarity 80.0%; Pred. No. 57;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 31 SYAMH 35

RESULT 36
S29546
Ig heavy chain V region (COS-8 / DP-46) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-Jan-1994 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
A:Accession: S29546; S26888
R/Tomlinson, M.; Walter, G.; Cook, G.P.; Winter, G.
submitted to the EMBL Data Library, October 1992
A:Reference number: S29543
A:Accession: S29546
A:Molecule type: DNA
A:Residues: 1-98 <TOM>
A:Cross-references: EMBL:Z12394; NID:G32843; PIDN:CAA78997.1; PID:G32844
A:Note: designated COS-8
R/Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26888
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <TOM>
A:Cross-references: EMBL:Z12346; NID:G32912; PIDN:CAA78216.1; PID:G32913
A:Note: designated DP-46

C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 86.2%; Score 25; DB 2; Length 98;
Best Local Similarity 80.0%; Pred. No. 58;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 31 SYAMH 35

RESULT 37
S53076
probable membrane protein YMR254c - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein YMR920.08c
C:Species: Saccharomyces cerevisiae
C:Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
A:Accession: S53076
R:Hunt, S.; Bowman, S.
submitted to the EMBL Data Library, March 1995
A:Reference number: S53069
A:Accession: S53076
A:Molecule type: DNA
A:Residues: 1-102 <HUN>
A:Cross-references: UNIPROT:Q04838; EMBL:Z48639; NID:G732924; PID:G732932; GSPDB:GN00013
C:Genetics:
A:Gene: MIP6:YMR254c
A:Cross-references: SGD:S0004867
A:Map position: 13R
C:Superfamily: Saccharomyces probable membrane protein YMR254c
C:Keywords: transmembrane protein
F:2-18/Domain: transmembrane #status predicted <TM1>
F:46-62/Domain: transmembrane #status predicted <TM2>

Query Match 86.2%; Score 25; DB 2; Length 102;
Best Local Similarity 80.0%; Pred. No. 60;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 47 TYTWH 51

RESULT 38
PH1665
Ig heavy chain V region (clone 6B68) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
A:Accession: PH1665
R/Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal protein A
A:Reference number: PH1642; MUID:93301610; PMID:8315388
A:Accession: PH1665
A:Molecule type: mRNA
A:Residues: 1-104 <HIL>
A:Experimental source: B cell
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 86.2%; Score 25; DB 2; Length 104;
Best Local Similarity 80.0%; Pred. No. 61;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 23 SYAMH 27

RESULT 39

PH1653
 Ig heavy chain V region (clone 3G11) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
 C:Accession: PH1653
 R:Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
 J. Exp. Med. 178, 331-336, 1993
 A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylo
 A:Reference number: PH1642; MUID:93301610; PMID:8315388
 A:Accession: PH1653
 A:Molecule type: mRNA
 A:Residues: 1-109 <HIL>
 A:Experimental source: B cell
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 86.2%; Score 25; DB 2; Length 109;
 Best Local Similarity 80.0%; Pred. No. 64;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
 :|||
 Db 23 SYAMH 27

RESULT 40

PH1646
 Ig heavy chain V region (clone 6H12) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
 C:Accession: PH1646
 R:Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
 J. Exp. Med. 178, 331-336, 1993
 A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylo
 A:Reference number: PH1642; MUID:93301610; PMID:8315388
 A:Accession: PH1646
 A:Molecule type: mRNA
 A:Residues: 1-109 <HIL>
 A:CROSS-references: UNIPROT:Q8WUK1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 86.2%; Score 25; DB 2; Length 109;
 Best Local Similarity 80.0%; Pred. No. 64;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
 :|||
 Db 23 SYAMH 27

Search completed: March 31, 2005, 12:11:13
 Job time : 8.10938 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: March 31, 2005, 11:42:54 ; Search time 33.2031 Seconds
(without alignments)
77.113 Million cell updates/sec

Title: US-10-614-959-10
Perfect score: 29
Sequence: 1 TYAMH 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	100.0	72	Q8R281	Q8R281 oryza sativ
2	29	100.0	122	1 HV3H HUMAN	P01769 homo sapien
3	29	100.0	158	2 Q8PKV7	Q8PKV7 xanthomonas
4	29	100.0	195	1 KADA PYRHO	O55443 pyrococcus
5	29	100.0	249	2 Q9HZZ6	Q9HZZ6 pseudomonas
6	29	100.0	356	2 Q962C9	Q962C9 podocoryne
7	29	100.0	481	2 Q6N097	Q6N097 homo sapien
8	29	100.0	493	2 Q68CN4	Q68CN4 homo sapien
9	29	100.0	531	2 Q83WR9	Q83WR9 escherichia
10	29	100.0	544	2 Q6A019	Q6A019 desulfofatale
11	29	100.0	648	2 Q9V6U4	Q9V6U4 diosiphila
12	29	100.0	690	2 Q9HGS1	Q9HGS1 aspergillus
13	29	100.0	690	2 Q9UVX9	Q9UVX9 aspergillus
14	29	100.0	747	1 V222 FOWPV	Q91513 fowlpox vir
15	29	100.0	1151	1 Y245 TREPA	O83273 treponema p
16	29	100.0	1377	2 Q88053	Q88053 escherichia
17	29	100.0	1377	2 Q47692	Q47692 escherichia
18	29	100.0	7488	2 Q6JHN6	Q6JHN6 saccharopol
19	29	89.7	65	2 Q62XJ3	Q62XJ3 bacillus li
20	29	89.7	95	2 Q23428	Q23428 caenorhabdi
21	29	89.7	108	2 Q6XNP8	Q6XNP8 hevea bras
22	29	89.7	138	2 Q8Z2A5	Q8Z2A5 pyrobaculum
23	29	89.7	160	2 Q72447	Q72447 homo sapien
24	29	89.7	169	2 Q66BK2	Q66BK2 yersinia ps
25	29	89.7	173	2 Q86SK1	Q86SK1 homo sapien
26	29	89.7	175	2 Q6LWV3	Q6LWV3 photobacter
27	29	89.7	187	2 Q67RR8	Q67RR8 symbiobacte
28	29	89.7	196	1 RETB CHICK	P41263 gallus gall
29	29	89.7	202	2 Q9CKO5	Q9CKO5 pasteuralla
30	29	89.7	213	2 Q9C6N1	Q9C6N1 arabidopsis
31	29	89.7	217	2 Q9DG60	Q9DG60 xenopus lae

32	26	89.7	222	2 Q9UX67	Q9UX67 bulfolobus
33	26	89.7	228	2 Q20984	Q20984 caenorhabdi
34	26	89.7	229	2 Q8SHP4	Q8SHP4 trichoderm
35	26	89.7	242	2 Q8Y918	Q8Y918 listeria mo
36	26	89.7	242	2 Q92DPO	Q92DPO listeria in
37	26	89.7	242	2 Q722H3	Q722H3 listeria mo
38	26	89.7	244	2 Q8WRC3	Q8WRC3 tetraymena
39	26	89.7	248	2 Q885R2	Q885R2 pseudomonas
40	26	89.7	266	2 Q7Q8W1	Q7Q8W1 anophel
41	26	89.7	296	2 Q7QJU6	Q7QJU6 anophel
42	26	89.7	302	2 Q65M55	Q65M55 bacillus li
43	26	89.7	304	2 Q635T5	Q635T5 bacillus ce
44	26	89.7	304	2 Q731K1	Q731K1 bacillus ce
45	26	89.7	304	2 Q818Z0	Q818Z0 bacillus ce

ALIGNMENTS

RESULT 1					
ID	Q8R281	PRELIMINARY;	PRT;	72 AA.	
AC	Q8R281				
DT	01-JUN-2002 (TREMBLrel. 21, Created)				
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)				
DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)				
DE	B1065G12.14 protein.				
GN	Name=B1065G12.14;				
OS	Oryza sativa (japonica cultivar-group).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;				
OC	Ehharitoidae; Oryzae; Oryza.				
OX	NCBI_TaxID=39947;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	PubMed=12447438; DOI=10.1038/nature01184;				
RA	Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,				
RA	Mu J., Nilmura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,				
RA	Hosokawa S., Maekawa M., Arikawa K., Chiden Y., Hayashi M.,				
RA	Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,				
RA	Hijishita S., Honda M., Ichikawa Y., Idenuma A., Iijima A., Ikeda M.,				
RA	Ikeno M., Itoh S., Itoh T., Itoh Y., Itoh Y., Iwabuchi A., Kamaya K.,				
RA	Karasaawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,				
RA	Maehata K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,				
RA	Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,				
RA	Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,				
RA	Shimokawa T., Shimura A., Song J., Takazaki Y., Teraawa K., Tsuji K.,				
RA	Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,				
RA	Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,				
RA	Yano M., Jiang J., Gojobori T.;				
RT	"The genome sequence and structure of rice chromosome 1.";				
RL	Nature 420:312-316(2002).				
DR	EMBL; AP003791; BAB90532.1; -.				
DR	Gene; Q8R281; -.				
SQ	SEQUENCE 72 AA; 7677 MW; 6A9368D674BE00A3 CRC64;				
Query Match					
Best local similarity 100.0%; Score 29; DB 2; Length 72;					
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1 TYAMH 5				
DB	25 TYAMH 29				
RESULT 2					
HY3H HUMAN	STANDARD;				
AC	P01769;				
DT	21-JUN-1986 (Rel. 01, Created)				
DT	21-JUN-1986 (Rel. 01, Last sequence update)				
DT	05-JUN-2004 (Rel. 44, Last annotation update)				
DE	Ig heavy chain V-III region GA.				

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=74175307; PubMed=4208843;
RA Florent G., Lehman D., Putnam F.W.;
RT "The switch point in mu heavy chains of human IGM immunoglobulins.";
RL Biochemistry 13:2482-2498(1974).
CC -1- MISCELLANEOUS: This chain was isolated from a Waldenstrom's
CC macroglobulin.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02052; M3HUGA.
DR HSSP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SMO0406; Igv; 1.
DR PROSITE; PS50835; Ig LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region;
KW Pyrolydione carboxylic acid.
FT DOMAIN 1 112 Ig-like.
FT MOD_RES 1 1 Pyrolydione carboxylic acid.
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 1316 MW; 74E5B659E84100A CRC64;

Query Match 100.0%; Score 29; DB 1; Length 122;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 31 TYAMH 35

RESULT 3
Q8PKV7 PRELIMINARY; PRT; 158 AA.
ID Q8PKV7;
AC Q8PKV7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein XAC2050.
GN OrderedLocustNames=XAC2050;
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCB1_TaxID=92829;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=306 / ATCC 13902 / XV 101;
RX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Queiroz R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Canhamar F., Cardoso J., Chambergo F., Clapina L.P.,
RA Chiarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Guber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sema J.A.D., Silva C., de Souza R.F.,
RA Spindola L.A.F., Takita M.A., Tamura R.B., Teixeira E.C., Tezsa R.I.D.,
RA Seubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
host specificities.";
```

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RL Nature 417:459-463(2002).
DR EMBL; AE011840; AAM6912.1; -.
DR InterPro; IPR001412; CRNA-synt_1.
DR PROSITE; PS00178; AA_TRNA_LIGASE_1; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 158 AA; 17289 MW; C1B1FB23AA6E930B CRC64;

Query Match 100.0%; Score 29; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 132 TYAMH 136

RESULT 4
KADA_PYRHO STANDARD; PRT; 196 AA.
ID KADA_PYRHO
AC 059443;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase).
GN Name-Adk1, OrderedLocustNames=PH1753;
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCB1_TaxID=53953;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OT3;
RX MEDLINE=98344137; PubMed=9679194;
RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohtoku Y.,
RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
RL DNA Res. 5:55-76(1998).
CC -1- CATALYTIC ACTIVITY: ATP + AMP = 2 ADP.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (by similarity).
CC -1- SIMILARITY: Belongs to the archaeal adenylate kinase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AP000007; BAA30867.1; -.
DR PIR; D71184; D71184.
DR HSSP; P43410; 1K19.
DR HAMAP; MF_00234; -.
KW ATP-binding; Complete proteome; Kinase; Transferase.
FT NP_BIND 9 ATP (Potential).
SQ SEQUENCE 196 AA; 22413 MW; 26C834A1BE9445DF CRC64;

Query Match 100.0%; Score 29; DB 1; Length 196;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 157 TYAMH 161

RESULT 5
Q9H2Z6
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ID Q9H2Z6 PRELIMINARY; PRT; 249 AA.
AC Q9H2Z6;
DT 01-MAR-2001 (TRENBLREL. 16, Created)
DT 01-MAR-2001 (TRENBLREL. 16, Last sequence update)
DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=PM2847;
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PAO1;
RX MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Glover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Gardner R.L., Goltz L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Ladwig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
DR EMBL; AE004711; AAG06235.1; -.
DR PIR; B83290; B83290.
DR InterPro; IPR002781; DUF81.
DR Pfam; PF01925; DUF81; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 249 AA; 25989 MW; 8B24827650F646DA CRC64;

Query Match 100.0%; Score 29; DB 2; Length 249;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 192 TYAMH 196

RESULT 6
Q962C9 PRELIMINARY; PRT; 356 AA.
AC Q962C9;
DT 01-DEC-2001 (TRENBLREL. 19, Created)
DT 01-DEC-2001 (TRENBLREL. 19, Last sequence update)
DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
DE Transcription factor Cnox4-PC.
OS Podocoryne carnea.
OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydrozoa; Anthomedusae;
OC Hydractiniidae; Podocoryne.
OX NCBI_TaxID=6096;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21349874; PubMed=11456446; DOI=10.1006/dbio.2001.0299;
RA Yanze N., Spring J., Schmidl C., Schmid V.;
RT "Conservation of Hox/Parahox-related genes in the early development of
RT a cnidarian.";
RL Dev. Biol. 236:89-98(2001).
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; AY036893; AAK63185.1; -.
DR HSBP; P03089; IKZ2.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR009057; Homeobox.
DR InterPro; IPR000047; HTH_lambrepresr.
DR Pfam; PF00046; Homeobox_1.
DR PRINTS; PR00024; HOMEBOX.
DR PRINTS; PR00031; HTHREPRESSR.
DR SMART; SM00389; Hox; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
RN [1]
RP SEQUENCE FROM N.A.
```

```
DR PROSITE; PS00771; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
SQ SEQUENCE 356 AA; 41170 MW; EAF5E2308D76C6BB CRC64;

Query Match 100.0%; Score 29; DB 2; Length 356;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 103 TYAMH 107

RESULT 7
Q6N097 PRELIMINARY; PRT; 481 AA.
AC Q6N097;
DT 05-JUL-2004 (TRENBLREL. 27, Created)
DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLREL. 27, Last annotation update)
DE Hypothetical protein DKFZp686H20196.
GN Name=DKFZp686H20196;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human esophagus tumor;
RG The German Human cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Well B., Amid C., Osanger A.,
RA Fodor G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640619; CA845773.1; -.
DR HSBP; P01861; IADQ.
DR InterPro; IPR003599; IG_1.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; CI-bet; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 481 AA; 52759 MW; 47220D9E64BDF98B CRC64;

Query Match 100.0%; Score 29; DB 2; Length 481;
Best Local Similarity 100.0%; Pred. No. 1,3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 50 TYAMH 54

RESULT 8
Q68CN4 PRELIMINARY; PRT; 493 AA.
AC Q68CN4;
DT 25-OCT-2004 (TRENBLREL. 28, Created)
DT 25-OCT-2004 (TRENBLREL. 28, Last sequence update)
DT 25-OCT-2004 (TRENBLREL. 28, Last annotation update)
DE Hypothetical protein DKFZp686E23209 (Fragment).
GN Name=DKFZp686E23209;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
```

```

RC TISSUE=Rectum tumor;
RA The German cDNA Consortium;
RA Bloecher H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C.,
RA Osaenger A., Fobo G., Han M., Wiemann S.;
RA Submitted (AUG-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL: CR749861; CAH18705.1; -
DR InterPro: IPR003599; IG_1like.
DR InterPro: IPR007110; IG_1like.
DR InterPro: IPR003597; IG_c1.
DR InterPro: IPR003596; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF07654; C1-act; 3.
DR Pfam: PF00047; Ig; 4.
DR SMART: SM00409; IG; 2.
DR SMART: SM00407; IGc1; 3.
DR SMART: SM00406; IGv; 1.
DR PROSITE: PS50835; IG_LIKE; 4.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_2.
KM Hypothetical protein.
FT NON_TER
SQ SEQUENCE 493 AA; 54117 MW; A1E4F5ED3FA8AB40 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 493;
Best Local Similarity 100.0%; Pred. NO. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 73 TYAMH 77

RESULT 9
Q83WR9 PRELIMINARY; PRT; 531 AA.
ID Q83WR9
AC Q83WR9;
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Tsh protein (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ABEC13;
RA Simoes R.C., Delicato E.R., Gaziri L.C.J., Vidotto M.C.;
RL Submitted (APR-2003) to the EMBL/Genbank/DBJ databases.
DR EMBL: AY280856; AAP33781.1; -
DR GO: GO:0004252; F:serine-type endopeptidase activity; IEA.
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR000710; Peptidase S6.
DR InterPro: IPR009003; Pept_Ser_Cyt.
DR Pfam: PF02395; IGA1; 1.
DR PRINTS: PR00921; IGASERPTASE.
FT NON_TER
SQ SEQUENCE 531 AA; 56485 MW; 60ACA4E859A7AFC03 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 531;
Best Local Similarity 100.0%; Pred. NO. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 341 TYAMH 345

RESULT 10
Q6A019 PRELIMINARY; PRT; 544 AA.
ID Q6A019
AC Q6A019;
DT 25-OCT-2004 (Tremblrel. 28, Created)
DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)

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DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)
DE Probable acetyl-coenzyme A synthetase.
GN Name=acs; OrderedLocustNames=DP0825;
OS Desulfotalea psychrophila.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacteriales;
OC Desulfobacteraceae; Desulfotalea.
OX NCBI_TaxID=84980;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=L5V54 / DSM 12343;
RX PubMed=15305914;
RA Rabus R., Ruegg A., Frickey T., Rattei T., Fartmann B., Stark M.,
RA Baer M., Zibat A., Lombardot T., Becker I., Amann U., Gellner K.,
RA Teeling H., Leuschner W.D., Gloeckner F.-O., Lupas A.N., Amann R.,
RA Kleink H.-P.;
RT "The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium
RT from permanently cold Arctic sediments.";
RL Environ. Microbiol. 6:887-902(2004).
CC -1- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
CC family.
DR EMBL: CR522870; CAG35554.1; -
DR GO: GO:0003824; F:catalytic activity; IEA.
DR GO: GO:0008152; P:metabolism; IEA.
DR InterPro: IPR000873; AMP-bind.
DR Pfam: PF00501; AMP-binding; 1.
DR PRINTS: PR00154; AMPBINDING.
DR PROSITE: PS00455; AMP_BINDING; 1.
SQ SEQUENCE 544 AA; 60412 MW; CAD62D99B4CCEBF7 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 544;
Best Local Similarity 100.0%; Pred. NO. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 307 TYAMH 311

RESULT 11
Q9V6J4 PRELIMINARY; PRT; 648 AA.
ID Q9V6J4
AC Q9V6J4;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)
DE CG3915-PB (GH27039p).
GN Name=Drl-2; ORFName=CG3915;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abriil J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballwey R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berna B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck U., Brokstein P., Brotlier P.,
RA Burlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasner K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

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RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
 RA Hostin M., Kalush F., Karpen G.H., Ke Z., Kennison J.G., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Neislo D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier B., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Massamman D.A., Weissstock G.M., Weissbach J.,
 RA Williams S.M., Woodgerf, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Ceiniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
 RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weissstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 RT "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*
 RT *melanogaster* euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminler J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Ceiniker S.E.;
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
 RT a genomic perspective.";
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Mierra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminler J.S., Millburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu I., Berman B.P.,
 RA Betencourt B.R., Ceiniker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RG FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RG FlyBase;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champagne M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
 RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Munoz J., Pacleb J., Paragas V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Ceiniker S.;
 Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AE003820; AAF58429.3; -
 DR EMBL; BT004493; AAC42657.1; -
 DR HSSP; P08581; IRW.
 DR FlyBase; FBgn003791; Dr1-2.
 DR GO; GO:0005524; P:ATP binding; IEA.
 DR GO; GO:0004713; F:Protein-tyrosine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:Protein amino acid phosphorylation; IEA.
 DR InterPro; IPR011009; Kinase like.
 DR InterPro; IPR000719; Prot. kinase.
 DR InterPro; IPR01245; Tyr_kinase.
 DR InterPro; IPR008266; Tyr_kinase_AS.
 DR InterPro; IPR003306; WIF.
 DR Pfam; PF02019; WIF; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot. kinase; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; UNKNOWN; 1.
 DR PROSITE; PS50814; WIF; 1.
 DR Kinase; Transferase; Tyrosine-protein kinase.
 SQ SEQUENCE 648 AA; 71139 MW; 1B4F6A0C84E457 CRC64;
 QY 1 TYAMH 5
 Db 56 TYAMH 60
 RESULT 12
 Q9HGS1 PRELIMINARY; PRT; 690 AA.
 AC Q9HGS1;
 DT 01-MAR-2001 (TRENBLrel. 16, Created)
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE Glutaminease (EC 3.5.1.12).
 OS Aspergillus oryzae.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eukaryota; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OX NCBI_TaxID=5062;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=U212;
 RA Thammavongtham C., Turner G., Moir A.J., Tanticharoen M.,
 RA Cheevadhanarak S.;
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY005477; AAG02575.1; -
 DR GO; GO:0004359; F:glutaminease activity; IEA.
 DR GO; GO:0016787; F:Hydrolase activity; IEA.
 KW Hydrolase.
 SQ SEQUENCE 690 AA; 76226 MW; 6546BE2499D8D43C CRC64;
 Query Match 100.0%; Score 29; DB 2; Length 690;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TYAMH 5
 Db 423 TYAMH 427
 RESULT 13
 Q9UVX9 PRELIMINARY; PRT; 690 AA.
 AC Q9UVX9;
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE Glutaminease A.
 GN Name=gtaa;

```

OS Aspergillus oryzae.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5062;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RIB40;
RX MEDLINE=20406523; PubMed=10952006;
RA Koibuchi K., Nagasaki H., Yusa A., Kataoka J., Kitamoto K.;
RT "Molecular cloning and characterization of a gene encoding glutaminase
  from Aspergillus oryzae.";
RL Appl. Microbiol. Biotechnol. 54:59-68 (2000).
DR EMBL; AB029552; BAA86934.1; -.
SQ SEQUENCE 690 AA; 76164 MW; E3D0B17841BEA00D CRC64;

Query Match
Best Local Similarity 100.0%; Score 29; DB 2; Length 690;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 423 TYAMH 427

RESULT 14
V222_FOWPV STANDARD; PRT; 747 AA.
ID V222_FOWPV
AC Q9513;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Putative ankylrin-repeat protein PPV222.
GN Name=PPV222;
OS Fowlpox virus (FPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Avipoxvirus.
OX NCBI_TaxID=10261;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20193820; PubMed=10729156;
RX DOI=10.1128/JVI.74.8.3815-3831.2000;
RA Afonso C.L., Tulman E.R., Lu Z., Zsak L., Kutish G.F., Rock D.L.;
RT "The genome of fowlpox virus.";
RL J. Virol. 74:3815-3831 (2000).
CC -1- SIMILARITY: Contains 14 ANK repeats.
CC -----
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CC -----
CC EMBL; AF198100; AAF4566.1; -.
DR HSP; Q60778; 1073.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR001810; F-box.
DR Pfam; PF00023; Ank; 13.
DR Pfam; PF00646; F-box; 1.
DR PRINTS; PR01415; ANKRIN.
DR SMART; SM00248; ANK; 15.
DR PROSITE; PS50297; ANK_REP_REGION; 1.
DR PROSITE; PS50088; ANK_REPEAT; 7.
KW ANK repeat; Hypothetical protein; Repeat.
FT REPEAT 38 67 ANK 1.
FT REPEAT 103 132 ANK 2.
FT REPEAT 136 165 ANK 3.
FT REPEAT 169 198 ANK 4.
FT REPEAT 202 231 ANK 5.
FT REPEAT 234 263 ANK 6.
FT REPEAT 294 323 ANK 7.
FT REPEAT 328 357 ANK 8.

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FT REPEAT 361 393 ANK 9.
FT REPEAT 397 426 ANK 10.
FT REPEAT 430 460 ANK 11.
FT REPEAT 464 493 ANK 12.
FT REPEAT 495 524 ANK 13.
FT REPEAT 529 559 ANK 14.
SQ SEQUENCE 747 AA; 85303 MW; 55F90AF28553D28 CRC64;

Query Match
Best Local Similarity 100.0%; Score 29; DB 1; Length 747;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 330 TYAMH 334

RESULT 15
Y245_TREPA STANDARD; PRT; 1151 AA.
ID Y245_TREPA
AC O83273;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Hypothetical protein TP0245.
GN OrderedLocustNames=TP0245;
OS Treponema pallidum.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=160;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Nichols;
RX MEDLINE=98332770; PubMed=965876; DOI=10.1126/science.281.5375.375;
RX Fraser C.M., Norris S.J., Weinstein G.M., White O., Sutton G.G.;
RA Dodson R.J., Gwinn M.L., Hickey B.K., Clayton R.A., Ketchum K.A.;
RA Sodergren E., Hardam J.M., McLeod M.P., Salzberg S.L., Peterson J.D.;
RA Khalak H.G., Richardson D.L., Howell J.K., Chidambaram M.;
RA Uteirack T.R., McDonald L.A., Artlich P., Bowman C., Cotton M.D.;
RA Fujii C., Garland S.A., Hatch B., Horst K., Roberts K.M., Sandusky M.;
RA Weidman J.F., Smith H.O., Venter J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
  spirochete.";
RL Science 281:375-388 (1998).
CC -----
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CC -----
CC EMBL; AB001206; AAC65239.1; -.
DR PIR; H71347; H71347.
DR TIGR; TP0245; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 1151 AA; 127556 MW; EDB6353C32CB4056 CRC64;

Query Match
Best Local Similarity 100.0%; Score 29; DB 1; Length 1151;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 700 TYAMH 704

RESULT 16
O88093 PRELIMINARY; PRT; 1377 AA.
AC O88093;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)

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DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Haemoglobin protease precursor.
GN Name=hbp;
OS Escherichia coli.
OC Plasmid pColy-K10.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=EB1.
RX MEDLINE=98416173; PubMed=9743528;
RA Otto B.R., van Dooren S.J.M., Nuijens J.H., Luijckink J., Oudega B.,
RT "Characterization of a hemoglobin protease secreted by the pathogenic
RT Escherichia coli strain EB1."
RL J. Exp. Med. 188:1091-1103(1998).
DR EMBL; AJ223631; CAA11507.1; -.
DR MEROPS; S06.003; -.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004252; F:serine-type endopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR006315; Autotransporter.
DR InterPro; IPR005546; Auto_transbeta.
DR InterPro; IPR01050; Pectin_lyas_like.
DR InterPro; IPR000710; Peptidase_S6.
DR Pfam; PF03797; Autotransporter; 1.
DR Pfam; PF03395; IGA1; 1.
DR PRINTS; PR00921; IGASERPTASE.
DR TIGRFPMS; TIGR01414; autotrans_bar1; 1.
KW Plasmid; Protease; Signal.
FT SIGNAL.
SQ SEQUENCE 1377 AA; 148256 MW; BB16D898EDAC0416 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 1377;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 341 TYAMH 345

RESULT 17
ID Q47692 PRELIMINARY; PRT; 1377 AA.
AC Q47692;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Tsh.
GN Name=tsh;
OS Escherichia coli.
OC Plasmid pAPBC-1.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=chi7122;
RX MEDLINE=94178945; PubMed=8132344;
RA Providence D.L., Curtiss R. III.;
RT "Isolation and characterization of a gene involved in hemagglutination
RT by an avian pathogenic Escherichia coli strain."
RL Infect. Immun. 62:1369-1380(1994).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=chi7122;
RX MEDLINE=20316042; PubMed=10858231;
RA DOI=10.1128/JAI.68.7.4145-4154.2000;
RA Dorais C.M., Dho-Moulin M., Bree A., Fairbrother J.M., Desautels C.,
RA Curtiss R. III.;
RT "Relationship between the Tsh autotransporter and pathogenicity of

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RT avian Escherichia coli and localization and analysis of the Tsh
RT genetic region."
RL Infect. Immun. 68:4145-4154(2000).
DR EMBL; AF218073; AAA24698.1; -.
DR PIR; I54632; I54632.
DR MEROPS; S06.003; -.
DR GO; GO:0004252; F:serine-type endopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR006315; Autotransporter.
DR InterPro; IPR005546; Auto_transbeta.
DR InterPro; IPR01050; Pectin_lyas_like.
DR InterPro; IPR000710; Peptidase_S6.
DR Pfam; PF03797; Autotransporter; 1.
DR Pfam; PF03395; IGA1; 1.
DR PRINTS; PR00921; IGASERPTASE.
DR TIGRFPMS; TIGR01414; autotrans_bar1; 1.
KW Plasmid.
SQ SEQUENCE 1377 AA; 148226 MW; 237423644D9AE012 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 1377;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 341 TYAMH 345

RESULT 18
ID Q6JUN6 PRELIMINARY; PRT; 7488 AA.
AC Q6JUN6;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Obsc.
OC Saccharopolyspora spinosa.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Pseudonocardiaceae; Pseudonocardiaceae; Saccharopolyspora.
OX NCBI_TaxID=60894;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRL1.18395;
RA Zirkle R., Black T.A., Goriach J., Tyson J.M., Molnar I.;
RT "Analysis of a 108-kb region of the Saccharopolyspora spinosa Genome
RT Covering the Obscurin Polyketide Synthase Locus."
RL DNA Seq. 15:123-134(2004).
DR EMBL; AY466441; AAS00421.1; -.
DR HSSP; 003133; 1KEZ.
DR GO; GO:0004024; F:alcohol dehydrogenase activity, zinc-dependent; IEA.
DR GO; GO:0048037; F:cofactor binding; IEA.
DR GO; GO:0016788; F:hydrolase activity, acting on ester bonds; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0009058; P:biosynthesis; IEA.
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
DR InterPro; IPR009081; ACP_like.
DR InterPro; IPR001227; Ac_transferase.
DR InterPro; IPR002085; Adh_zn_family.
DR InterPro; IPR011032; GroES_like.
DR InterPro; IPR000794; Ketoacyl_synth.
DR InterPro; IPR000209; Pept_S8_S53.
DR InterPro; IPR006163; Pnpanteteh_bind.
DR InterPro; IPR006162; Pantane_S.
DR InterPro; IPR001031; Thioesterase.
DR Pfam; PF00698; ACP1_transf.1; 4.
DR Pfam; PF00107; ADH_zinc_N; 1.
DR Pfam; PF02801; ketoacyl-synt; 4.
DR Pfam; PF00550; PP-binding; 4.
DR Pfam; PF00975; Thioesterase; 1.
DR PROSITE; PS50075; ACP_DOMAIN; 4.

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DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; 4.
 DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; 4.
 DR PROSITE; PS00136; SUBTILASE_ASP; UNKNOWN_1.
 KW Phosphopantetheine; Transferase.
 SQ SEQUENCE 7488 AA; 781833 MW; C54551IDF855B1A4 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 7488;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
 Db 7374 TYAMH 7378

RESULT 19

Q62XJ3 PRELIMINARY; PRT; 65 AA.
 AC Q62XJ3;
 DT 25-OCT-2004 (TReMBLrel. 28, Created)
 DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=BL05084;
 OS Bacillus licheniformis DSM 13.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 CX NCBI_TaxID=279010;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 14580;
 RA Rey M.W., Ramaiva P., Nelson B.A., Brody-Karpin S.D., Zaretsky E.J.,
 RA Tang M., de Leon A.L., Xiang H., Gueti V., Clausen I.G., Olsen P.B.,
 RA Rasmussen M.D., Andersen U.T., Jorgensen P.L., Larsen T.S.,
 RA Sorkin A., Bolotin A., Lapidus A., Galleron N., Ehrlich S.D.,
 RA Berka R.M.;
 RT "Complete genome sequence of the industrial bacterium Bacillus
 RT licheniformis and comparisons with closely related Bacillus species."
 RL Genome Biol. 5:R77-R77(2004).
 DR EMBL; CP000002; AA022515.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 65 AA; 7079 MW; 1D43A68FE26DC053 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 65;
 Best Local Similarity 80.0%; Pred. No. 90;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
 Db 33 TYALH 37

RESULT 20

Q23428 PRELIMINARY; PRT; 95 AA.
 AC Q23428;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE Hypothetical protein ZK1248.17;
 GN Name=ZK1248.17; ORFNames=ZK1248.17;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Pseudocercariae; Caenorhabditis.
 CX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=98063613; PubMed=9851916;
 RG WormBase Consortium;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Lactelle P.;
 RT "The sequence of C. elegans cosmid ZK1248."
 RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Wilson R.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Wilson R.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RG WormBase Consortium;
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.

-1- FUNCTION: Central component in molecular interactions underlying
 sperm crawling. Forms an extensive filament system that extends
 from sperm villipoda, along the leading edge of the pseudopod (By
 similarity).
 CC -1- SIMILARITY: Contains 1 MSP domain.
 DR EMBL; U29244; AAC71098.1; -.
 DR PIR; T34500; T34500.
 DR HSSP; P53017; IGRW.
 DR WormBase; WBGene00022884; ZK1248.17.
 DR WormPep; ZK1248.17; CE02901.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR000535; MSP.
 DR InterPro; IPR008962; PapD-like.
 DR Pfam; PF00635; Motile_Sperm; 1.
 DR PROSITE; PS50202; MSP; 1.
 KW Cytokeleton; Hypothetical protein.
 SQ SEQUENCE 95 AA; 10727 MW; E8D70FF0395004A8 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 95;
 Best Local Similarity 80.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
 Db 12 TYSMH 16

RESULT 21

Q6XNP8 PRELIMINARY; PRT; 108 AA.
 AC Q6XNP8;
 DT 05-JUL-2004 (TReMBLrel. 27, Created)
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
 DE ASR-like protein 1.
 GN Name=ASRBP1;
 OS Hevea brasiliensis (Para rubber tree).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Malpighiales; Euphorbiaceae; Crotonoideae; Microdreaceae;
 OC Hevea.
 CX NCBI_TaxID=3981;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ko J.-H., Han K.-H.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY221984; AAP46155.1; -.
 DR GO; GO:0006950; P:response to stress; IEA.

DR InterPro; IPR003496; ABA_WDS.
DR Pfam; PF02496; ABA_WDS; 1.
SQ SEQUENCE 108 AA; 12124 MW; 368E3B9C50D47AE7 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 108;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 TYAMH 5
DB 45 TYALH 49

RESULT 22

08ZZA5 PRELIMINARY; PRT; 138 AA.

AC 08ZZA5; 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Hypothetical protein PAE0353.
GN OrderedLocustNames=PAE0353;
OS Pyrobaculum aerophilum.
OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
OC Thermoproteaceae; Pyrobaculum.
OX NCBI_TaxID=13773;

RP SEQUENCE FROM N.A.
RC STRAIN=IM2 / ATCC 51768 / DSM 7523;
RX MEDLINE=21664397; PubMed=11792869; DOI=10.1073/pnas.241636498;
RA Flitz-Gibson S.T., Ladner H., Kim U.-U., Stetter K.O., Simon M.I.,
RA Miller J.H.;
RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
RT aerophilum".
RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
DR EMBL; AE009763; AAL62736.1; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 138 AA; 15372 MW; 662A04E963ABE921 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 138;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 TYAMH 5
DB 66 TYALH 70

RESULT 23

07Z447 PRELIMINARY; PRT; 160 AA.

AC 07Z447; 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Cytochrome P450 (Fragment).
GN Name=CYP3A5;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA MEDLINE=21835017; PubMed=11726664; DOI=10.1074/jbc.M109175200;
RX Finta C., Zaphiropoulos P.G.;
RT "Intergenic mRNA molecules resulting from trans-splicing";
RL J. Biol. Chem. 277:5882-5890(2002).

RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Zaphiropoulos P.G.;
RL Submitted (MAY-2003) to the EMBL/Genbank/DBJ databases.

CC -1 SIMILARITY: Belongs to the cytochrome P450 family.

DR EMBL; AJ563378; CAD91647.1; -.
DR HSSP; P14779; 1BU7.
DR GO; GO:0004497; F:monooxygenase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001128; Cytochrome_P450.
DR Pfam; PF00067; P450; 1.
DR PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
KW Heme; Monooxygenase; Oxidoreductase.
FT NON_TER
SQ SEQUENCE 160 AA; 18362 MW; A05FEDASB16A843 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 160;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 TYAMH 5
DB 56 TYALH 60

RESULT 24

06BK2 PRELIMINARY; PRT; 169 AA.

AC 06BK2; 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Regulatory protein CII bacteriophage 186.
GN ORFNames=YR7B1769;
OS Yersinia pseudotuberculosis IP 32953.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=273123;

RP SEQUENCE FROM N.A.
RC STRAIN=IP 32953;
RX PubMed=15358858;
RA Chain P.S.G., Carniel E., Larimer F.W., Lamerdin J., Stoutland P.O.,
RA Regala W.M., Georgescu A.M., Vergez L.M., Land M.L., Motin L.V.,
RA Brinkner R.R., Fowler J., Hinebusch B.J., Marceau M., Medigue C.,
RA Simion M., Chenal-Franciaque V., Souza B., Dacheux D., Elliott J.M.,
RA Derbise A., Hauser L.J., Garcia B.;
RT "Insights into the genome evolution of Yersinia pestis through whole
RT genome comparison with Yersinia pseudotuberculosis";
RL Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).
DR EMBL; BX936398; CAH21008.1; -.
DR InterPro; IPR009679; Phage_CP76.
DR Pfam; PF06892; Phage_CP76; 1.
SQ SEQUENCE 169 AA; 17796 MW; 8DD659B642CB5D4 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 169;
Best Local Similarity 80.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 TYAMH 5
DB 94 TYALH 98

RESULT 25

086SK1 PRELIMINARY; PRT; 173 AA.

AC 086SK1; 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=21839017; PubMed=11726664; DOI=10.1074/jbc.M109175200;
RA Finta C., Zaphiropoulos P.G.;
RT "Intergenic mRNA molecules resulting from trans-splicing.";
RL J. Biol. Chem. 277:5882-5890(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX Zaphiropoulos P.G.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
DR EMBL; A563378; CAD91347.1; -.
DR HSBP; P14779; 1B7.
DR GO; GO:0004497; F:monooxygenase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001128; Cytochrome_P450.
DR InterPro; IPR002403; EP4501V.
DR Pfam; PF00067; P450; 1.
DR PRINTS; PR00465; EP4501V.
DR PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
KW Heme; Hypothetical protein.
SQ SEQUENCE 173 AA; 19718 MW; AF01A03594D95A13 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 173;
Best Local Similarity 80.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 TYAMH 5
||:|
Db 69 TYALH 73

RESULT 26

O6LMV3 PRELIMINARY; PRT; 175 AA.
AC O6LMV3;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Putative autoinducer-2 production protein LuxS.
GN Name=S2901; OrderedLocNames=PBPA3045;
OS Photobacterium profundum (Photobacterium sp. (strain SS9)).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCBI_TaxID=74109;
RN [1]
RP SEQUENCE FROM N.A.
RA Verzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F.,
RA Cestaro A., Malacrida G., Simionati B., Cannata N., Bartlett D.,
RA Valle G.;
RT "Genome analysis of Photobacterium profundum reveals the complexity of
RT high pressure adaptations.";
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR318673; CAG21373.1; -.
DR GO; GO:0009372; P:quorum sensing; IEA.
DR InterPro; IPR003815; LuxS.
DR Pfam; PF02664; LuxS; 1.
DR PRINTS; PR01487; LUXSPROTEIN.
DR PRODOM; PD013172; LuxS; 1.
KW Complete proteome.
SQ SEQUENCE 175 AA; 19651 MW; 1191C0DCD26AB238 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 175;
Best Local Similarity 80.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 TYAMH 5
||:|
Db 133 TYSMH 137

RESULT 27
ID O67RR8 PRELIMINARY; PRT; 187 AA.
AC O67RR8;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Hypothetical protein.
GN ORFNames=STH640;
OS Symbiobacterium thermophilum.
OC Bacteria; Actinobacteria; Symbiobacterium.
OX NCBI_TaxID=2734;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IM14863;
RA Ueda K., Yamashita A., Ishikawa J., Shimada M., Watsui T.,
RA Morimura K., Ikeda H., Hattori M., Bepko T.;
RT "Complete genome sequence of an uncultured bacterium Symbiobacterium
RT thermophilum.";
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP006840; BAD39625.1; -.
DR InterPro; IPR003848; DUF218.
DR Pfam; PF02698; DUF218; 1.
KW Hypothetical protein.
SQ SEQUENCE 187 AA; 21555 MW; 421C8F241F2A81B8 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 187;
Best Local Similarity 80.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 TYAMH 5
||:|
Db 180 TYALH 184

RESULT 28

RETB_CHICK STANDARD; PRT; 196 AA.
AC P41263;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Plasma retinol-binding protein precursor (PRBP).
GN Name=RPB4;
OS Gallus gallus (chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95267350; PubMed=7748490;
RA Vieira A.V., Kuchler K., Schneider W.J.;
RT "Retinol in avian oogenesis: molecular properties of the carrier
RT protein.";
RL DNA Cell Biol. 14:403-410(1995).
CC -1- FUNCTION: Delivers retinol from the liver stores to the peripheral
CC tissues. In plasma, the RBP-retinol complex interacts with
CC transthyretin, this prevents its loss by filtration through the
CC kidney glomeruli (by similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the lipocalin family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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DR EMBL; X77960; CAA54922.1; -.
DR PIR; I50675; I50675.

DR PDB, 1IU, X-ray, A=23-196.
DR InterPro; IPR011038; Calycin.
DR InterPro; IPR002345; Lipocalin.
DR InterPro; IPR000566; Lipocalin cytochrome P-450.
DR InterPro; IPR002449; Retinol-binding.
DR Pfam; PF00061; Lipocalin; 1.
DR PRINTS; PR00179; LIPOCALIN.
DR PROSITE; PS00213; LIPOCALIN; 1.
KW 3D-structure; Lipocalin; Plasma; Retinol-binding; Signal; Transport;
vitamin A.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 196 Plasma retinol-binding protein.
FT DISULFID 25 181 By similarity.
FT DISULFID 91 195 By similarity.
FT DISULFID 141 150 By similarity.
FT STRAND 26 26
FT HELIX 27 29
FT TURN 34 35
FT HELIX 38 41
FT STRAND 43 51
FT STRAND 60 68
FT TURN 70 71
FT STRAND 74 83
FT TURN 85 86
FT STRAND 89 99
FT TURN 104 105
FT STRAND 106 113
FT STRAND 121 130
FT STRAND 135 144
FT TURN 146 147
FT STRAND 149 159
FT TURN 162 163
FT HELIX 167 178
FT TURN 179 181
FT TURN 183 184
FT TURN 187 188
SQ SEQUENCE 196 AA; 22515 MW; 5E9423A14578DA75 CRC64;
Query Match 89.7%; Score 26; DB 1; Length 196;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TYAMH 5
DB 134 TYALH 138
RESULT 29
Q9CKO5 PRELIMINARY; PRT; 202 AA.
ID Q9CKO5
AC Q9CKO5
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein PM1551.
GN OrderedLocusNames=PM1551;
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellales; Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Pm70;
RX MERLIN=21145866; PubMed=11248100; DOI=10.1073/pnas.051634598;
RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whitlam T.S., Kapur V.,
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465 (2001).
RL EMBL; AF006192; AAK03635.1; -.
DR HSSP; Q9ZVQ3; 1E6B.
DR InterPro; IPR004046; GST_Cterm.
DR InterPro; IPR010987; GST_C-like.
DR InterPro; IPR004045; GST_Nterm.
DR Pfam; PF02798; GST_N; 1.

KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 202 AA; 23181 MW; 5B6D95AE3FE02E73 CRC64;
Query Match 89.7%; Score 26; DB 2; Length 202;
Best Local Similarity 80.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TYAMH 5
DB 172 TYALH 176
RESULT 30
Q9CGN1 PRELIMINARY; PRT; 213 AA.
ID Q9CGN1
AC Q9CGN1
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein F28L5.12.
GN Name=F28L5.12;
OS Arabidopsis thaliana (mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,
Maiti R., Ronning C.M., Koo H., Fujii C.Y., Utechtack T.R.,
RA Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
RL Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AC079280; AAG50576.1; -.
DR PIR; H86403; H86403.
KW Hypothetical protein.
SQ SEQUENCE 213 AA; 25121 MW; D98C5F7BC5EC199C CRC64;
Query Match 89.7%; Score 26; DB 2; Length 213;
Best Local Similarity 80.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TYAMH 5
DB 202 TYALH 206
RESULT 31
Q9DG60 PRELIMINARY; PRT; 217 AA.
ID Q9DG60
AC Q9DG60
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Zinc finger protein Salt (Fragment).
GN Name=Salt;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Ruteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Mhlanga M., Brewster R., Ruiz i Altaba A.;
RL Submitted (AUG-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF11559; AAG09433.1; -.
FT NON_TER 1
SQ SEQUENCE 217 AA; 23167 MW; 44D3828F471668E2 CRC64;
Query Match 89.7%; Score 26; DB 2; Length 217;
Best Local Similarity 80.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 TYAMH 5

Db 132 TYSMH 136

RESULT 32

09UX67 PRELIMINARY; PRT; 222 AA.

AC 09UX67
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 25-OCT-2004 (TREMblrel. 28, Last annotation update)
 DE Hypothetical protein ORF-c16.036 (Hypothetical protein SSC0678).
 GN Name-ORF-c16.036; OrderedLocNames=SS00678;
 OS Sulfolobus solfataricus.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC Sulfolobus.
 NCBI_TaxID=2287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=P2.
 RX MEDLINE=20165948; PubMed=10701121; DOI=10.1139/gen-43-1-116;
 RA Charlebois R.L., Singh R.K., Chan-Weher C.C.Y., Allard G., Chow C.,
 RA Confalonieri F., Curtis B., Duguet M., Erasus G., Paquy D.,
 RA Gaasterland T., Garrett R.A., Gordon P., Jeffries A.C., Kozera C.,
 RA Kushwaha N., Lafleur E., Medina N., Peng X., Penny S.L., She Q.,
 RA St Jean A., Van Der Oost J., Young F., Zivanovic Y., Doolittle W.F.,
 RA Ragan M.A., Sengen C.W.;
 RT "Gene content and organization of a 281-kbp contig from the genome of
 RT the extremely thermophilic archaeon, Sulfolobus solfataricus P2.";
 RL Genome 43:116-136(2000).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 35092 / DSM 1617 / P2;
 RX MEDLINE=21332296; PubMed=11427726; DOI=10.1073/pnas.141222098;
 RA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
 RA Aveyez M.J., Chan-Weher C.C.-Y., Clausen I.G., Curtis B.A.,
 RA De Moers A., Erasus G., Fletcher C., Gordon P.M.K.,
 RA Heikamp-de Jong I., Jeffries A.C., Kozera C., Medina N., Peng X.,
 RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
 RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
 RA Garrett R.A., Ragan M.A., Sengen C.W., Van der Oost J.;
 RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
 DR EMBL; Y18930; CAB57625.1; -;
 DR EMBL; AE006695; AA40980.1; -;
 DR PIR; E90215; E90215.
 DR InterPro; IPR002761; DUF71.
 DR Pfam; PF01903; ATP_bind_4; 1.
 DR TIGRFAMs; TIGR00290; M0570_dom; 1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 222 AA; 25574 MW; C67F5F29712CE82F CRC64;

Query Match 89.7%; Score 26; DB 2; Length 222;
 Best Local Similarity 80.0%; Pred. No. 3.2e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
 |||:
 14 TYALH 18

RESULT 33

Q20984 PRELIMINARY; PRT; 228 AA.

AC 020984
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)
 DE Hypothetical protein F58B6.8.
 GN ORFNames=F58B6.8;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditia.

OX NCBI_TaxID=6239;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C.elegans: A platform for
 RT investigating biology.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA McMurray A.A.;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z70754; CA94778.1; -;
 DR PIR; T22924; T22924.
 DR WormBase; WBGene00010257; F58B6.8.
 DR WormPep; F58B6.8; CE06023.
 KW Hypothetical protein.
 SQ SEQUENCE 228 AA; 25181 MW; 55F66019EE3A882E CRC64;

Query Match 89.7%; Score 26; DB 2; Length 228;
 Best Local Similarity 80.0%; Pred. No. 3.3e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
 |||:
 177 TYALH 181

RESULT 34

Q8SHP4 PRELIMINARY; PRT; 229 AA.

AC Q8SHP4
 DT 01-JUN-2002 (TREMblrel. 21, Created)
 DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Trichoderma reesei (Hypocrea jecorina).
 OC Mitochondrion.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
 NCBI_TaxID=51453;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21950703; PubMed=11825887; DOI=10.1074/jbc.M107651200;
 RA Chambergo F.S., Bonaccorsi E.D., Ferreira A.J.S., Ramos A.S.P.,
 RA Ferreira J.R.J., Abramo-Neto J., Farah J.P.S., El-Dorry H.;
 RT "Elucidation of the metabolic fate of glucose in the filamentous
 RT fungus Trichoderma reesei using expressed sequence tag (EST) analysis
 RT and cDNA microarrays.";
 RL J. Biol. Chem. 277:13983-13988(2002).
 DR EMBL; AF447590; AL74168.1; -;
 DR GO; GO:0005739; C:mitochondrion; IEA.
 DR GO; GO:0003677; P:DNA binding; IEA.
 DR GO; GO:0003679; P:DNA binding; IEA.
 DR GO; GO:0006314; P:endonuclease activity; IEA.
 DR InterPro; IPR001982; P:intronic homing; IEA.
 DR Pfam; PF00961; LAGLIDADG_1; 2.
 KW Hypothetical protein; Mitochondrion.
 SQ SEQUENCE 229 AA; 26909 MW; BC5E7B377C19A3C CRC64;

Query Match 89.7%; Score 26; DB 2; Length 229;
 Best Local Similarity 80.0%; Pred. No. 3.3e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
 |||:
 46 TYALH 50

RESULT 35

Q8Y918

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ID 08Y918 PRELIMINARY; PRT; 242 AA.
AC Q8Y918;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE lmo0724 protein.
GN OrderedLocustNames=lmo0724;
OS Bacteria monocyctogenes.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EGD-e / Serovar 1/2a;
RX MEDLINE=21537279; PubMed=11679669; DOI=10.1126/science.1063447;
RA Glaser P., Frangoul L., Buchrieser C., Rusnok C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Checouani F., Couve E., de Daruvar P., Delhou P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Duesurget O.,
RA Entian K.-D., Fehli H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordsiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schueter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RL Science 294:849-852(2001).
DR EMBL; AL591976; CAC98802.1; -
DR PIR; AD1165; AD1165.
DR ListList; LMO0724; -
DR PROSITE; PS00639; THIOI_PROTEASE_HIS; UNKNOWN_1.
KM Complete proteome.
SQ SEQUENCE 242 AA; 26837 MW; E2D06DB33570BB8D CRC64;

Query Match 89.7%; Score 26; DB 2; Length 242;
Best Local Similarity 80.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 191 TYSMH 195

RESULT 36
ID Q92DT0 PRELIMINARY; PRT; 242 AA.
AC Q92DT0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE lmo0732 protein.
GN OrderedLocustNames=lmo0732;
OS Listeria innocua.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1642;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIP 11262 / Serovar 6a;
RX MEDLINE=21537279; PubMed=11679669; DOI=10.1126/science.1063447;
RA Glaser P., Frangoul L., Buchrieser C., Rusnok C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Checouani F., Couve E., de Daruvar P., Delhou P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Duesurget O.,
RA Entian K.-D., Fehli H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordsiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schueter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RL Science 294:849-852(2001).
DR EMBL; AL596166; CAC95964.1; -

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DR PIR; AD1524; AD1524.
DR ListList; LIN0732; -
DR InterPro; IPR000169; Pept_cys_acsite.
DR PROSITE; PS00639; THIOI_PROTEASE_HIS; UNKNOWN_1.
KM Complete proteome.
SQ SEQUENCE 242 AA; 26751 MW; 7AC7946460DF39A7 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 242;
Best Local Similarity 80.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 191 TYSMH 195

RESULT 37
ID Q722H3 PRELIMINARY; PRT; 242 AA.
AC Q722H3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE lmo0724 protein.
GN OrderedLocustNames=lmo0724;
OS Bacteria monocyctogenes (serotype 4b / strain F2365).
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=265669;
RN [1]
RP SEQUENCE FROM N.A.
RC PubMed=15115801; DOI=10.1093/nar/gkh562;
RX Nelson K.E., Fouts D.E., Mongodin E.F., Ravel J., DeBoy R.T.,
RA Kolonay J.F., Raeko D.A., Anguino S.V., Gill S.R., Paulsen I.T.,
RA Peterson J.D., White O., Nelson W.C., Niernan W.C., Beanan M.J.,
RA Brinkac L.M., Daugherty S.C., Dodson R.J., Durkin A.S., Madupu R.,
RA Haft D.H., Selengut J., Van Aken S.E., Khouri H.M., Fedorova N.,
RA Fothergill H.A., Tran B., Katharion S., Wonderling L.D., Ulrich G.A.,
RA Bayles D.O., Luchanansky J.B., Fraser C.M.;
RT "Whole genome comparisons of serotype 4b and 1/2a strains of the food-borne pathogen Listeria monocyctogenes reveal new insights into the core genome components of this species.";
RL Nucleic Acids Res. 32:2386-2395(2004).
DR EMBL; AE017324; AAT03541.1; -
DR InterPro; IPR000169; Pept_cys_acsite.
DR PROSITE; PS00639; THIOI_PROTEASE_HIS; UNKNOWN_1.
KM Complete proteome.
SQ SEQUENCE 242 AA; 26802 MW; 8C6903FDD8926A32 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 242;
Best Local Similarity 80.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 191 TYSMH 195

RESULT 38
ID Q8WRC3 PRELIMINARY; PRT; 244 AA.
AC Q8WRC3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE lmo0724 protein.
GN Endonuclease.
DE Name=TrEB1;
OS Tetrahymena thermophila.
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
OC Tetrahymenida; Tetrahymenidae; Tetrahymena.
OX NCBI_TaxID=5911;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=22030828; PubMed=12034842; DOI=10.1093/nar/30.11.2524;

```

RA Mutschick J.D., Gershan J.A., Lochowicz A.J., Li S., Karrer K.M.;
 RT "A novel family of mobile genetic elements is limited to the germline
 RL genome in *Tetrahymena thermophila*.";
 DR Nucleic Acids Res. 30:2524-2537(2002).
 DR EMBL/AF451862; AAL73456.1; -;
 DR GO:GO:0005634; C:nucleus; IEA.
 DR GO:GO:0004519; F:endonuclease activity; IEA.
 DR GO:GO:0003676; F:nucleic acid binding; IEA.
 DR GO:GO:0003700; F:transcription factor activity; IEA.
 DR GO:GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR Pfam; PF01844; HNH; 1.
 DR Pfam; PF07463; NUDOD4; 1.
 DR SMART; SM00507; HNHc; 1.
 KW Endonuclease.
 SQ SEQUENCE 244 AA; 28678 MW; C4805D4E8E2CA4CB CRC64;

Query March 89.7%; Score 26; DB 2; Length 244;
 Best Local Similarity 80.0%; Pred. No. 3.6e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 TYAMH 5
 |||:
 Db 128 TYSMH 132

RESULT 39
 Q885R2 PRELIMINARY; PRT; 248 AA.
 AC Q885R2;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Membrane protein, putative.
 GN OrderedLocusNames=PSPT01769;
 OS *Pseudomonas syringae* (pv. tomato).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OC NCBI_TaxID=323;
 OX [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=DC3000;
 RC MEDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.1731982100;
 RX Buell C.R., Joarist V., Lindeberg M., Selengut J., Paulsen I.T.,
 RA Gwyn M.T., Dodson R.J., DeBoy R.T., Durkin A.S., Kolonay J.F.,
 RA Madupu R., Daugherty S.C., Brinkac L.M., Beanan M.J., Haft D.H.,
 RA Nelson W.C., Davidson T.M., Zafar N., Zhou L., Liu J., Yuan Q.,
 RA Khouri H.M., Fedorova N.B., Tran B., Russell D., Berry K.J.,
 RA Uterback T.R., Van Aken S.E., Feldblyum T.V., D'Ascenzo M.,
 RA Deng W.-L., Ramos A.R., Alfano J.R., Cartinhour S., Chatterjee A.K.,
 RA Delaney T.P., Lazarowitz S.G., Martin G.B., Schneider D.J., Tang X.,
 RA Bender C.L., White O., Fraser C.M., Collier A.;
 RT "The complete genome sequence of the Arabidopsis and tomato pathogen
 RT *Pseudomonas syringae* pv. tomato DC3000.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186(2003).
 DR EMBL; AE016862; AA055289.1; -;
 DR TIGR; PSP01769; -;
 DR InterPro; IPR002781; DUF81.
 DR Pfam; PF01925; DUF81; 1.
 KW Complete proteome.
 SQ SEQUENCE 248 AA; 26313 MW; DCEADEE42B6161CE CRC64;

Query Match 89.7%; Score 26; DB 2; Length 248;
 Best Local Similarity 80.0%; Pred. No. 3.6e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 TYAMH 5
 |||:
 Db 191 TYALH 195

RESULT 40
 Q708W1 PRELIMINARY; PRT; 266 AA.
 ID Q708W1

AC Q708W1;
 DT 01-MAR-2004 (TREMBlrel. 26, Created)
 DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE AGCP11755
 GN Name=agCG46584; ORFNames=ENSANG00000018095;
 OS Anopheles gambiae str. PEST.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
 OX NCBI_TaxID=180454;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PEST;
 RA Anopheles Genome Sequencing Consortium;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC EMBL; AAB01008933; EAA09904.1; -;
 DR GO:GO:0008757; F:S-adenosylmethionine-dependent methyltransf. . .; IEA.
 DR InterPro; IPR001601; Methyltransf.
 DR InterPro; IPR000051; SAM bind.
 DR InterPro; IPR010233; UbiG_mtfase.
 DR TIGRfams; TIGR01983; UbiG_1.
 SQ SEQUENCE 266 AA; 30168 MW; 2F342C53863CFA08 CRC64;

Query Match 89.7%; Score 26; DB 2; Length 266;
 Best Local Similarity 80.0%; Pred. No. 3.9e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 TYAMH 5
 |||:
 Db 258 TYALH 262

Search completed: March 31, 2005, 12:09:37
 Job time : 35.3698 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 31, 2005, 11:42:18 ; Search time 131.75 Seconds
(without alignments)
49.905 Million cell updates/sec

Title: US-10-614-959-11

Sequence: 1 IISYDGSKYYADSVKG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqp1980s:*\n2: geneseqp1990s:*\n3: geneseqp2000s:*\n4: geneseqp2001s:*\n5: geneseqp2002s:*\n6: geneseqp2003as:*\n7: geneseqp2003bs:*\n8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	88	100.0	17	3	AA79069 Anti-Fact
2	87	98.9	118	5	AB07230 Anti-IL-4
3	87	98.9	248	5	ABP45312 Human Bly
4	87	98.9	248	5	ABP44905 Human Bly
5	87	98.9	248	5	ABP44903 Human Bly
6	87	98.9	248	7	ADG95730 Single ch
7	87	98.9	248	7	ADG95732 Single ch
8	87	98.9	248	7	ADG96139 Single ch
9	87	98.9	251	5	ABP45103 Human Bly
10	87	98.9	251	7	ADG95930 Single ch
11	86	97.7	135	7	ADG28319 Human het
12	85	96.6	119	5	AB07186 sHlgM22 h
13	84	95.5	17	7	AB033850 Anti-GPI-
14	84	95.5	112	7	AB033836 Human ant
15	84	95.5	119	5	AB07169 sHlgM22 h
16	84	95.5	119	8	AD126654 Human ant
17	83	94.3	17	8	AA79076 Anti-Fact
18	83	94.3	123	8	ADP22108 Human ant
19	83	94.3	125	7	ADP28443 Human ant
20	83	94.3	137	7	ADP28233 Human het
21	83	94.3	137	7	ADP28331 Human het
22	83	94.3	252	5	ABP45679 Human Bly
23	83	94.3	252	7	ADG96506 Single ch
24	83	94.3	470	7	ADP28467 Human ant
25	83	94.3	614	5	AB06275 Plasmid s

26	82	93.2	17	2	AAW90298 Human ant
27	82	93.2	17	3	AA79074 Anti-Fact
28	82	93.2	17	3	AA79078 Anti-Fact
29	82	93.2	17	5	AA017790 CDR2 regl
30	82	93.2	17	7	AD332094 Human int
31	82	93.2	17	8	ADH89402 Human tra
32	82	93.2	17	8	ADP47199 Human pho
33	82	93.2	17	8	ADP47199 Human pho
34	82	93.2	17	8	ADP47199 Human pho
35	82	93.2	17	8	ADP47199 Human pho
36	82	93.2	17	8	ADP47199 Human pho
37	82	93.2	17	8	ADP47199 Human pho
38	82	93.2	17	8	ADP47199 Human pho
39	82	93.2	17	8	ADP47199 Human pho
40	82	93.2	17	8	ADP47199 Human pho
41	82	93.2	17	8	ADP47199 Human pho
42	82	93.2	17	8	ADP47199 Human pho
43	82	93.2	17	8	ADP47199 Human pho
44	82	93.2	17	8	ADP47199 Human pho
45	82	93.2	17	8	ADP47199 Human pho

ALIGNMENTS

RESULT 1	AA79069	standard; peptide; 17 AA.
ID	AA79069	standard; peptide; 17 AA.
AC	AA79069;	
DT	12-JUN-2000	(first entry)
DE	Anti-factor IX/IXa antibody H chain V domain CDR2 amino acid sequence.	
XX	Complementarily determining region 2; CDR2; antibody; Gla domain;	
KW	factor IX/IXa; blood coagulation; deep venous thrombosis;	
KW	arterial thrombosis; unstable angina; post myocardial infarction;	
KW	coronary artery bypass graft; CABG; stroke; tumour growth; metastasis;	
KW	percutaneous transluminal coronary angioplasty; PTCA; inflammation;	
KW	septic shock; hypotension; adult respiratory distress syndrome; ARDS;	
KW	arterial fibrillation; disseminated intravascular coagulopathy; DIC.	
OS	Homo sapiens.	
XX		
PN	WO200012562-A1.	
XX		
PD	09-MAR-2000.	
XX		
PF	26-AUG-1999; 99WO-US019453.	
XX		
PR	28-AUG-1998; 98US-0098233P.	
XX		
PR	03-MAR-1999; 99US-0122767P.	
XX		
PA	(GETH) GENENTECH INC.	
XX		
PI	Adams CM, Devaux B, Eaton DL, Hass PE, Judice JK, Kirchhofer D;	
PI	Suggett S;	
XX		
DR	WPI; 2000-256595/22.	
XX		
PT	Novel human anti-factor IX/IXa antibodies against IX/IXa gamma-	
PT	carboxylglutamic acid domains useful as anti-coagulant in thrombosis,	
PT	stroke, and post myocardial infarction.	
XX		
XX	Claim 2; Fig 2; 84pp; English.	
CC	This sequence represents a complementarily determining region 2 (CDR2) of	
CC	antibody. Factor IXa is a vitamin K dependent plasma serine protease that	
CC	participates in the blood coagulation pathways. The Gla domain of factor	
CC	IXa and its zymogen factor IX contains important structural determinants	
CC	for interaction with high affinity binding sites on vascular endothelial	

CC cells and platelets. Compositions comprising the antibodies are used for
CC the treatment or prophylaxis of thrombotic or coagulopathic diseases or
CC disorders in a mammal for which inhibiting a FII/IXa mediated event is
CC indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable
CC angina, post myocardial infarction, post surgical thrombosis, coronary
CC artery bypass graft (CABG), percutaneous transluminal coronary
CC angioplasty (PTCA), stroke, tumour growth, invasion or metastasis,
CC inflammation, septic shock, hypotension, adult respiratory distress
CC syndrome (ARDS), arterial fibrillation and disseminated intravascular
CC coagulopathy (DIC)

CC Sequence 17 AA;
SQ

Query Match 100.0%; Score 88; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.2e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 IISYDGSKKYYADSVK 17
Db 1 IISYDGSKKYYADSVK 17

RESULT 2
ABR07230
ID ABR07230 standard; protein; 118 AA.
XX
AC ABR07230;
XX
DT 26-MAR-2002 (first entry)
XX
DE Anti-IL-4 receptor MAb 6-2 heavy chain variable region.
XX
KW Human; antibody; interleukin; IL-4; antagonist; receptor; IL-4 receptor;
KW antiarthritic; dermatological; antitumor; antiinflammatory; cytostatic;
KW anticaking; immunosuppressive; tuberculostatic; ophthalmological;
KW antianemic; antithyroid.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 31..35
FT /note="complementarity determining region (CDR) 1"
FT Region 50..66
FT /note="complementarity determining region (CDR) 2"
FT Region 99..107
FT /note="complementarity determining region (CDR) 3"
FT Region
XX
FN WO200192340-A2.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US017094.
XX
PR 26-MAY-2000; 2000US-00579808.
PR 19-SEP-2000; 2000US-00665343.
PR 15-FEB-2001; 2001US-00785934.
PR 01-MAY-2001; 2001US-00847816.
XX
PA (IMMUNEX CORP.
XX
PI Plueneke JD;
XX
DR WPI; 2002-114332/15.
DR N-PSDB; ABA94330.
XX
PT Novel human antibody which binds human interleukin (IL)-4 receptor and is
PT capable of inhibiting IL-4 induced biological activity, functions as IL-4
PT antagonist and is useful for treating septic arthritis, scleroderma.
XX
PS Claim 4; Page 73; 85pp; English.
XX
CC The invention relates to a human antibody (an interleukin (IL)-4
CC antagonist) (I) that binds human IL-4 receptor (IL-4R), and is capable of

CC inhibiting an IL-4-induced biological activity. (I) is also useful for
CC inhibiting both IL-4-induced biological activity and IL-13-induced
CC biological activity in vivo in a human, and for treating septic arthritis
CC in a human afflicted with septic arthritis. (I) is also used for treating
CC conditions such as septic/reactive arthritis, dermatitis herpetiformis,
CC urticaria (especially chronic idiopathic urticaria), ulcers, gastric
CC inflammation, mucosal inflammation, ulcerative colitis, Crohn's disease,
CC inflammatory bowel disease, other disorders of the digestive system in
CC which IL-4 plays a role (e.g. IL-4-induced inflammation of part of the
CC gastrointestinal tract), conditions in which IL-4-induced barrier
CC disruption plays a role (e.g. conditions characterized by decreased
CC epithelial barrier function in the lung or gastrointestinal tract),
CC scleroderma, hypertrophic scarring, Whipple's disease, benign prostatic
CC hyperplasia, IL-4-induced pulmonary conditions, allergic reactions to
CC medication, Kawasaki disease, sickle cell disease or crisis, Churg-
CC Strauss syndrome, Grave's disease, pre-eclampsia, Sjogren's syndrome,
CC autoimmune lymphoproliferative syndrome, autoimmune haemolytic anemia,
CC Barrett's esophagus, autoimmune uveitis, tuberculosis, nephrosis,
CC pemphigus vulgaris or bullous pemphigoid (autoimmune blistering
CC diseases), and myasthenia gravis (an autoimmune muscular disease). IL-4
CC antagonists also find use as adjuvants to allergy immunotherapy and as
CC vaccine adjuvants, especially when directing the immune response toward a
CC TH1 response would be beneficial in treating or preventing the disease.
CC The present sequence represents an anti-IL-4 receptor monoclonal antibody
CC (MAb) 6-2 heavy chain variable region
XX
SQ Sequence 118 AA;
XX

Query Match 98.9%; Score 87; DB 5; Length 118;
Best Local Similarity 94.1%; Pred. No. 4.1e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 IISYDGSKKYYADSVK 17
Db 50 IISYDGSKKYYADSVK 66

RESULT 3
ABP45312
ID ABP45312 standard; protein; 248 AA.
XX
AC ABP45312;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human BlyS binding scFv SEQ ID 1323.
XX
KW BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antineumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
XX
OS Homo sapiens.
XX
FN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US019110.
XX
PR 16-JUN-2000; 2000US-0212210P.
PR 17-OCT-2000; 2000US-0240816P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX

```

DR      WPI; 2002-114799/15.
XX
XX      Antibodies against B lymphocyte Stimulating polypeptides, useful for the
PT      diagnosis and treatment of cancers and immune disorders.
XX
XX      Claim 1; Page 1981-1982; 3148pp; English.
XX
XX      This invention describes novel antibodies that immunospecifically bind to
CC      B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC      tumour necrosis factor (TNF) super family and induces B cell
CC      proliferation and differentiation. The antibodies of the invention have
CC      cytosolic, immunosuppressive, immunostimulant, immunomodulatory,
CC      antirheumatic and antiAIDS activity and can be used in vaccines to
CC      inhibit the expression and activity of Blys. The antibodies bind to Blys
CC      and so may be used to detect and quantitate the presence of Blys in
CC      biological samples and may be used in this way to diagnose disease
CC      associated with aberrant expression of Blys. They may also be
CC      administered to treat diseases associated with aberrant Blys expression
CC      and activity such as cancer, immune, and autoimmune disorders and
CC      diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC      immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC      acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC      the antibodies and fragments of the antibodies described in the method of
CC      the invention
XX
XX      Sequence 248 AA;
SQ
XX
XX      Query Match          98.9%; Score 87; DB 5; Length 248;
XX      Best Local Similarity 94.1%; Pred. No. 9.3e-06;
XX      Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0.
XX
XX      1 IISYDGSKKYYADSVYKG 17
XX      :|||||
XX      50 VISYDGSKKYYADSVYKG 66
XX
XX
XX      RESULT 4
XX      ID      ABP44905
XX      ID      ABP44905 standard; protein; 248 AA.
XX
XX      ABP44905;
XX
XX      19-AUG-2002 (first entry)
XX
XX      Human Blys binding scFv SEQ ID 916.
XX
XX      Blys; B lymphocyte stimulator; TNF superfamily; human; cytosolic;
XX      tumour necrosis factor; B cell proliferation; B cell differentiation;
XX      immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
XX      antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
XX      systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
XX      common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
XX      Homo sapiens.
XX
XX      WO200202641-A1.
XX
XX      10-JAN-2002.
XX
XX      15-JUN-2001; 2001WO-US019110.
XX
XX      16-JUN-2000; 2000US-0212210P.
XX      17-OCT-2000; 2000US-0240816P.
XX      16-MAR-2001; 2001US-0275248P.
XX      21-MAR-2001; 2001US-0277379P.
XX      25-MAY-2001; 2001US-0293499P.
XX
XX      (HUMA-) HUMAN GENOME SCI INC.
XX      (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX      Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D,
XX      WPI; 2002-114799/15.

```

PT	XX	Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
XX	XX	diagnosis and treatment of cancers and immune disorders.
PS	XX	Claim 1; Page 1495-1496; 3148bp; English.
XX	XX	This invention describes novel antibodies that immunospecifically bind to
CC	CC	B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC	CC	tumour necrosis factor (TNF) super family and induces B cell
CC	CC	proliferation and differentiation. The antibodies of the invention have
CC	CC	cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC	CC	antipneumatic and antiAIDS activity and can be used in vaccines to
CC	CC	inhibit the expression and activity of Blys. The antibodies bind to Blys
CC	CC	and so may be used to detect and quantitate the presence of Blys in
CC	CC	biological samples and may be used in this way to diagnose disease
CC	CC	associated with aberrant expression of Blys. They may also be
CC	CC	administered to treat diseases associated with aberrant Blys expression
CC	CC	and activity such as cancer, immune, and autoimmune disorders and
CC	CC	diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC	CC	immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC	CC	acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC	CC	the antibodies and fragments of the antibodies described in the method of
CC	CC	the invention
XX	XX	
XX	XX	Sequence 248 AA;
XX	XX	
SO	SO	
Query Match	98.9%;	Score 87; DB 5; Length 248;
Best Local Similarity	94.1%;	Pred. No. 9.3e-06;
Matches 16;	Conservative 1;	Mismatches 0; Indels 0; Gaps 0;
OY	1	IIISYDGSKKYYADSVKG 17
	:	
Db	50	VISYDGSKKYYADSVKG 66
XX	XX	
RESULT 5		
ABP44903		
ID	ABP44903	standard; protein; 248 AA.
XX	XX	
AC	ABP44903;	
XX	XX	
DT	19-AUG-2002	(first entry)
XX	XX	
DE	Human Blys binding scFv SEQ ID 914.	
XX	XX	
Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;		
tumour necrosis factor; B cell proliferation; B cell differentiation;		
immunosuppressive; immunostimulant; immunomodulatory; antipneumatic;		
antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;		
systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;		
common variable immunodeficiency; acquired immunodeficiency syndrome.		
XX	XX	
OS	Homo sapiens.	
XX	XX	
XX	WO200202641-A1.	
XX	XX	
PD	10-JAN-2002.	
XX	XX	
PF	15-JUN-2001; 2001WO-US019110.	
XX	XX	
PR	16-JUN-2000; 2000US-0212210P.	
PR	17-OCT-2000; 2000US-0240816P.	
PR	16-MAR-2001; 2001US-0276248P.	
PR	21-MAR-2001; 2001US-0277379P.	
PR	25-MAY-2001; 2001US-0293499P.	
XX	XX	
PA	(HUMA-) HUMAN GENOME SCI INC.	
XX	XX	
PA	(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.	
XX	XX	
BT	Ruben SM, Baraah SC, Choi GH, Vaughan T, Hilbert D;	
XX	XX	
XX	XX	WPI; 2002-114799/15.
XX	XX	

PT Antibodies against B lymphocyte Stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.
XX
XX Claim 1; Page 1492-1493; 3148pp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cyostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antineumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). AB43990-AB47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
SQ Sequence 248 AA;
XX
Query Match 98.9%; Score 87; DB 5; Length 248;
Best Local Similarity 94.1%; Pred. No. 9.3e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 IISYDGSKKYYADSVKG 17
Db 50 VISYDGSKKYYADSVKG 66
XX
RESULT 6
ADG95730
ID ADG95730 standard; protein; 248 AA.
XX
AC ADG95730;
XX
DT 11-MAR-2004 (first entry)
XX
DE Single chain antibody that immunospecifically binds Blys Segid 914.
XX
KW antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
KW B cell proliferation; differentiation; scFv; myasthenia gravis;
KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
KW carcinoma; lymphoma; antineumatic; antiarthritic; neuroprotective;
KW antiinflammatory; antiaesthetic; antiallergic; cyostatic.
XX
OS Unidentified.
XX
PN WO2003055979-A2.
XX
PD 10-JUL-2003.
XX
PF 14-NOV-2002; 2002WO-US036496.
XX
PR 16-NOV-2001; 2001US-0331469P.
XX
PR 19-DEC-2001; 2001US-0340817P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan TV, Hilbert D;
XX
DR WPI; 2003-505530/47.
XX
PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator
PT (Blys), useful for detecting and treating diseases or disorders e.g.
PT rheumatoid arthritis, asthma and leukemia.
XX
PS Example 1; SEQ ID NO 914; 394pp; English.
XX

CC This invention relates to novel antibodies that immunospecifically bind
CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
CC chromosome 13q34 and encodes a protein that is a member of the tumour
CC necrosis factor superfamily and induces both in vivo and in vitro B cell
CC proliferation and differentiation. Specifically, it refers to single
CC chain antibody molecules (scFvs) derived, preferably, from the variable
CC heavy CDR3 region that immunospecifically bind to a polypeptide, or
CC fragment thereof, of either human, murine, rat or monkey Blys. The
CC present invention refers to the use of such antibodies in various methods
CC for the detection, diagnosis and prognosis of diseases related to the
CC aberrant expression or inappropriate function of Blys or its receptor. As
CC such, these compositions are useful for identifying immune disorders
CC including myasthenia gravis and multiple sclerosis, inflammatory
CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
CC as AIDS and proliferative disorders including leukaemia, carcinoma and
CC lymphoma. Accordingly, they can be described as exhibiting various
CC activities such as antineumatic, antiarthritic, neuroprotective,
CC antiinflammatory, antiaesthetic, antiallergic and cyostatic. This
CC polypeptide sequence is a single chain antibody that binds Blys of the
CC invention. NOTE: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 248 AA;
XX
Query Match 98.9%; Score 87; DB 7; Length 248;
Best Local Similarity 94.1%; Pred. No. 9.3e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 IISYDGSKKYYADSVKG 17
Db 50 VISYDGSKKYYADSVKG 66
XX
RESULT 7
ADG95732
ID ADG95732 standard; protein; 248 AA.
XX
AC ADG95732;
XX
DT 11-MAR-2004 (first entry)
XX
DE Single chain antibody that immunospecifically binds Blys Segid 916.
XX
KW antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
KW B cell proliferation; differentiation; scFv; myasthenia gravis;
KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
KW carcinoma; lymphoma; antineumatic; antiarthritic; neuroprotective;
KW antiinflammatory; antiaesthetic; antiallergic; cyostatic.
XX
OS Unidentified.
XX
PN WO2003055979-A2.
XX
PD 10-JUL-2003.
XX
PF 14-NOV-2002; 2002WO-US036496.
XX
PR 16-NOV-2001; 2001US-0331469P.
XX
PR 19-DEC-2001; 2001US-0340817P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan TV, Hilbert D;
XX
DR WPI; 2003-505530/47.
XX
PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator
PT (Blys), useful for detecting and treating diseases or disorders e.g.
PT rheumatoid arthritis, asthma and leukemia.
XX
PS Example 1; SEQ ID NO 916; 394pp; English.
XX

CC This invention relates to novel antibodies that immunospecifically bind
CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
CC chromosome 13q34 and encodes a protein that is a member of the tumour
CC necrosis factor superfamily and induces both in vivo and in vitro B cell
CC proliferation and differentiation. Specifically, it refers to single
CC chain antibody molecules (scFvs) derived, preferably, from the variable
CC heavy CDR3 region that immunospecifically bind to a polypeptide, or
CC fragment thereof, of either human, murine, rat or monkey Blys. The
CC present invention refers to the use of such antibodies in various methods
CC for the detection, diagnosis and prognosis of diseases related to the
CC aberrant expression or inappropriate function of Blys or its receptor. As
CC such, these compositions are useful for identifying immune disorders
CC including myasthenia gravis and multiple sclerosis, inflammatory
CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
CC as AIDS and proliferative disorders including leukaemia, carcinoma and
CC lymphoma. Accordingly, they can be described as exhibiting various
CC activities such as antirheumatic, antiarthritic, neuroprotective,
CC antiinflammatory, antiallergic and cytostatic. This
CC polypeptide sequence is a single chain antibody that binds Blys of the
CC invention. NOTE: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 248 AA;

Query Match 98.9%; Score 87; DB 7; Length 248;
Best Local Similarity 94.1%; Pred. No. 9.3e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSKKYYADSVKG 66

RESULT 8
ADG96139 ID ADG96139 standard; protein; 248 AA.

XX AC ADG96139;

XX DT 11-MAR-2004 (first entry)

XX DE Single chain antibody that immunospecifically binds Blys seqID 1323.

XX KW antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
KW B cell proliferation; differentiation; scFv; myasthenia gravis;
KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
KW carcinoma; lymphoma; antirheumatic; antiallergic; neuroprotective;
KW antiinflammatory; antisthmatic; antiallergic; cytostatic.

XX OS Unidentified.

XX PN WO2003055979-A2.

XX PD 10-JUL-2003.

XX PF 14-NOV-2002; 2002WO-US036496.

XX PR 16-NOV-2001; 2001US-0331469P.

XX PR 19-DEC-2001; 2001US-0340817P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Ruben SM, Baraah SC, Choi GH, Vaughan TJ, Hilbert D;

XX XX WPI; 2003-505530/47.

XX PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator
XX (Blys), useful for detecting and treating diseases or disorders e.g.
XX rheumatoid arthritis, asthma and leukemia.

XX PS Example 1; SEQ ID NO 1323; 394pp; English.

CC This invention relates to novel antibodies that immunospecifically bind
CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
CC chromosome 13q34 and encodes a protein that is a member of the tumour
CC necrosis factor superfamily and induces both in vivo and in vitro B cell
CC proliferation and differentiation. Specifically, it refers to single
CC chain antibody molecules (scFvs) derived, preferably, from the variable
CC heavy CDR3 region that immunospecifically bind to a polypeptide, or
CC fragment thereof, of either human, murine, rat or monkey Blys. The
CC present invention refers to the use of such antibodies in various methods
CC for the detection, diagnosis and prognosis of diseases related to the
CC aberrant expression or inappropriate function of Blys or its receptor. As
CC such, these compositions are useful for identifying immune disorders
CC including myasthenia gravis and multiple sclerosis, inflammatory
CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
CC as AIDS and proliferative disorders including leukaemia, carcinoma and
CC lymphoma. Accordingly, they can be described as exhibiting various
CC activities such as antirheumatic, antiarthritic, neuroprotective,
CC antiinflammatory, antisthmatic, antiallergic and cytostatic. This
CC polypeptide sequence is a single chain antibody that binds Blys of the
CC invention. NOTE: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 248 AA;

Query Match 98.9%; Score 87; DB 7; Length 248;
Best Local Similarity 94.1%; Pred. No. 9.3e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSKKYYADSVKG 66

RESULT 9
ABP45103 ID ABP45103 standard; protein; 251 AA.

XX AC ABP45103;

XX DT 19-AUG-2002 (first entry)

XX DE Human Blys binding scFv SEQ ID 1114.

XX KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.

XX OS Homo sapiens.

XX PN WO200202641-A1.

XX PD 10-JAN-2002.

XX PF 15-JUN-2001; 2001WO-US019110.

XX PR 16-JUN-2000; 2000US-0212210P.

XX PR 17-OCT-2000; 2000US-0240816P.

XX PR 16-MAR-2001; 2001US-0276248P.

XX PR 21-MAR-2001; 2001US-0277379P.

XX PR 25-MAY-2001; 2001US-0293499P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Ruben SM, Baraah SC, Choi GH, Vaughan T, Hilbert D;

XX XX WPI; 2002-114799/15.

XX PT Antibodies against B lymphocyte stimulating polypeptides, useful for the

PT diagnosis and treatment of cancers and immune disorders.
XX
PS Claim 1, Page 1731-1732; 3148bp; English.
XX
CC This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antineuritic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABR43390-ABR47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
SQ Sequence 251 AA;
XX
Query Match 98.9%; Score 87; DB 5; Length 251;
Best Local Similarity 94.1%; Pred. No. 9.4e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSKKYYADSVKG 66
XX
RESULT 10
ADG95930
ID ADG95930 standard; protein; 251 AA.
XX
AC ADG95930;
XX
DT 11-MAR-2004 (first entry)
XX
DE Single chain antibody that immunospecifically binds Blys Segid 1114.
XX
KW antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
KW B cell proliferation; differentiation; scfv; myasthenia gravis;
KW multiple sclerosis; aschma; rheumatoid arthritis; AIDS; leukaemia;
KW carcinoma; lymphoma; antineuritic; antiallergic; neuroprotective;
KW antiinflammatory; antiasthmatic; antiallergic; cytostatic.
XX
OS Unidentified.
XX
PN WO2003055979-A2.
XX
PD 10-JUL-2003.
XX
PF 14-NOV-2002; 2002WO-US036496.
XX
PR 16-NOV-2001; 2001US-0331469P.
XX
PR 19-DEC-2001; 2001US-0340817P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;
XX
DR WPI; 2003-505530/47.
XX
PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator
PT (Blys), useful for detecting and treating diseases or disorders e.g.
PT rheumatoid arthritis, asthma and leukemia.
XX
XX Example 1; SEQ ID NO 1114; 394pp; English.
XX
CC This invention relates to novel antibodies that immunospecifically bind

CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
CC chromosome 13q34 and encodes a protein that is a member of the tumour
CC necrosis factor superfamily and induces both in vivo and in vitro B cell
CC proliferation and differentiation. Specifically, it refers to single
CC chain antibody molecules (scfvs) derived, preferably, from the variable
CC heavy CD3 region that immunospecifically bind to a polypeptide, or
CC fragment thereof, of either human, murine, rat or monkey Blys. The
CC present invention refers to the use of such antibodies in various methods
CC for the detection, diagnosis and prognosis of diseases related to the
CC aberrant expression or inappropriate function of Blys or its receptor. As
CC such, these compositions are useful for identifying immune disorders
CC including myasthenia gravis and multiple sclerosis, inflammatory
CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
CC as AIDS and proliferative disorders including leukaemia, carcinoma and
CC lymphoma. Accordingly, they can be described as exhibiting various
CC activities such as antineuritic, antiallergic, neuroprotective,
CC antiinflammatory, antiasthmatic, antiallergic and cytostatic. This
CC polypeptide sequence is a single chain antibody that binds Blys of the
CC invention. NOTE: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 251 AA;
XX
Query Match 98.9%; Score 87; DB 7; Length 251;
Best Local Similarity 94.1%; Pred. No. 9.4e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSKKYYADSVKG 66
XX
RESULT 11
ADD28319
ID ADD28319 standard; protein; 135 AA.
XX
AC ADD28319;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human heterodimeric antibody heavy chain variable region SEQ ID NO:97.
XX
KW human heterodimeric antibody; human; antibody; binding affinity;
KW protective antigen; Bacillus anthracis; anthrax infection; cell receptor;
KW edema factor; lethal factor; virulence; antibacterial; immunotherapy;
KW anti-toxin; anti-infective; anthrax; botulinum; smallpox;
KW Venezuelan equine encephalomyelitis virus; VEEV; West Nile virus; WNV.
XX
OS Synthetic.
XX
OS Homo sapiens.
XX
PN WO2003076568-A2.
XX
PD 18-SEP-2003.
XX
PF 11-FEB-2003; 2003WO-US004206.
XX
PR 11-FEB-2002; 2002US-0356086P.
XX
PR 29-APR-2002; 2002US-0376408P.
XX
PR 27-SEP-2002; 2002US-0414053P.
XX
PR 25-NOV-2002; 2002US-0428807P.
XX
PA (ALEX-) ALEXION PHARM INC.
XX
PI Bowdish KS, Wild MA;
XX
DR WPI; 2003-722327/68.
XX
PT New human heterodimeric antibodies or their antibody fragments, useful as
PT anti-toxins or anti-infectives with respect to infective agents, e.g.
PT anthrax, botulinum, smallpox, Venezuelan equine encephalomyelitis or West
PT Nile virus.

XX
PS Claim 11, SEQ ID NO 97, 67bp; English.
XX
CC The present invention describes a human heterodimeric antibody (I)
CC (Fragment) having a binding affinity of at least 1X10⁻⁸ M to the
CC protective antigen of Bacillus anthracis or a molecule involved in
CC anthrax infection that blocks binding of the antigen or molecule to cell
CC receptors, edema factor and lethal factor. (I) has virucide and
CC antibacterial activities, and can be used in immunotherapy. The
CC antibodies (I) are useful as anti-toxins or anti-infectives with respect
CC to infective agents, such as anthrax, botulinum, smallpox, Venezuelan
CC equine encephalomyelitis virus (VEEV), or West Nile virus (WNV). The
CC present sequence represents a human heterodimeric antibody heavy chain
CC variable region amino acid sequence, which is used in the exemplification
CC of the present invention.
XX
SQ Sequence 135 AA;
Query Match 97.7%; Score 86; DB 7; Length 135;
Best Local Similarity 94.1%; Pred. No. 6.8e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 IISYDGSKKYYADSVKG 17
:|||||:|||||:
Db 52 LIISYDGSKKYYADSVKG 68
RESULT 12
ABO7186
ID ABO7186 standard; protein; 119 AA.
XX
AC ABO7186;
XX
DT 13-MAR-2002 (first entry)
XX
DE sHlgM22 heavy chain variable region clone B sequence.
XX
KM Neuromodulatory; central nervous system; CNS; sHlgM22; LYM 22; AKJR4;
KM ebvHlgM MS19D10; ebv HlgM CB2bG8; CB2iE12; CB2iE7; MS19E5; virucide;
KM antiParkinsonian; neuroprotective; nootropic; vulnerary.
XX
OS Homo sapiens.
XX
PN MO200185797-A1.
XX
PD 15-NOV-2001.
XX
PF 30-MAY-2000; 2000WO-US014902.
XX
PR 10-MAY-2000; 2000US-00568351.
XX
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION RES.
XX
PI Rodriguez M, Miller DJ, Pease LR;
XX
DR WPI: 2002-066596/09.
DR N-PSDB; ABA94243.
XX
PT Novel neuromodulatory agent (a human Igm monoclonal antibody), promoting
PT neurite outgrowth, regeneration, remyelination and neuroprotection in
PT central nervous system, useful to treat post-infectious
PT encephalomyelitis.
XX
PS Claim 23; Fig 17, 219pp; English.
XX
CC The invention provides a neuromodulatory agent (I) capable of promoting
CC neurite outgrowth, regeneration, remyelination and neuroprotection in
CC central nervous system (CNS). (I) is capable of inducing remyelination,
CC promoting cellular proliferation of glial cells, and promoting Ca²⁺-
CC signaling with oligodendrocytes. An humanised antibody to (I) can be
CC selected from antibody sHlgM22 (LYM 22), ebvHlgM MS19D10, ebv HlgM
CC CB2bG8, AKJR4, CB2iE12, CB2iE7 or MS19E5. (I) is useful for stimulating
CC remyelination of CNS axons, stimulating proliferation of glial cells in

CC CNS axons, or treating demyelinating disease of CNS in a mammal in need
CC of such therapy. (I) is capable of binding to structures and cells within
CC CNS. (I) is preferably useful for treating a demyelinating disease of CNS
CC of a mouse infected with Strain DA of Theiler's murine encephalomyelitis
CC (TMEV) or for treating a human being having multiple sclerosis, or a post-
CC human or domestic animal with a viral demyelinating disease, or a post-
CC neutral disease of CNS. (I) is also useful for an in vitro method of
CC stimulating the proliferation of glial cells from mixed cell culture. (I)
CC is also useful for stimulating remyelination of CNS axons. The antibodies
CC are useful for preventing infection by a bacterium, virus or like
CC pathogen that causes demyelination or other neurodegenerative condition
CC in a subject. Methods where (I) is administered to a patient are useful
CC for treating multiple sclerosis, Parkinson's disease, Alzheimer's
CC disease, amyotrophic lateral sclerosis (ALS), a viral demyelinating
CC disease, CNS diseases, and other conditions in the CNS where nerves are
CC damaged as by trauma. The present sequence represents the sHlgM22 heavy
CC chain variable region clone B amino acid sequence
XX
SQ Sequence 119 AA;
Query Match 96.6%; Score 85; DB 5; Length 119;
Best Local Similarity 94.1%; Pred. No. 8.6e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 IISYDGSKKYYADSVKG 17
:|||||:|||||:
Db 50 LIISYDGSKKYYADSVKG 66
RESULT 13
ABO33850
ID ABO33850 standard; peptide; 17 AA.
XX
AC ABO33850;
XX
DT 18-SEP-2003 (first entry)
XX
DE Anti-GPI-antibody heavy chain complementarity determining region #10.
XX
KM Human, anti-glucose-6-phosphate isomerase-antibody; immunopolypeptide;
KM anti-GPI-antibody; GPI; glucose-6-phosphate isomerase;
KM autoimmune disease; rheumatoid arthritis; heavy chain variable region;
KM VH; complementarity determining region; CDR.
XX
OS Homo sapiens.
XX
PN US2002146753-A1.
XX
PD 10-OCT-2002.
XX
PF 06-APR-2001; 2001US-00828708.
XX
PR 06-APR-2001; 2001US-00828708.
XX
PA (DITZEL H. BURTON D R.
PA (SCHA// SCHALLER M.
XX
PI Ditzel H, Burton DR, Schaller M;
XX
DR WPI, 2003-521517/49.
XX
PT Immunopolypeptide for diagnosis and treatment of human autoimmune
PT disease, e.g., human rheumatoid arthritis, comprises a polypeptide that
PT binds to human glucose-6-phosphate isomerase.
XX
PS Claim 3; Fig 4A; 47pp; English.
XX
CC The invention describes an immunopolypeptide comprising a polypeptide
CC that binds to human glucose-6-phosphate isomerase (GPI). The methods and
CC compositions are used for diagnosis and treatment of human autoimmune
CC disease, e.g., human rheumatoid arthritis. This is the amino acid
CC sequence of human anti-GPI-antibody heavy chain variable region

CC complementarity determining region
XX
SQ Sequence 17 AA;

Query Match 95.5%; Score 84; DB 7; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.4e-06;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 IISYDGSKKYADSVKG 17
:|||||:|||||
Db 1 VISYDGNKKYADSVKG 17

RESULT 14

ABO33836
ID ABO33836 standard; protein, 112 AA.

AC ABO33836;

XX 18-SEP-2003 (first entry)

XX Human anti-GPI-antibody heavy chain variable region #3.

XX Human; anti-glucose-6-phosphate isomerase-antibody; immunopolypeptide;

KM anti-GPI-antibody; GPI; glucose-6-phosphate isomerase;

KM autoimmune disease; rheumatoid arthritis; heavy chain variable region;

VH.

XX Homo sapiens.

XX US2002146753-A1.

XX 10-OCT-2002.

XX 06-APR-2001; 2001US-00828708.

XX 06-APR-2001; 2001US-00828708.

XX (DITZEL) DITZEL H.

XX (BURTON) BURTON D R.

XX (SCHALLER) SCHALLER M.

XX Ditzel H, Burton DR, Schaller M;

XX WPI; 2003-521517/49.

XX Immunopolypeptide for diagnosis and treatment of human autoimmune

XX disease, e.g., human rheumatoid arthritis, comprises a polypeptide that

XX binds to human glucose-6-phosphate isomerase.

XX Claim 11; Fig 3AH; 47pp; English.

XX The invention describes an immunopolypeptide comprising a polypeptide

XX that binds to human glucose-6-phosphate isomerase (GPI). The methods and

XX compositions are used for diagnosis and treatment of human autoimmune

XX disease, e.g., human rheumatoid arthritis. This is the amino acid

XX sequence of human anti-GPI-antibody heavy chain variable region

XX Sequence 112 AA;

Query Match 95.5%; Score 84; DB 7; Length 112;

Best Local Similarity 88.2%; Pred. No. 1.2e-05;

Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 IISYDGSKKYADSVKG 17
:|||||:|||||
Db 43 VISYDGNKKYADSVKG 59

RESULT 15

ABO7169
ID ABO7169 standard; protein, 119 AA.

AC ABO7169;

XX 13-MAR-2002 (first entry)

XX sHlgM22 heavy chain variable region clone A sequence.

XX Neuromodulatory; central nervous system; CNS; sHlgM22; LYM 22; AKR4;

KM ebvHlgM M6119D10; ebv HlgM CB2B68; CB21E12; CB21E7; MS119E5; Valutide;

XX antiparkinsonian; neuroprotective; nootropic; vulnerary.

XX Homo sapiens.

XX WO200185797-A1.

XX 15-NOV-2001.

XX 30-MAY-2000; 2000US-00568351.

XX 10-MAY-2000; 2000US-00568351.

XX (MAYO-) MAYO FOUND MEDICAL EDUCATION RES.

XX Rodriguez M, Miller DJ, Pease LR;

XX WPI; 2002-066596/09.

XX N-PSDB; ABA94216.

XX Claim 23; Fig 17; 219pp; English.

XX The invention provides a neuromodulatory agent (I) capable of promoting

XX neurite outgrowth, regeneration, remyelination and neuroprotection in

XX central nervous system (CNS). (I) is capable of inducing remyelination,

XX promoting cellular proliferation of glial cells, and promoting Ca2+

XX signaling with oligodendrocytes. An humanised antibody to (I) can be

XX selected from antibody sHlgM22 (LYM 22), ebvHlgM M6119D10, ebv HlgM

XX CB2B68, AKR4, CB21E12, CB21E7 or MS119E5. (I) is useful for stimulating

XX remyelination of CNS axons, stimulating proliferation of glial cells in

XX CNS axons, or treating demyelinating disease of CNS in a mammal in need

XX of such therapy. (I) is capable of binding to structures and cells within

XX CNS. (I) is preferably useful for treating a demyelinating disease of CNS

XX (THEBV) or for treating a human being having multiple sclerosis, or a

XX human or domestic animal with a viral demyelinating disease, or a post-

XX neural disease of CNS. (I) is also useful for an in vitro method of

XX stimulating the proliferation of glial cells from mixed cell culture. (I)

XX is also useful for preventing remyelination of CNS axons. The antibodies

XX are useful for preventing infection by a bacterium, virus or like

XX pathogen that causes demyelination or other neurodegenerative condition

XX in a subject. Methods where (I) is administered to a patient are useful

XX for treating multiple sclerosis, Parkinson's disease, Alzheimer's

XX disease, amyotrophic lateral sclerosis (ALS), a viral demyelinating

XX disease, CNS diseases, and other conditions in the CNS where nerves are

XX damaged as by trauma. The present sequence represents the sHlgM22 heavy

XX chain variable region clone A amino acid sequence

XX Sequence 119 AA;

Query Match 95.5%; Score 84; DB 5; Length 119;

Best Local Similarity 88.2%; Pred. No. 1.3e-05;

Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 IISYDGSKKYADSVKG 17
:|||||:|||||
Db 50 VISYDGSKKYADSVKG 66

RESULT 16
AD126654

AD126654 standard; protein; 119 AA.
 AD126654;
 15-APR-2004 (first entry)
 Human anti IGM antibody SHIGM22 VH protein.
 Human; antibody; IGM; remyelination; neuronal growth; autoantibody;
 demyelination disease; multiple sclerosis; central nervous system; CNS;
 axon; glial cell proliferation;
 Theiler's murine encephalomyelitis virus infection; CNS injury;
 spinal cord injury.
 Homo sapiens.
 US2003185827-A1.
 02-OCT-2003.
 13-NOV-2001; 2001US-00010729.
 29-APR-1994; 94US-00236520.
 08-AUG-1996; 96US-00692084.
 07-JAN-1997; 97US-00779784.
 28-MAY-1999; 99US-00322862.
 30-MAY-2000; 2000US-00580787.
 05-DEC-2000; 2000US-00730473.
 (MAYO-) MAYO FOUND.
 Rodriguez M, Miller DJ, Pease LR;
 WPI; 2004-119219/12.
 N-PSDB; AD126655.
 New human immunoglobulin M antibody for treating or preventing a
 demyelinating disease of the central nervous system in a human or
 domestic animal, such as multiple sclerosis.
 Claim 7; Fig 35; 159pp; English.

The invention relates to an antibody (I) produced by injecting an
 immunocompetent host with an antibody peptide, and harvesting the
 antibody, where the peptide comprises a human anti-IGM antibody fragment
 given in the specification, or active fragments. Also included are
 stimulating remyelination of central nervous system (CNS) axons in a
 mammal (comprising administering a monoclonal antibody, or mixtures,
 monomers, active fragments, or recombinant antibodies derived from it,
 characterised by their ability to bind structures and cells within the
 CNS, including oligodendrocytes), stimulating the proliferation of glial
 cells in CNS axons in a mammal (comprising administering a monoclonal
 antibody, or mixtures, monomers, active fragments, or recombinant
 antibodies derived from it, characterised by their ability to bind
 structures and cells within the CNS), treating or preventing a
 demyelinating disease of the CNS in a mammal (comprising administering a
 monoclonal antibody, or mixtures, monomers, active fragments, or
 recombinant antibodies derived from it, characterised by their ability to
 bind structures and cells within the CNS, and to stimulate remyelination
 of axons of the CNS), stimulating, in vitro, the proliferation of glial
 cells from mixed cell culture, stimulating remyelination of CNS axons in
 a mammal, a DNA sequence (or degenerate variant of it) which encodes an
 antibody (or a peptide analogue, hapten, or active fragment of it, where
 the DNA sequence consists of a sequence encoding an anti IGM antibody), a
 probe capable of screening for the antibody, an assay for screening drugs
 and other agents for the ability to modulate the production or mimic the
 activities of mAb SHIGM22, SHIGM46, or combinations of them, a
 recombinant virus transformed with recombinant antibody nucleic acids or
 vector, imaging a portion of the CNS using the antibody and diagnosing or
 monitoring demyelination and/or remyelination of the CNS comprising using
 CNS image. The antibody is used to stimulate remyelination of CNS axons,
 and to stimulate the proliferation of glial cells in CNS axons,
 optionally in vitro. The antibody is used to treat or prevent a

demyelinating disease of the CNS in a human or domestic animal, such as
 multiple sclerosis, or a disease, other injury or dysfunction of the CNS,
 preferably the mammal is a mouse infected with strain DA of Theiler's
 murine encephalomyelitis virus. The antibody is used to treat a spinal
 cord injury and used to screen drugs and other agents for the ability to
 modulate the production or mimic the activities of the antibody. The
 antibody can be used to image a portion of the CNS which can be used to
 diagnose or monitor demyelination and/or remyelination of the CNS. The
 present sequence is a variable region of a human anti-IGM antibody (or
 fragment).
 Sequence 119 AA:
 Query Match 95.5%; Score 84; DB 8; Length 119;
 Best Local Similarity 88.2%; Pred. No. 1.3e-05;
 Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 IISYDGRKRYADSVKG 17
 :|||||:|||||
 Db 50 VISYDGRKRYADSVKG 66
 RESULT 17
 AAY79076
 ID AAY79076 standard; peptide; 17 AA.
 XX AAY79076;
 AC AAY79076;
 XX
 DT 12-JUN-2000 (first entry)
 DE
 XX
 DE Anti-factor IX/IXa antibody H chain V domain CDR2 amino acid sequence.
 Complementarity determining region 2; CDR2; antibody; Gla domain;
 factor IX/IXa; blood coagulation; deep venous thrombosis;
 arterial thrombosis; unstable angina; post myocardial infarction;
 coronary artery bypass graft; CABG; stroke; tumour growth; metastasis;
 percutaneous transluminal coronary angioplasty; PTCA; inflammation;
 septic shock; hypotension; adult respiratory distress syndrome; ARDS;
 arterial fibrillation; disseminated intravascular coagulopathy; DIC.
 OS Homo sapiens.
 XX
 XX
 PN WO200012562-A1.
 XX
 XX 09-MAR-2000.
 PD
 XX 26-AUG-1999; 99WO-US019453.
 PF
 XX 28-AUG-1998; 98US-0098233P.
 PR
 XX 03-MAR-1999; 99US-0122767P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Adams CW, Devaux B, Baton DJ, Hase PE, Judice JK, Kirchofer D;
 PI Suggett S;
 XX
 XX WPI; 2000-256595/22.
 DR
 XX
 PT Novel human anti-Factor IX/IXa antibodies against IX/IXa gamma-
 PT carboxyglutamic acid domains useful as anti-coagulant in thrombosis,
 PT stroke, and post myocardial infarction.
 XX
 XX
 PS Claim 2; Fig 2; 84pp; English.

This sequence represents a complementarity determining region 2 (CDR2) of
 the heavy chain variable domain of a human anti-factor IX/IXa Gla domain
 antibody. Factor IXa is a vitamin K dependent plasma serine protease that
 participates in the blood coagulation pathways. The Gla domain of factor
 IXa and its zymogen factor IX contains important structural determinants
 for interaction with high affinity binding sites on vascular endothelial
 cells and platelets. Compositions comprising the antibodies are used for
 the treatment or prophylaxis of thrombotic or coagulopathic diseases or
 disorders in a mammal for which inhibiting a FIX/IXa mediated event is

CC indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable
 CC angina, post myocardial infarction, post surgical thrombosis, coronary
 CC artery bypass graft (CABG), percutaneous transluminal coronary
 CC angioplasty (PTCA), stroke, tumour growth, invasion or metastasis,
 CC inflammation, septic shock, hypotension, adult respiratory distress
 CC syndrome (ARDS), arterial fibrillation and disseminated intravascular
 CC coagulopathy (DIC)

XX
 SQ Sequence 17 AA;

Query Match 94.3%; Score 83; DB 3; Length 17;
 Best Local Similarity 94.1%; Pred. No. 2.1e-06;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
 |||||
 Db 1 IISYDGSNKYYADSVKG 17

RESULT 18
 ADP22108
 ID ADP22108 standard; protein; 123 AA.

XX
 AC ADP22108;
 XX
 DT 09-SEP-2004 (first entry)
 XX
 XX Human anti-TNFA antibody heavy chain variable region SEQ ID NO:14.

XX human; monoclonal antibody; tumour necrosis factor-alpha; TNFA;
 KM anti-TNFA antibody; anabolic; antiarteriosclerotic; antithrombotic;
 KM antibacterial; antiinflammatory; antiproliferative; antirheumatic;
 KM eating-disorder; immunomodulator; immunosuppressive; nephrotropic;
 KM neuroprotective; vasotropic; antiapoptotic; TNFA antagonist;
 KM TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;
 KM bladder cancer; lung cancer; glioblastoma; stomach cancer;
 KM endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;
 KM prostate cancer; immuno-mediated inflammatory disease;
 KM rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;
 KM restenosis; autoimmune disease; Crohn's disease; graft-host reaction;
 KM septic shock; cachexia; anorexia; multiple sclerosis.

XX
 OS Homo sapiens.
 XX
 FN WO2004050683-A2.
 XX
 PD 17-JUN-2004.
 XX
 PF 02-DEC-2003; 2003WO-US038281.
 XX
 PR 02-DEC-2002; 2002US-0430729P.
 XX
 PA (ABGE-) ABGENIX INC.

XX
 PI Babcock JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;
 PI Haak-Frendscho W, Rathnaswami P, Pigott C, Liang ML, Lee R;
 PI Manchulenko K, Faggioni R, Senaldi G, Qiaojuan JS;
 DR WPI: 2004-480601/45.
 DR N-PSDB; ADP22107.

XX
 PT New recombinant human monoclonal antibody that specifically binds to
 PT Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such
 PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid
 PT arthritis.

XX
 PS Example 10; SEQ ID NO 14; 213pp; English.

XX The present invention describes a human monoclonal antibody (I) that
 CC specifically binds to tumour necrosis factor-alpha (TNFA) and comprises:
 CC (a) a heavy chain complementarity determining region 1 (CDR1) having the
 CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);
 CC and (b) a light chain CDR1 having the two fully defined 11 amino acid

CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying
 CC (M1) the level of TNFA in a patient sample, comprising contacting with
 CC (I), and detecting the level of binding between the antibody and TNFA in
 CC the sample; (2) a composition comprising the antibody or its functional
 CC fragment and a carrier; (3) treating (M2) an animal suffering from a
 CC neoplastic, or an immuno-mediated inflammatory disease by selecting an
 CC animal in need of treatment for the disease by administering the human
 CC monoclonal antibody of (I); and (4) inhibiting (M3) TNFA induced
 CC apoptosis in an animal by selecting an animal in need of treatment for
 CC TNFA induced apoptosis by administering the human monoclonal antibody of
 CC (I). (I) has anabolic, antiarteriosclerotic, antithrombotic,
 CC antibacterial, antiinflammatory, antiproliferative, antirheumatic, eating-
 CC disorders, immunomodulator, immunosuppressive, nephrotropic,
 CC neuroprotective, vasotropic and antiapoptotic activities, and can be used
 CC as a TNFA antagonist. The antibody (I) is useful in the preparation of
 CC medicament for treating TNF induced apoptosis, neoplastic disease such as
 CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
 CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
 CC pancreatic cancer, and prostate cancer; or immuno-mediated inflammatory
 CC diseases such as rheumatoid arthritis, glomerulonephritis,
 CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's
 CC disease, graft-host reactions, septic shock, cachexia, anorexia, and
 CC multiple sclerosis. The present sequence represents a human anti-TNFA
 CC antibody heavy chain variable region, which is used in the
 CC exemplification of the present invention.

XX
 SQ Sequence 123 AA;

Query Match 94.3%; Score 83; DB 8; Length 123;
 Best Local Similarity 94.1%; Pred. No. 1.9e-05;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
 |||||
 Db 50 IISYDGSNKYYADSVKG 66

RESULT 19
 ADE28443
 ID ADE28443 standard; protein; 125 AA.

XX
 AC ADE28443;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 XX Human anti-CD40 antibody 22-1-1 variable region heavy chain protein.

XX anti-CD40 monoclonal antibody; CD40; cytotoxic; virucide; antibacterial;
 KM immunostimulant; anti-HIV; hyperproliferative; cancer; viral;
 KM bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;
 KM human; variable region heavy chain; 22-1-1.

XX
 OS Homo sapiens.
 XX
 FN WO2003040170-A2.
 XX
 PD 15-MAY-2003.
 XX
 PF 08-NOV-2002; 2002WO-US036107.
 XX
 PR 09-NOV-2001; 2001US-0348980P.
 XX
 PA (PF12) PFIZER PROD INC.
 PA (ABGE-) ABGENIX INC.

XX
 PI Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;
 DR WPI: 2003-441521/41.
 DR N-PSDB; ADE28442.

XX
 PT New chimeric or human monoclonal antibody or its antigen-binding portion
 PT that specifically binds to and activates human CD40, useful for enhancing
 PT an immune response in a human, or treating cancer, HIV, neutropenia or

PT viral infections.
 XX
 PS Claim 1; SEQ ID NO 50; 177pp; English.
 XX
 CC The invention relates to a novel chimeric or human monoclonal antibody or
 CC its antigen-binding portion that specifically binds to and activates
 CC human CD40. The anti-CD40 antibody of the invention demonstrates
 CC cytostatic, virucide, antibacterial, immunostimulant and anti-HIV
 CC activities and may be useful for treating a hyperproliferative disorder
 CC such as cancer, viral and bacterial infection or genetic, primary or
 CC combined immunodeficiency conditions including neutropenia or HIV
 CC infection. The anti-CD40 antibodies may also be useful for detecting CD40
 CC in a biological sample in vitro or in vivo, as well as during gene
 CC therapy procedures. The current sequence is that of the human anti-CD40
 CC antibody variable region heavy chain protein of the invention.
 XX
 SQ Sequence 125 AA;
 Query Match 94.3%; Score 83; DB 7; Length 125;
 Best Local Similarity 94.1%; Pred. No. 1.9e-05;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 IISYDGSKKYYADSVYKG 17
 Db 50 IISYDGSKKYYADSVYKG 66
 RESULT 20
 ADD28233
 ID ADD28233 standard; protein; 137 AA.
 XX
 AC ADD28233;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Human heterodimeric antibody heavy chain variable region SEQ ID NO:11.
 XX
 KW human heterodimeric antibody; human; antibody; binding affinity;
 KW protective antigen; Bacillus anthracis; anthrax infection; cell receptor;
 KW edema factor; lethal factor; virucide; antibacterial; immunotherapy;
 KW anti-toxin; anti-infective; anthrax; botulinum; smallpox;
 KW Venezuelan equine encephalomyelitis virus; VEEV; West Nile virus; MNV.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO2003076568-A2.
 XX
 PD 18-SEP-2003.
 XX
 PF 11-FEB-2003; 2003WO-US004206.
 XX
 PR 11-FEB-2002; 2002US-0356086P.
 PR 29-APR-2002; 2002US-0376408P.
 PR 27-SEP-2002; 2002US-0414053P.
 PR 25-NOV-2002; 2002US-0428807P.
 XX
 PA (ALEX-) ALEXION PHARM INC.
 XX
 PI Bowditch KS, Wild MA;
 XX
 DR WPI; 2003-722327/68.
 XX
 PT New human heterodimeric antibodies or their antibody fragments, useful as
 PT anti-toxins or anti-infectives with respect to infective agents, e.g.
 PT anthrax, botulinum, smallpox, Venezuelan equine encephalomyelitis or West
 PT Nile virus.
 XX
 PS Claim 6; SEQ ID NO 11; 67pp; English.
 CC The present invention describes a human heterodimeric antibody (I)
 CC (fragment) having a binding affinity of at least 1x10⁻⁸ M to the
 CC protective antigen of Bacillus anthracis or a molecule involved in

CC anthrax infection that blocks binding of the antigen or molecule to cell
 CC receptors, edema factor and lethal factor. (I) has virucide and
 CC antibacterial activities, and can be used in immunotherapy. The
 CC antibodies (I) are useful as anti-toxins or anti-infectives with respect
 CC to infective agents, such as anthrax, botulinum, smallpox, Venezuelan
 CC equine encephalomyelitis virus (VEEV), or West Nile virus (MNV). The
 CC present sequence represents a human heterodimeric antibody heavy chain
 CC variable region amino acid sequence, which is used in the exemplification
 CC of the present invention.
 XX
 SQ Sequence 137 AA;
 Query Match 94.3%; Score 83; DB 7; Length 137;
 Best Local Similarity 88.2%; Pred. No. 2.1e-05;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 IISYDGSKKYYADSVYKG 17
 Db 52 IISYDGSKKYYADSVYKG 68
 RESULT 21
 ADD28321
 ID ADD28321 standard; protein; 137 AA.
 XX
 AC ADD28321;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Human heterodimeric antibody heavy chain variable region SEQ ID NO:99.
 XX
 KW human heterodimeric antibody; human; antibody; binding affinity;
 KW protective antigen; Bacillus anthracis; anthrax infection; cell receptor;
 KW edema factor; lethal factor; virucide; antibacterial; immunotherapy;
 KW anti-toxin; anti-infective; anthrax; botulinum; smallpox;
 KW Venezuelan equine encephalomyelitis virus; VEEV; West Nile virus; MNV.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO2003076568-A2.
 XX
 PD 18-SEP-2003.
 XX
 PF 11-FEB-2003; 2003WO-US004206.
 XX
 PR 11-FEB-2002; 2002US-0356086P.
 PR 29-APR-2002; 2002US-0376408P.
 PR 27-SEP-2002; 2002US-0414053P.
 PR 25-NOV-2002; 2002US-0428807P.
 XX
 PA (ALEX-) ALEXION PHARM INC.
 XX
 PI Bowditch KS, Wild MA;
 XX
 DR WPI; 2003-722327/68.
 XX
 PT New human heterodimeric antibodies or their antibody fragments, useful as
 PT anti-toxins or anti-infectives with respect to infective agents, e.g.
 PT anthrax, botulinum, smallpox, Venezuelan equine encephalomyelitis or West
 PT Nile virus.
 XX
 PS Claim 11; SEQ ID NO 99; 67pp; English.
 CC The present invention describes a human heterodimeric antibody (I)
 CC (fragment) having a binding affinity of at least 1x10⁻⁸ M to the
 CC protective antigen of Bacillus anthracis or a molecule involved in
 CC anthrax infection that blocks binding of the antigen or molecule to cell
 CC receptors, edema factor and lethal factor. (I) has virucide and
 CC antibacterial activities, and can be used in immunotherapy. The
 CC antibodies (I) are useful as anti-toxins or anti-infectives with respect
 CC to infective agents, such as anthrax, botulinum, smallpox, Venezuelan
 CC equine encephalomyelitis virus (VEEV), or West Nile virus (MNV). The

CC present sequence represents a human heterodimeric antibody heavy chain
CC variable region amino acid sequence, which is used in the exemplification
CC of the present invention.

XX Sequence 137 AA;

Query Match 94.3%; Score 83; DB 7; Length 137;
Best Local Similarity 88.2%; Pred. No. 2.1e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 52 VISYDGSKKYYGDSVKG 68

RESULT 22
ADP45679
ID ABP45679 standard; protein; 252 AA.

XX AC ABP45679;

XX DT 19-AUG-2002 (first entry)

XX DE Human Blys binding scfv SEQ ID 1690.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
XX tumour necrosis factor; B cell proliferation; B cell differentiation;
XX immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
XX common variable immunodeficiency; acquired immunodeficiency syndrome.

OS Homo sapiens.

XX WO200202641-A1.

XX PD 10-JAN-2002.

XX PF 15-JUN-2001; 2001WO-US019110.

XX PR 16-JUN-2000; 2000US-0212210P.

XX PR 17-OCT-2000; 2000US-0240816P.

XX PR 16-MAR-2001; 2001US-0276248P.

XX PR 21-MAR-2001; 2001US-0277379P.

XX PR 25-MAY-2001; 2001US-0293499P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX WPI; 2002-114799/15.

XX DR WPI; 2002-114799/15.

XX PT Antibodies against B lymphocyte stimulating polypeptides, useful for the

XX diagnosis and treatment of cancers and immune disorders.

XX PS Claim 1; Page 2419-2420; 3148pp; English.

XX CC This invention describes novel antibodies that immunospecifically bind to

XX CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the

XX CC tumour necrosis factor (TNF) super family and induces B cell

XX CC proliferation and differentiation. The antibodies of the invention have

XX CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,

XX CC antirheumatic and antiAIDS activity and can be used in vaccines to

XX CC inhibit the expression and activity of Blys. The antibodies bind to Blys

XX CC and so may be used to detect and quantitate the presence of Blys in

XX CC biological samples and may be used in this way to diagnose disease

XX CC associated with aberrant expression of Blys. They may also be

XX CC administered to treat diseases associated with aberrant Blys expression

XX CC and activity such as cancer, immune, and autoimmune disorders and

XX CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,

XX CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and

XX CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent

CC the antibodies and fragments of the antibodies described in the method of
CC the invention

XX Sequence 252 AA;

Query Match 94.3%; Score 83; DB 5; Length 252;
Best Local Similarity 88.2%; Pred. No. 4.2e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSKKYYGDSVKG 66

RESULT 23
ADG96506
ID ADG96506 standard; protein; 252 AA.

XX AC ADG96506;

XX DT 11-MAR-2004 (first entry)

XX DE Single chain antibody that immunospecifically binds Blys SeqID 1690.

XX antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
XX B cell proliferation; differentiation; scfv; myasthenia gravis;
XX multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
XX carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;
XX antiinflammatory; antiasthmatic; antiallergic; cytostatic.

XX Unidentified.

OS WO2003055979-A2.

XX PD 10-JUL-2003.

XX PF 14-NOV-2002; 2002WO-US036496.

XX PR 16-NOV-2001; 2001US-0331469P.

XX PR 19-DEC-2001; 2001US-0340817P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Ruben SM, Barash SC, Choi GH, Vaughan TU, Hilbert D;

XX WPI; 2003-505530/47.

XX DR WPI; 2003-505530/47.

XX PS Example 1; SEQ ID NO 1690; 394pp; English.

XX CC This invention relates to novel antibodies that immunospecifically bind

XX CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to

XX CC chromosome 13q34 and encodes a protein that is a member of the tumour

XX CC necrosis factor superfamily and induces both in vivo and in vitro B cell

XX CC proliferation and differentiation. Specifically, it refers to single

XX CC chain antibody molecules (scfvs) derived, preferably, from the variable

XX CC heavy CD3 region that immunospecifically bind to a polypeptide, or

XX CC fragment thereof, of either human, murine, rat or monkey Blys. The

XX CC present invention refers to the use of such antibodies in various methods

XX CC for the detection, diagnosis and prognosis of diseases related to the

XX CC aberrant expression or inappropriate function of Blys or its receptor. As

XX CC such, these compositions are useful for identifying immune disorders

XX CC including myasthenia gravis and multiple sclerosis, inflammatory

XX CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such

XX CC as AIDS and proliferative disorders including leukaemia, carcinoma and

XX CC lymphoma. Accordingly, they can be described as exhibiting various

XX CC activities such as antirheumatic, antiarthritic, neuroprotective,

XX CC antiinflammatory, antiasthmatic, antiallergic and cytostatic. This

XX CC polypeptide sequence is a single chain antibody that binds Blys of the

XX CC invention. NOTE: The sequence data for this patent did not form part of

CC the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 252 AA;

Query Match 94.3%; Score 83; DB 7; Length 252;
 Best Local Similarity 88.2%; Pred. No. 4.2e-05;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
 :|||||
 DB 50 VISYDGSKKYYADSVKG 66

RESULT 24
 ADE28467
 ID ADE28467 standard; protein; 470 AA.

AC ADE28467;
 DT 29-JAN-2004 (first entry)
 XX Human anti-CD40 antibody 23-29-1 variable region heavy chain protein.
 XX anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;
 KW immunostimulant; anti-HIV; hyperproliferative; cancer; viral;
 KW bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;
 KW human; variable region heavy chain; 23-29-1.

XX Homo sapiens.
 OS
 PN WO2003040170-A2.
 XX
 PD 15-MAY-2003.
 XX
 PF 08-NOV-2002; 2002WO-US036107.
 XX
 PR 09-NOV-2001; 2001US-0348980P.
 XX
 XX (PFIZ) PRIZER PROD INC.
 PA (ABGE-) ABGENIX INC.

PI Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;
 XX
 DR WPI; 2003-441521/41.
 DR N-PSDB; ADE28466.

PT New chimeric or human monoclonal antibody or its antigen-binding portion
 PT that specifically binds to and activates human CD40, useful for enhancing
 PT an immune response in a human, or treating cancer, HIV, neutropenia or
 PT viral infections.

XX Claim 1; SEQ ID NO 74; 177bp; English.

XX The invention relates to a novel chimeric or human monoclonal antibody or
 CC its antigen-binding portion that specifically binds to and activates
 CC human CD40. The anti-CD40 antibody of the invention demonstrates
 CC cytostatic, virucide, antibacterial, immunostimulant and anti-HIV
 CC activities and may be useful for treating a hyperproliferative disorder
 CC such as cancer, viral and bacterial infection or genetic, primary or
 CC combined immunodeficiency conditions including neutropenia or HIV
 CC infection. The anti-CD40 antibodies may also be useful for detecting CD40
 CC in a biological sample in vitro or in vivo, as well as during gene
 CC therapy procedures. The current sequence is that of the human anti-CD40
 CC antibody variable region heavy chain protein of the invention.

XX Sequence 470 AA;

Query Match 94.3%; Score 83; DB 7; Length 470;
 Best Local Similarity 94.1%; Pred. No. 8.4e-05;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17

DB 69 IISYDGSNNKYADSVKG 85
 |||||

RESULT 25
 ABB06275
 ID ABB06275 standard; protein; 614 AA.
 AC ABB06275;
 DT 24-MAY-2002 (first entry)

XX Plasmid scFv(CO046N2)-CL-GFP protein sequence.
 DE Construction; scFv antibody; green fluorescent protein; GFP; immunoassay;
 KW fluorescent protein; antigen binding; immunostaining; fusion protein;
 KW immunological assay.

XX Homo sapiens.
 OS Synthetic.

PN WO200196401-A1.

PD 20-DEC-2001.

XX 12-JUN-2001; 2001WO-JP004964.

PR 14-JUN-2000; 2000JP-00178880.

XX (MED1-) MEDICAL & BIOLOGICAL LAB CO LTD.

PI Morino K, Akahori Y, Iba Y, Shinohara M, Ukai Y, Kurosawa Y;

XX WPI; 2002-098056/13.
 DR N-PSDB; ABL49526.

PT Producing scFv antibody fused to a fluorescent protein, useful for
 PT immunoassay and immunostaining, comprises expressing a scFv gene
 PT (extracted from selected clones) fused to a fluorescent protein gene.

XX Example; Fig 14; 105bp; Japanese.

XX The present invention describes a method for producing a scFv antibody
 CC fused to a fluorescent protein. The method comprises constructing a scFv
 CC antibody library composed of phage clones expressing scFv antibody on
 CC their surface, screening this library with an antigen, extracting the
 CC gene for scFv antibody from the selected phage clones and inserting it
 CC into an expression vector that expresses the gene fused to a fluorescent
 CC protein. Also described are: (1) a fusion protein comprising the scFv
 CC antibody fused to a fluorescent protein; (2) immunological assays using
 CC the fusion protein of (1); (3) an expression vector encoding the fusion
 CC protein of (1); and (4) a kit for producing the fusion protein of (1).
 CC The fusion protein can be used in immunoassays and immunostaining.
 CC Immunological assays using the fusion protein do not require a secondary
 CC or tertiary antibody. Direct intracellular and even in vivo assays are
 CC possible. ABL49521 to ABL49591 and ABB06268 to ABB06276 represent
 CC sequences used in the exemplification of the present invention

XX Sequence 614 AA;

Query Match 94.3%; Score 83; DB 5; Length 614;
 Best Local Similarity 88.2%; Pred. No. 0.00011;
 Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
 :|||||
 DB 53 VISYDGSKKYYADSVKG 69

RESULT 26
 AAW90298
 ID AAW90298 standard; protein; 17 AA.
 XX

AC AAM90298;
 XX 07-SEP-1999 (first entry)
 XX
 XX Human anti-GPIIb/IIIa auto-antibody heavy chain protein CDR2 region 2.
 DE
 XX
 XX Antibody; GPIIb/IIIa; human; auto-antibody; anti-idiotypic; diagnosis;
 KW blood platelet membrane protein; predisposition; prevention; treatment;
 KW autoimmune thrombocytopenic purpura; AITP; fibrinogen binding; thrombi;
 KW thrombocyte; cardiac infarction; pulmonary embolism; heavy chain.
 XX
 OS Homo sapiens.
 XX
 XX MO9855619-A1.
 XX
 PD 10-DEC-1998.
 XX
 XX 05-JUN-1998; 98WO-EP003357.
 XX
 XX 06-JUN-1997; 97DE-01023904.
 PR 12-DEC-1997; 97DE-01055227.
 PR 08-MAY-1998; 98DE-01020663.
 XX
 PA (ASAT-) ASAT AG APPLIED SCI & TECHNOLOGY.
 XX
 FI Berchold P, Beecher RFA;
 XX
 DR WPI; 1999-105496/09.
 XX
 XX Nucleic acid encoding human autoantibodies against platelet glycoprotein
 PT IIL/IIla - used for diagnosis; treatment and prevention of autoimmune
 PT thrombocytopenic purpura and for modulation of fibrinogen binding.
 XX
 PS Claim 3b; Page 5; 93pp; German.
 XX
 CC This invention describes novel nucleic acid fragments that encode human
 CC auto-antibodies and anti-idiotypic antibodies against blood platelet
 CC membrane protein, GPIIb/IIIa. The products of the invention are used for
 CC diagnosis (including monitoring and determining predisposition),
 CC prevention and treatment of autoimmune thrombocytopenic purpura (AITP)
 CC and also for modulating binding of fibrinogen to thrombocytes
 CC (particularly to dissolve thrombi and/or prevent their formation, e.g. in
 CC cases of cardiac infarction or pulmonary embolism). Unlike murine
 CC antibodies, human antibodies (hAb) do not induce adverse side effects and
 CC persist for longer in vivo than small peptides. AAM90293-W90337 represent
 CC antibody fragments used in the method of the invention
 CC
 XX Sequence 17 AA;
 SQ
 Query Match 93.2%; Score 82; DB 2; Length 17;
 Best Local Similarity 88.2%; Pred. No. 3e-06;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 IISYDGSKKYADSVKG 17
 :|||||
 Db 1 VISYDGSNKRYADSVKG 17

RESULT 27
 AAY79074
 ID AAY79074 standard; peptide; 17 AA.
 XX
 AC AAY79074;
 XX
 DT 12-JUN-2000 (first entry)
 XX
 XX Anti-factor IX/IXa antibody H chain V domain CDR2 amino acid sequence.
 XX
 XX Complementarity determining region 2; CDR2; antibody; Gla domain;
 KW factor IX/IXa; blood coagulation; deep venous thrombosis;
 KW arterial thrombosis; unstable angina; post myocardial infarction;
 KW coronary artery bypass graft; CABG; stroke; tumour growth; metastasis;
 KW percutaneous transluminal coronary angioplasty; PTCA; inflammation;
 KW percutaneous transluminal coronary angioplasty; PTCA; inflammation;

KW septic shock; hypotension; adult respiratory distress syndrome; ARDS;
 KW arterial fibrillation; disseminated intravascular coagulopathy; DIC.
 XX
 OS Homo sapiens.
 XX
 XX WO200012562-A1.
 XX
 XX 09-MAR-2000.
 XX
 XX 26-AUG-1999; 99WO-US019453.
 XX
 XX 28-AUG-1998; 98US-0098233P.
 PR 03-MAR-1999; 99US-0122767P.
 XX
 XX (GERTH) GENENTECH INC.
 XX
 XX Adams CW, Devaux B, Baton DL, Haas PE, Judice JK, Kirchhofer D;
 PI Suggett S;
 XX
 XX WPI; 2000-256595/22.
 XX
 XX Novel human anti-Factor IX/IXa antibodies against IX/IXa gamma-
 PT carboxyglutamic acid domains useful as anti-coagulant in thrombosis,
 PT stroke, and post myocardial infarction.
 XX
 XX Claim 2; Fig 2; 84pp; English.
 PS
 CC This sequence represents a complementarity determining region 2 (CDR2) of
 CC the heavy chain variable domain of a human anti-Factor IX/IXa Gla domain
 CC antibody. Factor IXa is a vitamin K dependent plasma serine protease that
 CC participates in the blood coagulation pathways. The Gla domain of factor
 CC IXa and its zymogen factor IX contains important structural determinants
 CC for interaction with high affinity binding sites on vascular endothelial
 CC cells and platelets. Compositions comprising the antibodies are used for
 CC the treatment or prophylaxis of thrombotic or coagulopathic diseases or
 CC disorders in a mammal for which inhibiting a FIX/IXa mediated event is
 CC indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable
 CC angina, post myocardial infarction, post surgical thrombosis, coronary
 CC artery bypass graft (CABG), percutaneous transluminal coronary
 CC angioplasty (PTCA), stroke, tumour growth, invasion or metastasis,
 CC inflammation, septic shock, hypotension, adult respiratory distress
 CC syndrome (ARDS), arterial fibrillation and disseminated intravascular
 CC coagulopathy (DIC)
 CC
 XX Sequence 17 AA;
 SQ
 Query Match 93.2%; Score 82; DB 3; Length 17;
 Best Local Similarity 88.2%; Pred. No. 3e-06;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 IISYDGSKKYADSVKG 17
 :|||||
 Db 1 VISYDGSNKRYADSVKG 17

RESULT 28
 AAY79078
 ID AAY79078 standard; peptide; 17 AA.
 XX
 AC AAY79078;
 XX
 DT 12-JUN-2000 (first entry)
 XX
 XX Anti-factor IX/IXa antibody H chain V domain CDR2 amino acid sequence.
 XX
 XX Complementarity determining region 2; CDR2; antibody; Gla domain;
 KW factor IX/IXa; blood coagulation; deep venous thrombosis;
 KW arterial thrombosis; unstable angina; post myocardial infarction;
 KW coronary artery bypass graft; CABG; stroke; tumour growth; metastasis;
 KW percutaneous transluminal coronary angioplasty; PTCA; inflammation;
 KW septic shock; hypotension; adult respiratory distress syndrome; ARDS;
 KW arterial fibrillation; disseminated intravascular coagulopathy; DIC.

OS	Homo sapiens.
XX	
PN	WO200012562-A1.
XX	
PD	09-MAR-2000.
XX	
PF	26-AUG-1999; 99WO-US019453.
XX	
PR	28-AUG-1998; 98US-0098233P.
PR	03-MAR-1999; 99US-0122767P.
XX	
PA	(GETH) GENENTECH INC.
XX	
PI	Adams CW, Devaux B, Eaton DL, Hass PE, Judice JK, Kirchhofer D,
PI	Suggett S;
XX	
DR	WPI; 2000-256595/22.
XX	
PT	Novel human anti-Factor IX/IXa antibodies against IX/IXa gamma-
PT	carboxyglutamic acid domains useful as anti-coagulant in thrombosis,
XX	stroke, and post myocardial infarction.
PS	Claim 2, Fig 2, 84pp; English.

CC This sequence represents a complementarily determining region 2 (CDR2) of
CC the heavy chain variable domain of a human anti-factor IX/IXa Glu domain
CC antibody. Factor IXa is a vitamin K dependent plasma serine protease that
CC participates in the blood coagulation pathways. The Glu domain of factor
CC IXa and its zymogen factor IX contains important structural determinants
CC for interaction with high affinity binding sites on vascular endothelial
CC cells and platelets. Compositions comprising the antibodies are used for
CC the treatment or prophylaxis of thrombotic or coagulopathic diseases or
CC disorders in a mammal for which inhibiting a FIX/IXa mediated event is
CC indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable
CC angina, post myocardial infarction, post surgical thrombosis, coronary
CC artery bypass graft (CABG), percutaneous transluminal coronary
CC angioplasty (PTCA), stroke, tumour growth, invasion or metastasis,
CC inflammation, septic shock, hypotension, adult respiratory distress
CC syndrome (ARDS), arterial fibrillation and disseminated intravascular
CC coagulopathy (DIC)

Query Match Similarity	93.2%	Score 82;	DB 3;	Length 17;
Best Local Similarity	100.0%	Pred. No. 3e-06;		
Matches 16; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

```
QY 1 IISYDGSKKYYADSVK 16
    |||||
Db 1 IISYDGSKKYYADSVK 16
```

	RESULT 29
AA017790	AA017790 standard; peptide; 17 AA.
ID	
XX	
AC	AA017790;
XX	
DT	15-AUG-2002 (first entry)
XX	
DE	CDR2 region of antibody for glycoprotein IIb/IIIa receptor #2.
XX	
KM	CDR2; complementarity determining region 2; antibody; metastasis;
KM	glycoprotein IIb/IIIa; GPIIb/IIIa; angiogenesis; cancer; cytostatic;
KM	antiangiogenic; vasotropic; intimal hyperplasia; vascular occlusion.
XX	
OS	Unidentified.
XX	
PN	DE10057443-A1.
XX	
PD	23-MAY-2002.
XX	
PF	20-NOV-2000; 2000DE-01057443.

XX 20-NOV-2000; 2000DE-01057443.
PR
XX
XX (ASAT-) ASAT AG APPLIED SCI & TECHNOLOGY
PA
PI
XX Peter B, Escher RF;
XX
XX
XX WPI; 2002-472625/51.
DR

PT Use of specific antibodies, or individual chains, for treating tumors and
 PR vascular occlusions, by inhibition of the gp1b/IIla receptor.
 XX
 PS Claim 3, Page 9, 10pp; German.

Claim 3; Page 9; 10pp; German.

CC The present invention relates to the use of heavy or light chains or
CC their functional derivatives or fragments, having specific CDR
CC (complementarily determining region) sequences of antibodies. The
CC peptides can be used for the combined inhibition of the binding of
CC fibrinogen to thrombocytes and of vitronectin to endothelial cells, the
CC inhibition of angiogenesis, the inhibition of tumour metastasis and/or
CC the inhibition of intimal hyperplasia after vascular injury. They are
CC useful for prevention and treatment of vascular occlusion and for
CC treating tumours. The present sequence is a CDR2 region of the invention
XX
XX Sequence 17 AA;
SQ

Sequence 17 AA;

Query Match	93.2%	Score 82;	DB 5;	Length 17;
Best Local Similarity	88.2%;	Pred. No. 3e-06;		
Matches 15; Conservative	1;	Mismatches	1;	Indels 0; Gaps 0;

```
QY 1 IISYDGSKKYYADSVKG 17
    :||||| |||||
Db 1 VISYDGSNKYYADSVKG 17
```

RESULT 30
ADJ32094
ID ADJ32094 standard; peptide; 17 AA

KX	
DT	22-APR-2004 (first entry)
XX	
DE	Human interferon-gamma antibody heavy chain CDR2 peptide SegID48
XX	
KW	antibody; antigen binding domain; interferon-gamma; INF-gamma;
KM	antagonist antibody; antiinflammatory; immunosuppressive;
KK	autoimmune disease; inflammatory condition; human;
KW	complementarity determining region; CDR.

Homo sapiens.

US2003099647-A1.

29-MAY-2003

05-OCT-2001; 2001US-00972656.

05-OCT-2001; 2001US-00972656.

(DESH/) DESHPANDE R V.

PT New antibody or antigen binding domain, or its fragment, variant or PT derivative, which binds to an interferon-gamma protein, useful for PT preparing a composition for preventing or treating inflammatory or PT autoimmune disorders.

PS Claim 14; SEQ ID NO 48; 113pp; English.

CC protein is useful for preparing a composition for treating a disease or

Best Local Similarity	88.2%;	Pred. No. 3e-06;
Matched	15	Conservation
Matched	1	Mismatches
Matched	1	Indels
Matched	0	Gaps
Matched	0	Other

Qy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 1 VISYDGSNKYYADSVKG 17

RESULT 33
ADSS82565
ID ADSS82565 standard; peptide; 17 AA.

AC ADSS82565;

XX 16-DEC-2004 (first entry)

DE Anti-IL-21R antibody MW1 H2 CDR, SEQ ID 23.

XX Immunosuppressive; Cytostatic; Antirheumatic; Antiarthritic;
KM Antinflammatory; Gastrointestinal; Antipsoriatic; Gene therapy;
KM antibody; interleukin-21 receptor; interleukin-21; receptor; IL-21;
KM IL-21R; autoimmune disorder; rheumatoid arthritis;
KM inflammatory bowel disease; Crohn's disease; transplant rejection;
KM psoriasis; hyperproliferative disorder; MUII;
KM complementarity determining region; CDR; heavy chain; H2 CDR.

XX Homo sapiens.

PN WO2004083249-A2.

XX 30-SEP-2004.

PF 12-MAR-2004; 2004WO-US007444.

PR 14-MAR-2003; 2003US-0454336P.

XX (AMHP) WYETH.

PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

PI Young DA, Witters MJ, Valge-Archer V, Collins M, Williams AJ;
PI Witek J;

XX WPI; 2004-691025/67.

DR N-PSDB; ADS82574.

XX New human antibodies that selectively bind to human interleukin-21
PT receptor, useful for diagnosing, preventing or treating autoimmune
PT disorders (e.g. rheumatoid arthritis) or hyperproliferative disorders.

XX Claim 4; SEQ ID NO 23; 143pp; English.

XX The present invention relates to human antibodies, or their antigen-
CC binding fragments, that selectively bind to a human interleukin-21
CC receptor (IL-21R). The antibodies of the invention are referred to as
CC MDP, MDP-germline, MW1, 18G4, 18A5, 19F5, CP5G2 and R18. The antibodies
CC selectively bind the extracellular domain of human IL-21R, or inhibit the
CC binding of IL-21 to an IL-21R. Pharmaceutical compositions comprising an
CC antibody or fragment of the invention are useful for diagnosing,
CC preventing or treating autoimmune disorders (e.g. rheumatoid arthritis,
CC inflammatory bowel disease, Crohn's disease, transplant rejection or
CC psoriasis) or hyperproliferative disorders. The present sequence is an
CC anti-IL-21R antibody heavy chain complementarity determining region of
CC the invention.

XX Sequence 17 AA;

Query Match 93.2%; Score 82; DB 8; Length 17;

Best Local Similarity 88.2%; Pred. No. 3e-06;

Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 1 VISYDGSNKYYADSVKG 17

RESULT 34

ADSS2370
ID ADSS2370 standard; peptide; 17 AA.

XX ADSS2370;

XX 16-DEC-2004 (first entry)

DE Fab targeting HLA-A2/Tax11-19, T3F2, heavy chain CDR 2.

XX Antibody; Fab; HLA-A2; Tax 11-19; human leukocyte antigen; antigen;
KM T lymphocyte; antigen-presenting cell; B cell; dendritic cell;
KM major histocompatibility complex; MHC class I; viral infection;
KM human T lymphotropic virus-1 infection; viral oncoprotein;
KM mycoplasma infection; bacterial infection; fungal infection;
KM protozoal infection; phage display; heavy chain; CDR;
KM complementarity determining region.

XX Homo sapiens.

PN US2004191260-A1.

XX 30-SEP-2004.

PF 26-MAR-2003; 2003US-00396578.

PR 26-MAR-2003; 2003US-00396578.

PA (TECR) TECHNION RES & DEV FOUND LTD.

PI Reiter Y, Cohen C;

XX WPI; 2004-735863/72.

XX New composition comprising a multimeric form of an antibody or fragment
PT which specifically binds an antigen-presenting portion of a complex,
PT useful for treating pathogen-associated diseases e.g., HIV.

XX Claim 5; SEQ ID NO 21; 68pp; English.

XX The invention relates to a composition-of-matter comprising (a multimeric
CC form of) an antibody or antibody fragment including an antigen-binding
CC region capable of specifically binding an antigen-presenting portion of a
CC complex composed of a human antigen-presenting molecule and an antigen
CC derived from a pathogen. Also included are an isolated polynucleotide
CC comprising a nucleic acid sequence encoding an antibody fragment (the
CC antibody fragment including an antigen-binding region capable of
CC specifically binding an antigen-presenting portion of a complex composed
CC of a human antigen-presenting molecule and an antigen derived from a
CC pathogen), a nucleic acid construct comprising the isolated
CC polynucleotide above (and a promoter sequence for directing transcription
CC of the isolated polynucleotide in a host cell), a host cell comprising
CC the nucleic acid construct above, a host virus comprising the nucleic
CC acid construct above, a virus comprising a coat protein fused to the
CC antibody fragment, detecting an antigen-presenting portion of a complex
CC composed of a human antigen-presenting molecule and an antigen derived
CC from a pathogen, a method of diagnosing an infection by a pathogen in an
CC individual, a method of killing or damaging a target cell
CC (expressed/displaying an antigen-presenting portion of a complex
CC composed of a human antigen-presenting molecule and an antigen derived
CC from a pathogen) and a method of detecting in a biological sample an
CC antigen-presenting portion of a complex as described above. The target
CC cell is a T lymphocyte or an antigen-presenting cell, which is a B cell
CC or a dendritic cell. The composition-of-matter further comprises a
CC detectable moiety attached to the antibody or antibody fragment. The
CC detectable moiety is a recognition sequence of a biotin protein ligase, a
CC biotin molecule, a streptavidin molecule, a fluorophore, an enzyme or a
CC polystyrene tag. The biotin protein ligase is BirA, the fluorophore is
CC phycoerythrin, and the enzyme is horseradish peroxidase. The toxin is
CC pseudomonas exotoxin A or its portion, which is a translocation domain
CC and/or an ADP ribosylation domain. The human antigen-presenting molecule
CC is a major histocompatibility complex (MHC), preferably MHC class I
CC molecule, more preferably HLA-A2 molecule. The pathogen is viral,
CC preferably a retrovirus, more preferably human T lymphotropic virus-1.

CC The antigen derived from a pathogen is restricted by the antigen-
CC presenting molecule and is a polypeptide selected from a segment of a
CC viral oncoprotein or a segment of a Tax protein. A pharmaceutical
CC composition comprising as an active ingredient the composition-of-matter
CC is useful in a method for treating a disease associated with a pathogen
CC in an individual such as viruses (HIV), mycoplasmas, bacteria, fungi and
CC protozoans. The composition-of-matter or the methods are useful for
CC diagnosing an infection by a pathogen in an individual and for killing or
CC damaging a target cell expressing or displaying an antigen-presenting
CC portion of a complex composed of a human antigen-presenting molecule and
CC an antigen derived from a pathogen. A phage displayed library of human
CC Fab antibodies which recognise an HLA-A2/Tax 11-19 complex was generated
CC and tested for specific binding to HLA-A2/Tax 11-19, individual clones
CC were then sequenced and their CDR (complementarity determining region)
CC sequences compared. The present sequence is a CDR from the heavy chain of
CC an isolated Fab clone.
CX
CQ
Sequence 17 AA:
CQ

Query Match	93.2%	Score 82;	DB 8;	Length 17;
Best Local Similarity	88.2%;	Pred. NO.	3e-06;	
Matches 15;	Conservative 1;	Mismatches	0;	Gaps 0;

```
Qy      1 IISYDGSKKYYADSVKG 17
          :||||| |||||
Db      1 VISYDGSNKYYADSVKG 17
```

```

RESULT 35
ADDS2400
ID   ADDS2400 standard; peptide; 17 AA.

```

comprising a nucleic acid sequence encoding an antibody fragment (the antibody fragment including an antigen-binding region capable of specifically binding an antigen-presenting portion of a complex composed of a human antigen-presenting molecule and an antigen derived from a pathogen), a nucleic acid construct comprising the isolated polynucleotide above (and a promoter sequence for directing transcription of the isolated polynucleotide in a host cell), a host cell comprising the nucleic acid construct above, a host virus comprising the nucleic acid construct above, a virus comprising a coat protein fused to the antibody fragment, detecting an antigen-presenting portion of a complex composed of a human antigen-presenting molecule and an antigen derived from a pathogen, a method of diagnosing an infection by a pathogen in an individual, a method of killing or damaging a target cell expressing/displaying an antigen-presenting portion of a complex (composed of a human antigen-presenting molecule and an antigen derived from a pathogen) and a method of detecting in a biological sample an antigen-presenting portion of a complex as described above. The target cell is a T lymphocyte or an antigen-presenting cell, which is a B cell or a dendritic cell. The composition-of-matter further comprises a detectable moiety attached to the antibody or antibody fragment. The detectable moiety is a recognition sequence of a biotin protein ligase, a biotin molecule, a streptavidin molecule, a fluorophore, an enzyme or a polystyridine tag. The biotin protein ligase is BirA, the fluorophore is phycoerythrin, and the enzyme is horseradish peroxidase. The toxin is pseudomonas exotoxin A or its portion, which is a translocation domain and/or an ADP ribosylation domain. The human antigen-presenting molecule is a major histocompatibility complex (MHC), preferably MHC class I molecule, more preferably HLA-A2 molecule. The pathogen is viral, preferably a retrovirus, more preferably human T lymphotropic virus-1. The antigen derived from a pathogen is restricted by the antigen-presenting molecule and is a polypeptide selected from a segment of a viral oncoprotein or a segment of a Tax protein. A pharmaceutical composition comprising as an active ingredient the composition-of-matter is useful in a method for treating a disease associated with a pathogen in an individual such as viruses (HIV), mycoplasmas, bacteria, fungi and protozoans. The composition-of-matter or the methods are useful for diagnosing an infection by a pathogen in an individual and for killing or damaging a target cell expressing or displaying an antigen-presenting portion of a complex composed of a human antigen-presenting molecule and an antigen derived from a pathogen. A phase displayed library of human Fab antibodies which recognise an HLA-A2/Tax 11-19 complex was generated and tested for specific binding to HLA-A2/Tax 11-19, individual clones were then sequenced and their CDR (complementarily determining region) sequences compared. The present sequence is a CDR from the heavy chain of an isolated Fab clone.

SQ Sequence 17 AA;

Query Match	93.2%	Score 82;	DB 8;	Length 17;
Best Local Similarity	88.2%	Pred. NO. 3e-06;		
Matches	15;	Conservative	1;	Mismatches 0;
			Indels	Gaps 0;

```
Qy      1 IISYDGSKKYYADSVKG 17
        :||||| |||||||
Db      1 VISYDGSNKYYADSVKG 17
```

RESULT 36
AD552430
ID AD552430 standard; peptide; 17 AA

KW complementarity determining region.
 XX Homo sapiens.
 OS
 XX US2004191260-A1.
 PN
 XX 30-SEP-2004.
 PD
 XX 26-MAR-2003; 2003US-00396578.
 PE
 XX 26-MAR-2003; 2003US-00396578.
 PR
 XX (TECR) TECHNION RES & DEV FOUND LTD.
 PA
 XX Reiter Y, Cohen C;
 PI
 XX WPI; 2004-735863/72.
 DR
 XX
 PT New composition comprising a multimeric form of an antibody or fragment
 PT which specifically binds an antigen-presenting portion of a complex,
 PT useful for treating pathogen-associated diseases e.g., HIV.
 PS
 XX Claim 5; SEQ ID NO 81; 68bp; English.
 XX
 XX The invention relates to a composition-of-matter comprising (a multimeric
 CC form of) an antibody or antibody fragment including an antigen-binding
 CC region capable of specifically binding an antigen-presenting portion of a
 CC complex composed of a human antigen-presenting molecule and an antigen
 CC derived from a pathogen. Also included are an isolated polynucleotide
 CC comprising a nucleic acid sequence encoding an antibody fragment (the
 CC antibody fragment including an antigen-binding region capable of
 CC specifically binding an antigen-presenting portion of a complex composed
 CC of a human antigen-presenting molecule and an antigen derived from a
 CC pathogen), a nucleic acid construct comprising the isolated
 CC polynucleotide above (and a promoter sequence for directing transcription
 CC of the isolated polynucleotide in a host cell), a host cell comprising
 CC the nucleic acid construct above, a host virus comprising the nucleic
 CC acid construct above, a virus comprising a coat protein fused to the
 CC antibody fragment, detecting an antigen-presenting portion of a complex
 CC composed of a human antigen-presenting molecule and an antigen derived
 CC from a pathogen, a method of diagnosing an infection by a pathogen in an
 CC individual, a method of killing or damaging a target cell
 CC expressing/displaying an antigen-presenting portion of a complex
 CC (composed of a human antigen-presenting molecule and an antigen derived
 CC from a pathogen) and a method of detecting in a biological sample an
 CC antigen-presenting portion of a complex as described above. The target
 CC cell is a T lymphocyte or an antigen-presenting cell, which is a B cell
 CC or a dendritic cell. The composition-of-matter further comprises a
 CC detectable moiety attached to the antibody or antibody fragment. The
 CC detectable moiety is a recognition sequence of a biotin protein ligase, a
 CC biotin molecule, a streptavidin molecule, a fluorophore, an enzyme or a
 CC polystyrene tag. The biotin protein ligase is BirA, the fluorophore is
 CC phycoerythrin, and the enzyme is horseradish peroxidase. The toxin is
 CC Pseudomonas exotoxin A or its portion, which is a translocation domain
 CC and/or an ADP-ribosylation domain. The human antigen-presenting molecule
 CC is a major histocompatibility complex (MHC), preferably MHC class I
 CC molecule, more preferably HLA-A2 molecule. The pathogen is viral,
 CC preferably a retrovirus, more preferably human T lymphotropic virus-1.
 CC The antigen derived from a pathogen is restricted by the antigen-
 CC presenting molecule and is a polypeptide selected from a segment of a
 CC viral oncoprotein or a segment of a Tax protein. A pharmaceutical
 CC composition comprising an active ingredient the composition-of-matter
 CC is useful in a method for treating a disease associated with a pathogen
 CC in an individual such as viruses (HIV), mycoplasmas, bacteria, fungi and
 CC protozoans. The composition-of-matter or the methods are useful for
 CC diagnosing an infection by a pathogen in an individual and for killing or
 CC damaging a target cell expressing or displaying an antigen-presenting
 CC portion of a complex composed of a human antigen-presenting molecule and
 CC an antigen derived from a pathogen. A phage displayed library of human
 CC Fab antibodies which recognise an HLA-A2/Tax 11-19 complex was generated
 CC and tested for specific binding to HLA-A2/Tax 11-19, individual clones
 CC were then sequenced and their CDR (complementarity determining region)
 CC (composed of a human antigen-presenting molecule and an antigen derived

CC an isolated Fab clone.
 XX
 XX Sequence 17 AA;
 SQ
 XX Query Match 93.2%; Score 82; DB 8; Length 17;
 XX Best Local Similarity 88.2%; Pred. No. 3e-06;
 XX Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 IISYDGSKKYYADSVKG 17
 :|||||
 Db 1 VISYDGSNKKYYADSVKG 17
 RESULT 37
 ADS52388
 ID ADS52388 standard; peptide; 17 AA.
 XX
 XX ADS52388;
 AC
 XX 16-DEC-2004 (first entry)
 DT
 XX
 DE Fab targeting HLA-A2/Tax11-19, T3D1, heavy chain CDR 2.
 XX
 XX Antibody; Fab; HLA-A2; Tax 11-19; human leukocyte antigen; antigen;
 KW T lymphocyte; antigen-presenting cell; B cell; dendritic cell;
 KW major histocompatibility complex; MHC class I; viral infection;
 KW human T lymphotropic virus-1 infection; viral oncoprotein;
 KW mycoplasma infection; bacterial infection; fungal infection;
 KW protozoan infection; phage display; heavy chain; CDR;
 KW complementarity determining region.
 OS
 XX Homo sapiens.
 XX
 XX US2004191260-A1.
 PN
 XX 30-SEP-2004.
 PD
 XX 26-MAR-2003; 2003US-00396578.
 PE
 XX 26-MAR-2003; 2003US-00396578.
 PR
 XX (TECR) TECHNION RES & DEV FOUND LTD.
 PA
 XX Reiter Y, Cohen C;
 PI
 XX WPI; 2004-735863/72.
 DR
 XX
 PT New composition comprising a multimeric form of an antibody or fragment
 PT which specifically binds an antigen-presenting portion of a complex,
 PT useful for treating pathogen-associated diseases e.g., HIV.
 PS
 XX Claim 5; SEQ ID NO 39; 68bp; English.
 XX
 XX The invention relates to a composition-of-matter comprising (a multimeric
 CC form of) an antibody or antibody fragment including an antigen-binding
 CC region capable of specifically binding an antigen-presenting portion of a
 CC complex composed of a human antigen-presenting molecule and an antigen
 CC derived from a pathogen. Also included are an isolated polynucleotide
 CC comprising a nucleic acid sequence encoding an antibody fragment (the
 CC antibody fragment including an antigen-binding region capable of
 CC specifically binding an antigen-presenting portion of a complex composed
 CC of a human antigen-presenting molecule and an antigen derived from a
 CC pathogen), a nucleic acid construct comprising the isolated
 CC polynucleotide above (and a promoter sequence for directing transcription
 CC of the isolated polynucleotide in a host cell), a host cell comprising
 CC the nucleic acid construct above, a host virus comprising the nucleic
 CC acid construct above, a virus comprising a coat protein fused to the
 CC antibody fragment, detecting an antigen-presenting portion of a complex
 CC composed of a human antigen-presenting molecule and an antigen derived
 CC from a pathogen, a method of diagnosing an infection by a pathogen in an
 CC individual, a method of killing or damaging a target cell
 CC expressing/displaying an antigen-presenting portion of a complex
 CC (composed of a human antigen-presenting molecule and an antigen derived

CC from a pathogen) and a method of detecting in a biological sample an
 CC antigen-presenting portion of a complex as described above. The target
 CC cell is a T lymphocyte or an antigen-presenting cell, which is a B cell
 CC or a dendritic cell. The composition-of-matter further comprises a
 CC detectable moiety attached to the antibody or antibody fragment. The
 CC detectable moiety is a recognition sequence of a biotin protein ligase, a
 CC biotin molecule, a streptavidin molecule, a fluorophore, an enzyme or a
 CC polystyrene tag. The biotin protein ligase is BirA, the fluorophore is
 CC phycoerythrin, and the enzyme is horseradish peroxidase. The toxin is
 CC pseudomonas exotoxin A or its portion, which is a translocation domain
 CC and/or an ADP-ribosylation domain. The human antigen-presenting molecule
 CC is a major histocompatibility complex (MHC), preferably MHC class I
 CC molecule, more preferably HLA-A2 molecule. The pathogen is viral,
 CC preferably a retrovirus, more preferably human T lymphotropic virus-1.
 CC The antigen derived from a pathogen is restricted by the antigen-
 CC presenting molecule and is a polypeptide selected from a segment of a
 CC viral oncoprotein or a segment of a Tax protein. A pharmaceutical
 CC composition comprising as an active ingredient the composition-of-matter
 CC is useful in a method for treating a disease associated with a pathogen
 CC in an individual such as viruses (HIV), mycoplasmas, bacteria, fungi and
 CC protozoans. The composition-of-matter or the methods are useful for
 CC diagnosing an infection by a pathogen in an individual and for killing or
 CC damaging a target cell expressing or displaying an antigen-presenting
 CC portion of a complex composed of a human antigen-presenting molecule and
 CC an antigen derived from a pathogen. A phage displayed library of human
 CC Fab antibodies which recognise an HLA-A2/Tax 11-19 complex was generated
 CC and tested for specific binding to HLA-A2/Tax 11-19, individual clones
 CC were then sequenced and their CDR (complementarity determining region)
 CC sequences compared. The present sequence is a CDR from the heavy chain of
 CC an isolated Fab clone.

SO Sequence 17 AA;

Query Match 93.2%; Score 82; DB 8; Length 17;
 Best Local Similarity 88.2%; Pred. No. 3e-06;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKITYADSVKG 17
 :|||||
 Db 1 VISYDGSNKITYADSVKG 17

RESULT 38
 ADS84420
 ID ADS84420 standard; protein; 41 AA.

AC ADS84420;

DT 18-NOV-2004 (first entry)

DE Human anti-EPO-R antibody heavy chain variable region CDR SEQ ID NO:59.

human; erythropoietin receptor; EPO receptor;
 erythropoietin receptor binding antibody; EPO receptor binding antibody;
 antihaemic; neuroprotective; vulnerary; gene therapy; aplasia; anaemia;
 wound healing; neural cell damage protection;
 neural tissue damage protection; brain injury; spinal cord injury;
 stroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody;
 complementarity determining region; CDR.

OS Homo sapiens.

PN WO2004035603-A2.

PD 29-APR-2004.

PF 14-OCT-2003; 2003WO-US032243.

PR 14-OCT-2002; 2002US-00269711.
 PR 10-OCT-2003; 2003US-00684109.

PA (ABBO) ABBOTT LAB.

XX

PI Devices PU, Green LL, Ostrow DH, Reilly EB, Wieler J;
 XX WPI; 2004-348433/32.

PT New antibodies that bind to or activate an endogenous human
 PT erythropoietin receptor, useful for diagnosing, preventing or treating
 PT disorders associated with dysfunctional erythropoietin receptor, e.g.
 PT anemia.

PS Claim 40; SEQ ID NO 59; 192pp; English.

CC The present invention describes an antibody or its fragment that binds to
 CC or activates an endogenous activity of a human erythropoietin (EPO)
 CC receptor in a mammal, but does not interact with a peptide having a
 CC sequence of 30 amino acids (SEQ ID NO:1, ADS84362). Also described: (1)
 CC methods of modulating or activating an endogenous activity of a human EPO
 CC receptor in a mammal, comprising administering to the mammal a
 CC therapeutic amount of the above antibody or its fragment to modulate or
 CC activate the receptor; (2) a method of treating a mammal suffering from
 CC aplasia, comprising administering to the mammal a therapeutic amount of
 CC the above antibody or its fragment to modulate or activate the receptor;
 CC (3) a pharmaceutical composition comprising a therapeutic amount of the
 CC above antibody or antibody fragment, and a pharmaceutical excipient; (4)
 CC an isolated and purified polynucleotide sequence, and their fragments,
 CC complements and degenerate codon equivalents; and (5) an isolated and
 CC purified amino acid sequence, and their fragments. The EPO receptor
 CC binding antibody has antihaemic, neuroprotective and vulnerary
 CC activities, and can be used in gene therapy. The compositions and methods
 CC from the present invention can be used for modulating an endogenous
 CC activity of a human EPO receptor or for treating mammals suffering from
 CC aplasia or anaemia. They may also be used for identifying mammals having
 CC a dysfunctional EPO receptor. The composition may also be used in
 CC promoting wound healing or in protecting against neural cell and/or
 CC tissue damage resulting from brain/spinal cord injury, stroke and the
 CC like. The present sequence represents a human anti-EPO-R antibody heavy
 CC chain variable region complementarity determining region (CDR), which is
 CC given in the exemplification of the present invention.

SO Sequence 41 AA;

Query Match 93.2%; Score 82; DB 8; Length 41;
 Best Local Similarity 88.2%; Pred. No. 8.1e-06;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKITYADSVKG 17
 :|||||
 Db 11 VISYDGSNKITYADSVKG 27

RESULT 39
 ADR68562
 ID ADR68562 standard; peptide; 41 AA.

AC ADR68562;

DT 02-DEC-2004 (first entry)

DE Human EPO-R heavy chain variable region seqid 59.

antihaemic; respiratory; vulnerary; gene therapy; vaccine;
 erythropoietin receptor; EPO-R; anti-EPO-R-antibody; aplasia; anaemia;
 hypoxaemia; chronic tissue hypoxia; blood circulation; blood flow;
 wound healing; neural tissue damage; tissue damage; brain injury;
 spinal cord injury; stroke; human; heavy chain variable region;
 anti-EPO-R-antibody.

OS Homo sapiens.

PN US2004175379-A1.

PD 09-SEP-2004.

PF 10-OCT-2003; 2003US-00684109.

XX

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: March 31, 2005, 11:51:44 ; Search time 33.2031 Seconds
(without alignments)
38.220 Million cell updates/sec

Title: US-10-614-959-11

Perfect score: 88
Sequence: 1 IISYDGSKKYYADSVKG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: Issued_Patents_AA.*
- 2: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
- 3: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
- 4: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
- 5: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
- 6: /cgn2_6/ptodata/1/1aa/6CTUS.COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	88	100.0	17	4	US-09-383-667-11
2	83	94.3	17	4	US-09-383-667-18
3	82	93.2	17	4	US-09-383-667-16
4	82	93.2	17	4	US-09-383-667-20
5	82	93.2	17	4	US-09-424-840B-36
6	82	93.2	17	4	US-09-424-840B-95
7	82	93.2	17	4	US-09-424-840B-108
8	82	93.2	17	4	US-09-424-840B-97
9	82	93.2	17	4	US-08-211-202-118
10	82	93.2	115	4	US-08-211-202-118
11	82	93.2	115	4	US-08-211-202-141
12	82	93.2	115	4	US-08-211-202-141
13	82	93.2	115	4	US-08-545-809A-115
14	82	93.2	119	2	US-08-331-398A-46
15	82	93.2	119	2	US-08-331-397B-46
16	82	93.2	119	2	US-08-759-804A-46
17	82	93.2	119	3	US-09-227-693-46
18	82	93.2	120	1	US-08-211-202-135
19	82	93.2	120	1	US-07-942-245-35
20	82	93.2	123	3	US-08-983-607-38
21	82	93.2	128	1	US-09-424-840B-6
22	82	93.2	128	1	US-08-478-039-96
23	82	93.2	248	4	US-08-476-349A-96
24	81	92.0	17	4	US-09-315-926A-80
25	81	92.0	17	4	US-09-424-840B-77
26	81	92.0	124	4	US-09-424-840B-111
27	81	92.0	179	3	US-08-862-124-2

28	81	92.0	225	4	US-09-456-090A-102	Sequence 102, App
29	81	92.0	225	4	US-09-456-090A-108	Sequence 108, App
30	81	92.0	225	4	US-09-456-090A-110	Sequence 110, App
31	81	92.0	225	4	US-09-453-234-102	Sequence 102, App
32	81	92.0	225	4	US-09-453-234-108	Sequence 108, App
33	81	92.0	225	4	US-09-453-234-110	Sequence 110, App
34	81	92.0	287	3	US-08-862-124-17	Sequence 17, App
35	81	92.0	304	3	US-08-862-124-14	Sequence 14, App
36	79	89.8	17	4	US-09-560-198A-12	Sequence 12, App
37	79	89.8	17	4	US-09-424-840B-84	Sequence 84, App
38	79	89.8	17	4	US-09-424-840B-113	Sequence 113, App
39	79	89.8	123	4	US-09-560-198A-2	Sequence 2, App
40	79	89.8	123	4	US-09-560-198A-4	Sequence 4, App
41	79	89.8	123	4	US-09-560-198A-10	Sequence 10, App
42	79	89.8	123	4	US-09-424-840B-22	Sequence 22, App
43	77	87.5	126	1	US-08-276-852-81	Sequence 81, App
44	77	87.5	126	1	US-08-899-575-81	Sequence 81, App
45	77	87.5	126	1	US-08-899-575-81	Sequence 81, App

ALIGNMENTS

RESULT 1
US-09-383-667-11
Sequence 11, Application US/09383667
Patent No. 6624295
GENERAL INFORMATION:
APPLICANT: Adams, Camelia W.
APPLICANT: Devaux, Brigitte
APPLICANT: Baton, Dan L.
APPLICANT: Haas, Philip E.
APPLICANT: Judice, J. Kevin
APPLICANT: Kirchofer, Daniel
APPLICANT: Suggest, Shelley
TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
FILE REFERENCE: Pl661R2
CURRENT APPLICATION NUMBER: US/09/383,667
CURRENT FILING DATE: 1999-08-26
EARLIER APPLICATION NUMBER: US 60/098,233
EARLIER FILING DATE: 1998-08-28
EARLIER APPLICATION NUMBER: US 60/122,767
EARLIER FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 32
SEQ ID NO 11
LENGTH: 17
TYPE: PRT
ORGANISM: Homo sapiens
US-09-383-667-11
Query Match 100.0%; Score 88; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 IISYDGSKKYYADSVKG 17
Db 1 IISYDGSKKYYADSVKG 17
RESULT 2
US-09-383-667-18
Sequence 18, Application US/09383667
Patent No. 6624295
GENERAL INFORMATION:
APPLICANT: Adams, Camelia W.
APPLICANT: Devaux, Brigitte
APPLICANT: Baton, Dan L.
APPLICANT: Haas, Philip E.
APPLICANT: Judice, J. Kevin
APPLICANT: Kirchofer, Daniel
APPLICANT: Suggest, Shelley
TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
FILE REFERENCE: Pl661R2

;; CURRENT APPLICATION NUMBER: US/09/383,667
;; EARLIER FILING DATE: 1999-08-26
;; EARLIER APPLICATION NUMBER: US 60/098,233
;; EARLIER FILING DATE: 1998-08-28
;; EARLIER APPLICATION NUMBER: US 60/122,767
;; EARLIER FILING DATE: 1999-03-03
;; NUMBER OF SEQ ID NOS: 32
;; SEQ ID NO 18
;; LENGTH: 17
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-383-667-18

Query Match 94.3%; Score 83; DB 4; Length 17;
Best Local Similarity 94.1%; Pred. No. 8.1e-07;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
Db 1 IISYDGSNNKYADSVKG 17

RESULT 3

US-09-383-667-16
;; Sequence 16, Application US/09383667
;; Patent No. 6624295
;; GENERAL INFORMATION:
;; APPLICANT: Adams, Camelia W.
;; APPLICANT: Devaux, Brigitte
;; APPLICANT: Baton, Dan L.
;; APPLICANT: Hase, Philip B.
;; APPLICANT: Judice, J. Kevin
;; APPLICANT: Kirchofer, Daniel
;; APPLICANT: Suggett, Shelley
;; TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
;; FILE REFERENCE: P1661R2
;; CURRENT APPLICATION NUMBER: US/09/383,667
;; CURRENT FILING DATE: 1999-08-26
;; EARLIER APPLICATION NUMBER: US 60/098,233
;; EARLIER FILING DATE: 1998-08-28
;; EARLIER APPLICATION NUMBER: US 60/122,767
;; EARLIER FILING DATE: 1999-03-03
;; NUMBER OF SEQ ID NOS: 32
;; SEQ ID NO 16
;; LENGTH: 17
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-383-667-16

Query Match 93.2%; Score 82; DB 4; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
Db 1 VISYDGSNNKYADSVKG 17

RESULT 4

US-09-383-667-20
;; Sequence 20, Application US/09383667
;; Patent No. 6624295
;; GENERAL INFORMATION:
;; APPLICANT: Adams, Camelia W.
;; APPLICANT: Devaux, Brigitte
;; APPLICANT: Baton, Dan L.
;; APPLICANT: Hase, Philip B.
;; APPLICANT: Judice, J. Kevin
;; APPLICANT: Kirchofer, Daniel
;; APPLICANT: Suggett, Shelley
;; TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
;; FILE REFERENCE: P1661R2
;; CURRENT APPLICATION NUMBER: US/09/383,667

;; CURRENT FILING DATE: 1999-08-26
;; EARLIER APPLICATION NUMBER: US 60/098,233
;; EARLIER FILING DATE: 1998-08-28
;; EARLIER APPLICATION NUMBER: US 60/122,767
;; EARLIER FILING DATE: 1999-03-03
;; NUMBER OF SEQ ID NOS: 32
;; SEQ ID NO 20
;; LENGTH: 17
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-383-667-20

Query Match 93.2%; Score 82; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVK 16
Db 1 IISYDGSKKYYADSVK 16

RESULT 5

US-09-424-840B-36
;; Sequence 36, Application US/09424840B
;; Patent No. 6790938
;; GENERAL INFORMATION:
;; APPLICANT: Berchtold, Peter
;; APPLICANT: Escher, Robert F. A.
;; TITLE OF INVENTION: ANTI-GPIIb/IIIa RECOMBINANT ANTIBODIES
;; FILE REFERENCE: 100564-09049
;; CURRENT APPLICATION NUMBER: US/09/424,840B
;; CURRENT FILING DATE: 1999-12-03
;; PRIOR APPLICATION NUMBER: DE 19820663.1
;; PRIOR FILING DATE: 1998-05-08
;; PRIOR APPLICATION NUMBER: DE 19755227.7
;; PRIOR FILING DATE: 1997-12-12
;; PRIOR APPLICATION NUMBER: DE 19723904.8
;; PRIOR FILING DATE: 1997-06-06
;; NUMBER OF SEQ ID NOS: 128
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 36
;; LENGTH: 17
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-424-840B-36

Query Match 93.2%; Score 82; DB 4; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
Db 1 VISYDGSNNKYADSVKG 17

RESULT 6

US-09-424-840B-95
;; Sequence 95, Application US/09424840B
;; Patent No. 6790938
;; GENERAL INFORMATION:
;; APPLICANT: Berchtold, Peter
;; APPLICANT: Escher, Robert F. A.
;; TITLE OF INVENTION: ANTI-GPIIb/IIIa RECOMBINANT ANTIBODIES
;; FILE REFERENCE: 100564-09049
;; CURRENT APPLICATION NUMBER: US/09/424,840B
;; CURRENT FILING DATE: 1999-12-03
;; PRIOR APPLICATION NUMBER: DE 19820663.1
;; PRIOR FILING DATE: 1998-05-08
;; PRIOR APPLICATION NUMBER: DE 19755227.7
;; PRIOR FILING DATE: 1997-12-12
;; PRIOR APPLICATION NUMBER: DE 19723904.8
;; PRIOR FILING DATE: 1997-06-06
;; NUMBER OF SEQ ID NOS: 128

SOFTWARE: PatentIn version 3.1
SEQ ID NO 95
LENGTH: 17
TYPE: PRT
ORGANISM: Homo sapiens
US-09-424-840B-95

Query Match 93.2%; Score 82; DB 4; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 1 VISYDGSNKYYADSVKG 17

RESULT 7
US-09-424-840B-97
Sequence 97, Application US/09424840B
Patent No. 6790938
GENERAL INFORMATION:
APPLICANT: Escher, Robert F. A.
TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES
FILE REFERENCE: 100564-09049
CURRENT FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: DE 19820663.1
PRIOR FILING DATE: 1998-05-08
PRIOR APPLICATION NUMBER: DE 19755227.7
PRIOR FILING DATE: 1997-12-12
PRIOR APPLICATION NUMBER: DE 19723904.8
PRIOR FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 128
SOFTWARE: PatentIn version 3.1
SEQ ID NO 97
LENGTH: 17
TYPE: PRT
ORGANISM: Homo sapiens
US-09-424-840B-97

Query Match 93.2%; Score 82; DB 4; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 1 VISYDGSNKYYADSVKG 17

RESULT 8
US-09-424-840B-108
Sequence 108, Application US/09424840B
Patent No. 6790938
GENERAL INFORMATION:
APPLICANT: Berchtold, Peter
TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES
FILE REFERENCE: 100564-09049
CURRENT FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: US/09/424, 840B
PRIOR FILING DATE: 1998-05-08
PRIOR APPLICATION NUMBER: DE 19755227.7
PRIOR FILING DATE: 1997-12-12
PRIOR APPLICATION NUMBER: DE 19723904.8
PRIOR FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 128
SOFTWARE: PatentIn version 3.1
SEQ ID NO 108
LENGTH: 17
TYPE: PRT
ORGANISM: Homo sapiens

US-09-424-840B-108

Query Match 93.2%; Score 82; DB 4; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 1 VISYDGSNKYYADSVKG 17

RESULT 9
US-08-211-202-118
Sequence 118, Application US/08211202
Patent No. 5565332
GENERAL INFORMATION:
APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Mattheus
APPLICANT: BAIER, Michael
APPLICANT: JESPER, Laurence Stephane Anne Therese
APPLICANT: WINTER, Gregory Paul
TITLE OF INVENTION: Production of chimeric antibodies - a
TITLE OF INVENTION: combinatorial approach
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211,202
FILING DATE: 23-SEP-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120252.3
FILING DATE: 23-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120377.8
FILING DATE: 25-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/31960
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 118:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-211-202-118

Query Match 93.2%; Score 82; DB 1; Length 98;
Best Local Similarity 88.2%; Pred. No. 7.3e-06;

Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 10
US-09-726-219A-167
; Sequence 167; Application US/09726219A
; Patent No. 6806079
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kaaper
; APPLICANT: Marks, James
; APPLICANT: Clackson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 213839-00013
; CURRENT FILING DATE: US/09/726,219A
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 167
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-726-219A-167

Query Match 93.2%; Score 82; DB 4; Length 115;
Best Local Similarity 88.2%; Pred. No. 8.6e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 11
US-08-211-202-141
; Sequence 141; Application US/08211202
; Patent No. 5565332
; GENERAL INFORMATION:
; APPLICANT: HOOGENBOOM, Hendricus
; APPLICANT: BAIRER, Michael

APPLICANT: JESPER, Laurent Stephane Anne Therese
; APPLICANT: WINTER, Gregory Paul
; TITLE OF INVENTION: Production of chimeric antibodies - a
; TITLE OF INVENTION: combinatorial approach
; NUMBER OF SEQUENCES: 144
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (ERO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/211,202
; FILING DATE: 23-SEP-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9120252.3
; FILING DATE: 23-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9120377.8
; FILING DATE: 25-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206372.6
; FILING DATE: 24-MAR-1992
; APPLICATION NUMBER: PCT/GB92/00883
; APPLICATION DATA:
; FILING DATE: 15-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: David W. Clough
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/31960
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 141:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-211-202-141

Query Match 93.2%; Score 82; DB 1; Length 116;
Best Local Similarity 88.2%; Pred. No. 8.7e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 12
US-08-545-809A-115
; Sequence 115; Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tadamu
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: PastSRO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545, 809A
FILING DATE: 27-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06501/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 115:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-545-809A-115

Query Match 93.2%; Score 82; DB 3; Length 117;
Best Local Similarity 88.2%; Pred. No. 8.8e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:|||||
DB 69 VISYDGSNKYYADSVKG 85

RESULT 13
US-08-331-398A-46
Sequence 46, Application US/08331398A
GENERAL INFORMATION:
APPLICANT: Pastan, Ira
APPLICANT: Willingham, Mark
APPLICANT: Fitzgerald, David
APPLICANT: Brinkmann, Ulrich
APPLICANT: Pal, Lee
TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
TITLE OF INVENTION: and Their Uses (as amended)
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Plaza
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,398A
FILING DATE: 28-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331

FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-126110US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..119
OTHER INFORMATION: /note= "Human fetal immunoglobulin
OTHER INFORMATION: 56P1 CL Variable Heavy chain (V-H)"
US-08-331-398A-46
Query Match 93.2%; Score 82; DB 1; Length 119;
Best Local Similarity 88.2%; Pred. No. 8.9e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:|||||
DB 50 VISYDGSNKYYADSVKG 66

RESULT 14
US-08-331-397B-46
Sequence 46, Application US/08331397B
GENERAL INFORMATION:
APPLICANT: Pastan, Ira
APPLICANT: Benhar, Itai
TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Uses
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Plaza
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,397B
FILING DATE: 28-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-126120US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600

TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..119
; OTHER INFORMATION: /note="Human fetal immunoglobulin
; OTHER INFORMATION: 56p1/CL Variable Heavy chain (V-H)"
US-08-331-397B-46

Query Match 93.2%; Score 82; DB 2; Length 119;
Best Local Similarity 88.2%; Pred. No. 8.9e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
Db 50 VISYDGSNKYYADSVKG 66

RESULT 15
US-08-759-804A-46
; Sequence 46, Application US/08759804A
; Patent No. 5990296
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Willingham, Mark
; APPLICANT: Fitzgerald, David J.
; APPLICANT: Brinkmann, Ulrich
; APPLICANT: Pal, Lee
; TITLE OF INVENTION: Tumor-Specific Antibody Fragments,
; TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/759,804A
; FILING DATE: 03-DEC-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/331,398
; FILING DATE: 28-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen L.
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 015280-126140US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid

STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..119
; OTHER INFORMATION: /note="Human fetal immunoglobulin
; OTHER INFORMATION: 56p1/CL Variable Heavy chain (V-H)"
US-08-759-804A-46

Query Match 93.2%; Score 82; DB 2; Length 119;
Best Local Similarity 88.2%; Pred. No. 8.9e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
Db 50 VISYDGSNKYYADSVKG 66

RESULT 16
US-09-227-693-46
; Sequence 46, Application US/09227693
; Patent No. 6287562
; GENERAL INFORMATION:
; APPLICANT: PASTAN, Ira
; APPLICANT: BENHAR, Itai
; APPLICANT: PADLAN, Eduardo A.
; APPLICANT: JUNG, Sun-Hee
; APPLICANT: LEE, Byungkook
; TITLE OF INVENTION: HUMANIZED TUMOR-SPECIFIC ANTIBODY
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourile and Crew
; STREET: Stewart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/227,693
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/331,396
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 15280-126-1-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..119

OTHER INFORMATION: /note="Human fetal immunoglobulin
OTHER INFORMATION: 56P1/CL VH region"
US-09-227-693-46

Query Match 93.2%; Score 82; DB 3; Length 119;
Best Local Similarity 88.2%; Pred. No. 8.9e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 17
US-08-211-202-135
Sequence 135, Application US/08211202
Patent No. 5565332
GENERAL INFORMATION:
APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Matteus
APPLICANT: BAIRER, Michael
APPLICANT: JESPER, Laurent Stephane Anne Therese
APPLICANT: WINTER, Gregory Paul
TITLE OF INVENTION: Production of chimeric antibodies - a
NUMBER OF INVENTION: combinatorial approach
CORRESPONDENCE ADDRESSES: 144
ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
ADDRESS: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211.202
FILING DATE: 23-SEP-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120252.3
FILING DATE: 23-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120377.8
FILING DATE: 25-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/31960
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 135:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-211-202-135

Query Match 93.2%; Score 82; DB 1; Length 120;
Best Local Similarity 88.2%; Pred. No. 9e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 18
US-07-942-245-35
Sequence 35, Application US/07942245
Patent No. 5639641
GENERAL INFORMATION:
APPLICANT: PEDERSEN, Jan T.
APPLICANT: SEARLE, Stephen M.J.
APPLICANT: REES, Anthony R.
APPLICANT: ROGUSKA, Michael A.
APPLICANT: GUILD, Braydon C.
TITLE OF INVENTION: SURFACE RESIDUE VENERING OF RODENT
NUMBER OF INVENTION: ANTIBODIES
CORRESPONDENCE ADDRESSES: 522
ADDRESSEE: Sughrue, Miron, Zimm, Macpeak & Seas
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: United States
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HP 9000/700 Workstation
OPERATING SYSTEM: UNIX
SOFTWARE: In house
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/942.245
FILING DATE: 09-SEP-1992
CLASSIFICATION: 530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-942-245-35

Query Match 93.2%; Score 82; DB 1; Length 120;
Best Local Similarity 88.2%; Pred. No. 9e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 19
US-08-983-607-38
Sequence 38, Application US/08983607
Patent No. 6140470
GENERAL INFORMATION:
APPLICANT: Aiah Garen
APPLICANT: Xiaohong Cai
TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
TITLE OF INVENTION: bodies
NUMBER OF INVENTION: 51
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Department of Molecular Biophysics
ADDRESSEE: and Biochemistry, Yale University
STREET: 266 Whitney Avenue

CITY: New Haven
STATE: Connecticut
COUNTRY: United States of America
ZIP: 06520-8114
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER: IBM PC
OPERATING SYSTEM: MS DOS
SOFTWARE: Word Processing
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/983.607
FILING DATE: April 27, 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB96/01032
FILING DATE: June 28, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mary M. Kineky
REGISTRATION NUMBER: 32423
REFERENCE/DOCKET NUMBER: OCR-679
TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-773-9544
TELEFAX: 203-773-1183
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 residues
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: polypeptide
ORIGINAL SOURCE:
ORGANISM: Homo sapiens (melanoma patient
ORGANISM: immunized with autologous tumor cells)
INDIVIDUAL ISOLATE: peripheral blood lympho-
INDIVIDUAL ISOLATE: cytes
IMMEDIATE SOURCE:
LIBRARY: DM414 scFv antibodies obtained from
LIBRARY: fuses fusion phage construct
CLONE: V575
FEATURE:
NAME/KEY: heavy chain
US-08-983-607-38
Query Match 93.2%; Score 82; DB 3; Length 123;
Best Local Similarity 88.2%; Pred. No. 9.2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Oy 1 IISYDSKXYADSVKG 17
Db 50 VISYDSNKXYADSVKG 66
RESULT 20
US-09-424-840B-6
Sequence 6, Application US/09424840B
Patent No. 6790938
GENERAL INFORMATION:
APPLICANT: Berchtold, Peter
APPLICANT: Escher, Robert F. A.
TITLE OF INVENTION: ANTI-GPIIb/IIIa RECOMBINANT ANTIBODIES
FILE REFERENCE: 100564-09049
CURRENT APPLICATION NUMBER: US/09/424.840B
CURRENT FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: DE 19820663.1
PRIOR FILING DATE: 1998-05-08
PRIOR APPLICATION NUMBER: DE 19755227.7
PRIOR FILING DATE: 1997-12-12
PRIOR APPLICATION NUMBER: DE 19723904.8
PRIOR FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 128
SOFTWARE: PatentIn version 3.1

SEQ ID NO 6
LENGTH: 123
TYPE: PRT
ORGANISM: Homo sapiens
US-09-424-840B-6
Query Match 93.2%; Score 82; DB 4; Length 123;
Best Local Similarity 88.2%; Pred. No. 9.2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Oy 1 IISYDSKXYADSVKG 17
Db 50 VISYDSNKXYADSVKG 66
RESULT 21
US-08-478-039-96
Sequence 96, Application US/08478039
Patent No. 5681722
GENERAL INFORMATION:
APPLICANT: Newman, Roland A.
APPLICANT: Hanna, Nabil
APPLICANT: Raab, Ronald W.
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince St.
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478.039
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379.072
FILING DATE: 25-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912.292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856.281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735.064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Teekin Esq., Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-160
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
POSITION IN GENOME:
CHROMOSOME/SEGMENT: RF SJ2
US-08-478-039-96
Query Match 93.2%; Score 82; DB 1; Length 128;
Best Local Similarity 88.2%; Pred. No. 9.6e-06;

Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 22
US-08-476-349A-96
; Sequence 96, Application US/08476349A
; Patent No. 5750105
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SNECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-161
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 96:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: RF SJ2
US-08-476-349A-96

Query Match 93.2%; Score 82; DB 1; Length 128;
Best Local Similarity 88.2%; Pred. No. 9.6e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 23

US-09-315-926A-80
; Sequence 80, Application US/09315926A
; Patent No. 6498027
; GENERAL INFORMATION:
; APPLICANT: Es van, Helmut
; APPLICANT: Havenga, Menzo
; APPLICANT: Verlinden, Stefan
; TITLE OF INVENTION: TARGETED DELIVERY THROUGH A CATIONIC AMINO ACID TRANSPORTER
; FILE REFERENCE: 2183-4080US
; CURRENT APPLICATION NUMBER: US/09/315,926A
; CURRENT FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: EP 99201593.3
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: EP 98201693.3
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 80
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Description of Artificial Sequence: phage
; LOCATION: (1)..(248)
; OTHER INFORMATION: /note="hCAR1 amino acid sequence"
US-09-315-926A-80

Query Match 93.2%; Score 82; DB 4; Length 248;
Best Local Similarity 88.2%; Pred. No. 1.9e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 72 VISYDGSNKYYADSVKG 88

RESULT 24
US-09-424-840B-77
; Sequence 77, Application US/09424840B
; Patent No. 6790938
; GENERAL INFORMATION:
; APPLICANT: Berchtold, Peter
; TITLE OF INVENTION: ANTI-GPIIb/IIIa RECOMBINANT ANTIBODIES
; FILE REFERENCE: 100564-09049
; CURRENT APPLICATION NUMBER: US/09/424,840B
; CURRENT FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: DE 19820663.1
; PRIOR FILING DATE: 1998-05-08
; PRIOR APPLICATION NUMBER: DE 19755227.7
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: DE 19723904.8
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 77
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-424-840B-77

Query Match 92.0%; Score 81; DB 4; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.7e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 1 LISYDGSNKYYADSVKG 17

RESULT 25

US-09-424-840B-111
; Sequence 111, Application US/09424840B
; Patent No. 6790938
; GENERAL INFORMATION:
; APPLICANT: Berchtold, Peter
; TITLE OF INVENTION: ANTI-GPIIb/IIIa RECOMBINANT ANTIBODIES
; FILE REFERENCE: 100564-09049
; CURRENT FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: DE 19820663.1
; PRIOR FILING DATE: 1998-05-08
; PRIOR APPLICATION NUMBER: DE 19755227.7
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: DE 19723904.8
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 111
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-424-840B-111

Query Match 92.0%; Score 81; DB 4; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.7e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
Db 1 LISYDGSNKYYADSVKG 17

RESULT 26
US-09-424-840B-16
; Sequence 16, Application US/09424840B
; Patent No. 6790938
; GENERAL INFORMATION:
; APPLICANT: Berchtold, Peter
; TITLE OF INVENTION: ANTI-GPIIb/IIIa RECOMBINANT ANTIBODIES
; FILE REFERENCE: 100564-09049
; CURRENT FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: DE 19820663.1
; PRIOR FILING DATE: 1998-05-08
; PRIOR APPLICATION NUMBER: DE 19755227.7
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: DE 19723904.8
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-424-840B-16

Query Match 92.0%; Score 81; DB 4; Length 124;
Best Local Similarity 88.2%; Pred. No. 1.3e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
Db 50 LISYDGSNKYYADSVKG 66

RESULT 27
US-08-862-124-2
; Sequence 2, Application US/08862124
; Patent No. 6207153
; GENERAL INFORMATION:
; APPLICANT: Dan, Michael D.

APPLICANT: Maiti, Pradip K.
; APPLICANT: Kaplan, Howard A.
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT
; TITLE OF INVENTION: SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE
; TITLE OF INVENTION: FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
; TITLE OF INVENTION: DETECTION OF CANCERS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster LLP
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/862,124
; FILING DATE: 22-MAY-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnhardt, Susan K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 31608-20001.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 179 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-862-124-2

Query Match 92.0%; Score 81; DB 3; Length 179;
Best Local Similarity 88.2%; Pred. No. 2e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
Db 111 VISYDGSSTKYADSVKG 127

RESULT 28
US-09-456-090A-102
; Sequence 102, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkiers, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lomberg, Nile
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT FILING DATE: 1999-12-06
; CURRENT APPLICATION NUMBER: US/09/456,090A
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 102
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-31H
US-09-456-090A-102

Query Match 92.0%; Score 81; DB 4; Length 225;
Best Local Similarity 88.2%; Pred. No. 2.5e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 LISYDGSNKYYADSVKG 66

RESULT 29
US-09-456-090A-108
; Sequence 108, Application US/09456090A
; Patent No. 6680209

GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lomborg, Nils
TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
FILE REFERENCE: 020015-000200US
CURRENT APPLICATION NUMBER: US/09/456,090A
CURRENT FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 110
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 108
LENGTH: 225
TYPE: PRT
ORGANISM: Homo sapiens
OTHER INFORMATION: M2-34H
US-09-456-090A-108

Query Match 92.0%; Score 81; DB 4; Length 225;
Best Local Similarity 88.2%; Pred. No. 2.5e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 LISYDGSNKYYADSVKG 66

RESULT 30
US-09-456-090A-110
; Sequence 110, Application US/09456090A
; Patent No. 6680209

GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lomborg, Nils
TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
FILE REFERENCE: 020015-000200US
CURRENT APPLICATION NUMBER: US/09/456,090A
CURRENT FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 110
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 110
LENGTH: 225
TYPE: PRT
ORGANISM: Homo sapiens
OTHER INFORMATION: M2-35H
US-09-456-090A-110

Query Match 92.0%; Score 81; DB 4; Length 225;
Best Local Similarity 88.2%; Pred. No. 2.5e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 LISYDGSNKYYADSVKG 66

RESULT 31
US-09-453-234-102
; Sequence 102, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:

APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lomborg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: Genpharm International
TITLE OF INVENTION: Human Antibodies
FILE REFERENCE: 020015-000110US
CURRENT APPLICATION NUMBER: US/09/453,234
CURRENT FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: US 60/157,415
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 102
LENGTH: 225
TYPE: PRT
ORGANISM: Homo sapiens
OTHER INFORMATION: M2-31H
US-09-453-234-102

Query Match 92.0%; Score 81; DB 4; Length 225;
Best Local Similarity 88.2%; Pred. No. 2.5e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 LISYDGSNKYYADSVKG 66

RESULT 32
US-09-453-234-108
; Sequence 108, Application US/09453234
; Patent No. 6794132

GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lomborg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: Genpharm International
TITLE OF INVENTION: Human Antibodies
FILE REFERENCE: 020015-000110US
CURRENT APPLICATION NUMBER: US/09/453,234
CURRENT FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: US 60/157,415
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 108
LENGTH: 225
TYPE: PRT
ORGANISM: Homo sapiens
OTHER INFORMATION: M2-34H
US-09-453-234-108

Query Match 92.0%; Score 81; DB 4; Length 225;
Best Local Similarity 88.2%; Pred. No. 2.5e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 LISYDGSNKYYADSVKG 66

RESULT 33
US-09-453-234-110
; Sequence 110, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff

APPLICANT: Lonberg, Nils
APPLICANT: Bioscience Diagnostics, Inc.
FILE REFERENCE: 020015-000110US
CURRENT APPLICATION NUMBER: US/09/453,234
CURRENT FILING DATE: 1999-12-01
PRIORITY APPLICATION NUMBER: US 60/157,415
PRIORITY FILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 112
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 110
LENGTH: 225
TYPE: PRT
ORGANISM: Homo sapiens
OTHER INFORMATION: M2-35H
US-09-453-234-110

Query Match 92.0%; Score 81; DB 4; Length 225;
Best Local Similarity 88.2%; Pred. No. 2.5e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 IISYDGSKKYYADSVKG 66

RESULT 34
US-08-862-124-17
Sequence 17, Application US/08862124
Patent No. 6207153
GENERAL INFORMATION:
APPLICANT: Dan, Michael D.
APPLICANT: Maiti, Pradip K.
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT
SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE
TITLE OF INVENTION: FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
TITLE OF INVENTION: DETECTION OF CANCERS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster LLP
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/862,124
FILING DATE: 22-MAY-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 31608-20001.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 287 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-862-124-17

Query Match 92.0%; Score 81; DB 3; Length 287;

Best Local Similarity 88.2%; Pred. No. 3.2e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 192 VISYDGSSTKYADSVKG 208

RESULT 35
US-08-862-124-14
Sequence 14, Application US/08862124
Patent No. 6207153
GENERAL INFORMATION:
APPLICANT: Dan, Michael D.
APPLICANT: Maiti, Pradip K.
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT
SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE
TITLE OF INVENTION: FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
TITLE OF INVENTION: DETECTION OF CANCERS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster LLP
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/862,124
FILING DATE: 22-MAY-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 31608-20001.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 304 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-862-124-14

Query Match 92.0%; Score 81; DB 3; Length 304;
Best Local Similarity 88.2%; Pred. No. 3.4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 209 VISYDGSSTKYADSVKG 225

RESULT 36
US-09-560-198A-12
Sequence 12, Application US/09560198A
Patent No. 6492497
GENERAL INFORMATION:
APPLICANT: Thompson, Julia E
APPLICANT: Leonard, Simon J
APPLICANT: Wilton, Alison J
APPLICANT: Bradlock, Peter SH
APPLICANT: Du Fou, Sarah L
APPLICANT: McCafferty, John G

```

? APPLICANT: Conroy, Louise R
? APPLICANT: Tempst, Philip R
? TITLE OF INVENTION: Specific binding members for TGFbeta1
? FILE REFERENCE: 2811/35620A
? CURRENT APPLICATION NUMBER: US/09/560,198A
? CURRENT FILING DATE: 2000-04-28
? PRIOR APPLICATION NUMBER: US 60/131,983
? PRIOR FILING DATE: 1999-04-30
? NUMBER OF SEQ ID NOS: 25
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 12
? LENGTH: 17
? TYPE: PR1
? ORGANISM: Homo sapiens
? US-09-560-198A-12

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Query Match	89.8%	Score	79;	DB	4;	length	17;
Best Local Similarity	88.2%	Pred.	No.	3.5e-06;			
Matches	15;	Conservative	1;	Mismatches	0;	Gaps	0;

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QY      1 IISYDGSKKYYADSVKG 17
          : ||||| ||||| |||||
Db      1 VISYDGSIKYYADSVKG 17
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RESULT 37
US-09-424-840B-84
Sequence 84, Application US/09424840B
Patent No. 6790938
GENERAL INFORMATION:
APPLICANT: Berchtold, Peter
APPLICANT: Escher, Robert F. A.
TITLE OF INVENTION: ANTI-GPIIb/IIIa RECOMBINANT ANTIBODIES
FILE REFERENCE: 100564-09049
CURRENT APPLICATION NUMBER: US/09/424,840B
CURRENT FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: DE 19820663.1
PRIOR FILING DATE: 1998-05-08
PRIOR APPLICATION NUMBER: DE 19755227.7
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: DE 19723904.8
PRIOR FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 128
SOFTWARE: PatentIn version 3.1
SEQ ID NO 84
LENGTH: 17
TYPE: PRT
ORGANISM: Homo sapiens
US-09-424-840B-84

Query Match	89.8%	Score	79	DB	4	Length	17
Best Local Similarity	93.8%	Pred	No.	3.5e-06			
Matches	15	Conservative	0	Mismatches	1	Indels	0
						Gaps	0

Qy	2	ISYDGSKKYYADSVKG	17
Db	2	ISYDGSNKYYADSVKG	17

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RESULT 38
US-09-424-840B-113
: Sequence 113, Application US/09242480B
: Patent No. 6790938
: GENERAL INFORMATION:
: APPLICANT: Berchold, Peter
: APPLICANT: Escher, Robert F. A.
: TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES
: FILE REFERENCE: 100564-09049
: CURRENT APPLICATION NUMBER: US/09/424,840B
: CURRENT FILING DATE: 1999-12-03
: PRIOR APPLICATION NUMBER: DE 19820663.1
: PRIOR FILING DATE: 1998-05-08
: PRIOR APPLICATION NUMBER: DE 19755227.7

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? PRIOR FILLING DATE: 1997-12-12
? PRIOR APPLICATION NUMBER: DE_19723904.8
? PRIOR FILLING DATE: 1997-06-06
? NUMBER OF SEQ ID NOS: 128
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO: 113
? LENGTH: 17
? TYPE: prt
? ORGANISM: Homo sapiens
US-03-424-840B-113

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Query Match	89.8%	Score 79	DB 4	Length 17
Best Local Similarity	93.8%	Pred. No.	3.5e-06	
Matches	15	Conservative	0	Mismatches 1
				Indels 0
				Gaps 0

QY 2 ISYDGSKKYYADSVKG 17
|||
Db 2 ISYDGSNNKYADSVKG 17

RESULT 39
 US-09-560-198A-2
 Sequence 2, Application US/09560198A
 Patent No. 6492497
 GENERAL INFORMATION:
 APPLICANT: Thompson, Julia E
 APPLICANT: Leonard, Simon N
 APPLICANT: Wilson, Allison J
 APPLICANT: Braddock, Peta SH
 APPLICANT: Du Fou, Sarah L
 APPLICANT: McCallister, John G
 APPLICANT: Conroy, Louise A
 APPLICANT: Tempest, Philip R
 TITLE OF INVENTION: Specific binding members for TGFbeta1
 FILE REFERENCE: 2811/35620A
 CURRENT APPLICATION NUMBER: US/09/560,198A
 CURRENT FILING DATE: 2000-04-28
 PRIOR APPLICATION NUMBER: US 60/131,983
 PRIOR FILING DATE: 1999-04-30
 NUMBER OF SEQ ID NOS: 25
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 2
 LENGTH: 123
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-560-198A-2

Query Match	89.8%	Score 79:	DB 4:	Length 123;
Best Local Similarity	88.2%	Pred. No.	2.8e-05;	
Matches 15; Conservative	1;	Mismatches	1;	Indels 0; Gaps 0

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QY      1 IISYDGSKYYADSVKG 17
          : ||||| ||||| |||
Db      50 VISYDGSIKYYADSVKG 66
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US-RESULT 40
US-09-560-198A-4
; Sequence 4, Application US/09560198A
; Patent No. 6492497
; GENERAL INFORMATION:
; APPLICANT: Thompson, Julia E
; APPLICANT: Lennard, Simon N
; APPLICANT: Wilton, Alison J
; APPLICANT: Braddock, Peta SH
; APPLICANT: Du Fou, Sarah L
; APPLICANT: McCaferry, John G
; APPLICANT: Conroy, Louise A
; APPLICANT: Tempest, Philip R
; TITLE OF INVENTION: Specific binding members for TGFbeta
; FILE REFERENCE: 2811/35620A
; CURRENT APPLICATION NUMBER: US/09/560,198A
; CURRENT FILING DATE: 2000-04-28

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; PRIOR APPLICATION NUMBER: US 60/131,983
 ; PRIOR FILING DATE: 1999-04-30
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 4
 ; LENGTH: 123
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-560-198A-4

Query Match 89.8%; Score 79; DB 4; Length 123;
 Best Local Similarity 88.2%; Pred. No. 2.8e-05;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 IISYDGSKKYYADSVKG 17
 :|||||
 Db 50 VISYDGSIKYYADSVKG 66

Search completed: March 31, 2005, 12:13:25
 Job time : 34.2031 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 31, 2005, 12:10:00 ; Search time 95.0938 Seconds
(without alignments)
59.279 Million cell updates/sec

Title: US-10-614-959-11

Perfect score: 88
Sequence: 1 IISYDGSKKYYADSVKG 17

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1413372 seqs, 331592847 residues

Total number of hits satisfying chosen parameters: 1413372

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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20: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	87	98.9	248 10 US-09-880-748-914	Sequence 914, App
2	87	98.9	248 10 US-09-880-748-916	Sequence 916, App
3	87	98.9	248 10 US-09-880-748-1323	Sequence 1323, App
4	87	98.9	248 15 US-10-293-418-914	Sequence 914, App
5	87	98.9	248 15 US-10-293-418-916	Sequence 916, App
6	87	98.9	248 15 US-10-293-418-1323	Sequence 1323, App
7	87	98.9	251 10 US-09-880-748-1114	Sequence 1114, App
8	87	98.9	251 15 US-10-293-418-1114	Sequence 1114, App
9	86	97.7	135 15 US-10-364-743-97	Sequence 97, App
10	84	95.5	17 9 US-09-828-708-24	Sequence 24, App
11	84	95.5	101 9 US-09-828-708-10	Sequence 10, App
12	84	95.5	119 14 US-10-010-729-7	Sequence 7, App
13	83	94.3	123 17 US-10-727-155-14	Sequence 14, App

14	83	94.3	125 15 US-10-292-088-58	Sequence 58, App
15	83	94.3	137 15 US-10-364-743-11	Sequence 11, App
16	83	94.3	137 15 US-10-364-743-99	Sequence 99, App
17	83	94.3	252 10 US-09-880-748-1690	Sequence 1690, App
18	83	94.3	252 15 US-10-293-418-1690	Sequence 1690, App
19	83	94.3	470 15 US-10-292-088-62	Sequence 62, App
20	82	93.2	17 10 US-09-972-656-66	Sequence 46, App
21	82	93.2	17 15 US-10-384-060-46	Sequence 46, App
22	82	93.2	17 15 US-10-399-701-6	Sequence 6, App
23	82	93.2	17 16 US-10-396-578-21	Sequence 21, App
24	82	93.2	17 16 US-10-396-578-39	Sequence 39, App
25	82	93.2	17 16 US-10-396-578-51	Sequence 51, App
26	82	93.2	17 16 US-10-396-578-81	Sequence 81, App
27	82	93.2	17 17 US-10-726-332-114	Sequence 114, App
28	82	93.2	41 15 US-10-269-711-47	Sequence 47, App
29	82	93.2	41 15 US-10-269-711-48	Sequence 48, App
30	82	93.2	41 16 US-10-684-109-59	Sequence 59, App
31	82	93.2	83 14 US-10-078-958-7	Sequence 7, App
32	82	93.2	95 16 US-10-884-830-653	Sequence 15, App
33	82	93.2	98 9 US-09-948-939-15	Sequence 15, App
34	82	93.2	98 14 US-10-194-975-23	Sequence 23, App
35	82	93.2	98 14 US-10-194-975-24	Sequence 24, App
36	82	93.2	98 14 US-10-194-975-25	Sequence 25, App
37	82	93.2	98 15 US-10-308-817-63	Sequence 63, App
38	82	93.2	98 15 US-10-308-817-64	Sequence 64, App
39	82	93.2	98 15 US-10-308-817-65	Sequence 65, App
40	82	93.2	98 15 US-10-032-0378-74	Sequence 74, App
41	82	93.2	98 15 US-10-032-0378-75	Sequence 75, App
42	82	93.2	98 15 US-10-032-0378-76	Sequence 76, App
43	82	93.2	98 15 US-10-032-0378-80	Sequence 80, App
44	82	93.2	98 15 US-10-029-9888-74	Sequence 74, App
45	82	93.2	98 15 US-10-029-9888-75	Sequence 75, App

ALIGNMENTS

RESULT 1
US-09-880-748-914
; Sequence 914, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P523
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 914
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-880-748-914

Query Match 98.9%; Score 87; DB 10; Length 248;
Best Local Similarity 94.1%; Pred. No. 1.9e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
CY 1 IISYDGSKKYYADSVKG 17
DB 50 IISYDGSKKYYADSVKG 66


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RESULT 5
US-10-293-418-916
Sequence 916, Application US/10293418
Publication No. US2003022396A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
FILE REFERENCE: p5523p2
CURRENT APPLICATION NUMBER: US/10/293,418
PRIOR FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 916
LENGTH: 248

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TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-418-916

Query Match
Best Local Similarity 98.9%; Score 87; DB 15; Length 248;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
Db 50 VISYDGSKKYYADSVKG 66

RESULT 6
US-10-293-418-1323
Sequence 1323, Application US/10293418
Publication No. US20030223996A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
FILE REFERENCE: PFS23P2

CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1323
LENGTH: 248
TYPE: PRT

ORGANISM: Homo sapiens
US-10-293-418-1323

Query Match
Best Local Similarity 98.9%; Score 87; DB 15; Length 248;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
Db 50 VISYDGSKKYYADSVKG 66

RESULT 7
US-09-880-748-1114
Sequence 1114, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
FILE REFERENCE: PFS23
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1114
LENGTH: 251
TYPE: PRT

ORGANISM: Homo sapiens
US-10-293-418-1114

Query Match
Best Local Similarity 98.9%; Score 87; DB 15; Length 251;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
Db 50 VISYDGSKKYYADSVKG 66

RESULT 8
US-10-293-418-1114
Sequence 1114, Application US/10293418
Publication No. US20030223996A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
FILE REFERENCE: PFS23P2

CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1114
LENGTH: 251
TYPE: PRT

ORGANISM: Homo sapiens
US-10-293-418-1114

PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1114
LENGTH: 251
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-1114

Query Match
Best Local Similarity 98.9%; Score 87; DB 10; Length 251;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
Db 50 VISYDGSKKYYADSVKG 66

RESULT 9
US-10-364-743-97
Sequence 97, Application US/10364743
Publication No. US20040009178A1
GENERAL INFORMATION:
APPLICANT: Bowditch, Katherine S.
APPLICANT: Frederickson, Shana
APPLICANT: Wild, Martha A.
APPLICANT: Maruyama, Yoshiaki
APPLICANT: No. US20040009178A1, Mary Jean
TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
FILE REFERENCE: 84 (1087-73)

CURRENT APPLICATION NUMBER: US/10/364,743
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1114
LENGTH: 251
TYPE: PRT

ORGANISM: Homo sapiens
US-10-293-418-1114

Query Match
Best Local Similarity 98.9%; Score 87; DB 15; Length 251;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
Db 50 VISYDGSKKYYADSVKG 66

RESULT 9
US-10-364-743-97
Sequence 97, Application US/10364743
Publication No. US20040009178A1
GENERAL INFORMATION:
APPLICANT: Bowditch, Katherine S.
APPLICANT: Frederickson, Shana
APPLICANT: Wild, Martha A.
APPLICANT: Maruyama, Yoshiaki
APPLICANT: No. US20040009178A1, Mary Jean
TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
FILE REFERENCE: 84 (1087-73)

CURRENT APPLICATION NUMBER: US/10/364,743
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1114
LENGTH: 251
TYPE: PRT

ORGANISM: Homo sapiens
US-10-293-418-1114

Query Match
Best Local Similarity 98.9%; Score 87; DB 15; Length 251;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
Db 50 VISYDGSKKYYADSVKG 66

RESULT 9
US-10-364-743-97
Sequence 97, Application US/10364743
Publication No. US20040009178A1
GENERAL INFORMATION:
APPLICANT: Bowditch, Katherine S.
APPLICANT: Frederickson, Shana
APPLICANT: Wild, Martha A.
APPLICANT: Maruyama, Yoshiaki
APPLICANT: No. US20040009178A1, Mary Jean
TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
FILE REFERENCE: 84 (1087-73)

CURRENT APPLICATION NUMBER: US/10/364,743
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1114
LENGTH: 251
TYPE: PRT

ORGANISM: Homo sapiens
US-10-293-418-1114

```

; CURRENT APPLICATION NUMBER: US/10/364,743
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US 60/428,807
; PRIOR FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 97
; LENGTH: 135
; TYPE: PRT
; ORGANISM: human
US-10-364-743-97

Query Match          97.7%  Score 86; DB 15; Length 135;
Best Local Similarity 94.1%; Pred. NO. 1.5e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 IISYDGSKKYYADSVKG 17
       :||||:|||||
Db      52 LISYDGSKKYYADSVKG 68

RESULT 10
US-09-828-708-24
; Sequence 24, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partic
; FILE REFERENCE: 1361.005US1
; CURRENT APPLICATION NUMBER: US/09/828,708
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-708-24

Query Match          95.5%  Score 84; DB 9; Length 17;
Best Local Similarity 88.2%; Pred. NO. 3.5e-06;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 IISYDGSKKYYADSVKG 17
       :||||:|||||
Db      1 VISYDGNKKYYADSVKG 17

RESULT 11
US-09-828-708-10
; Sequence 10, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partic
; FILE REFERENCE: 1361.005US1
; CURRENT APPLICATION NUMBER: US/09/828,708
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-708-10

Query Match          95.5%  Score 84; DB 9; Length 101;

```

```

Best Local Similarity 88.2%; Pred. NO. 2.2e-05;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 IISYDGSKKYYADSVKG 17
       :||||:|||||
Db      43 VISYDGNKKYYADSVKG 59

RESULT 12
US-10-010-729-7
; Sequence 7, Application US/10010729
; Publication No. US20030185827A1
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; APPLICANT: Pease, Larry R.
; TITLE OF INVENTION: Human IGM Antibodies and Diagnostic and
; TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous
; FILE REFERENCE: 1199-1-005C1P2
; CURRENT APPLICATION NUMBER: US/10/010,729
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 09/730,473
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 09/580,787
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: 09/322,862
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 08/779,784
; PRIOR FILING DATE: 1997-01-07
; PRIOR APPLICATION NUMBER: 08/692,084
; PRIOR FILING DATE: 1996-08-08
; PRIOR APPLICATION NUMBER: 08/236,520
; PRIOR FILING DATE: 1994-04-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-010-729-7

Query Match          95.5%  Score 84; DB 14; Length 119;
Best Local Similarity 88.2%; Pred. NO. 2.6e-05;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 IISYDGSKKYYADSVKG 17
       :||||:|||||
Db      50 VISYDGSKKYYADSVKG 66

RESULT 13
US-10-727-155-14
; Sequence 14, Application US/10727155
; Publication No. US20050049402A1
; GENERAL INFORMATION:
; APPLICANT: John S. Babcock
; APPLICANT: Jaapal S. Kang
; APPLICANT: Orit Foord
; APPLICANT: Larry Green
; APPLICANT: Xiao Feng
; APPLICANT: Scott Klakamp
; APPLICANT: Mary Haak-Frendachio
; APPLICANT: Palaniswami Rathanaswami
; APPLICANT: Craig Pigott
; APPLICANT: Meina Liang
; APPLICANT: Rozanne Lee
; APPLICANT: Kathy Manchulenchio
; APPLICANT: Rafiaella Faggioni
; APPLICANT: Giorgio Senaldi
; APPLICANT: Qiaojuan Jane Su
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO TUMOR NECROSIS
; TITLE OF INVENTION: FACTOR AND USES THEREOF

```

```
FILE REFERENCE: ABGENIX.073A
; CURRENT APPLICATION NUMBER: US/10/727,155
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 60/430729
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 320
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-727-155-14

Query Match          94.3%; Score 83; DB 17; Length 123;
Best Local Similarity 94.1%; Pred. No. 3.9e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 IISYDGSKKYYADSVKG 17
        |||||
        50 IISYDGSNNYYADSVKG 66

RESULT 14
US-10-292-088-58
; Sequence 58, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHR
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PR/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 58
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-58

Query Match          94.3%; Score 83; DB 15; Length 125;
Best Local Similarity 94.1%; Pred. No. 3.9e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 IISYDGSKKYYADSVKG 17
        |||||
        50 IISYDGSNNYYADSVKG 66

RESULT 15
US-10-364-743-11
; Sequence 11, Application US/10364743
; Publication No. US20040009178A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Wild, Martha A.
; APPLICANT: Maruyama, Toshiaki
; APPLICANT: No. US20040009178A1an, Mary Jean
; TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
; FILE REFERENCE: 84 (1087-73)
; CURRENT APPLICATION NUMBER: US/10/364,743
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: 60/428,807
; PRIOR FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.2
```

```
; SEQ ID NO 11
; LENGTH: 137
; TYPE: PRT
; ORGANISM: human
US-10-364-743-11

Query Match          94.3%; Score 83; DB 15; Length 137;
Best Local Similarity 88.2%; Pred. No. 4.3e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 IISYDGSKKYYADSVKG 17
        :|||||
        52 VISYDGSKKYYGDSVKG 68

RESULT 16
US-10-364-743-99
; Sequence 99, Application US/10364743
; Publication No. US20040009178A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Wild, Martha A.
; APPLICANT: Maruyama, Toshiaki
; APPLICANT: No. US20040009178A1an, Mary Jean
; TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
; FILE REFERENCE: 84 (1087-73)
; CURRENT APPLICATION NUMBER: US/10/364,743
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US 60/428,807
; PRIOR FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 99
; LENGTH: 137
; TYPE: PRT
; ORGANISM: human
US-10-364-743-99

Query Match          94.3%; Score 83; DB 15; Length 137;
Best Local Similarity 88.2%; Pred. No. 4.3e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 IISYDGSKKYYADSVKG 17
        :|||||
        52 VISYDGSKKYYGDSVKG 68

RESULT 17
US-09-880-748-1690
; Sequence 1690, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1690
; LENGTH: 252
; TYPE: PRT
```

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; ORGANISM: Homo sapiens
US-09-860-748-1690

Query Match      94.3%; Score 83; DB 10; Length 252;
Best Local Similarity 88.2%; Pred. No. 8.1e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 IISYDGSKKYYADSVKG 17
       :|||||
Db      50 VISYDGSKKYYGDSVKG 66

RESULT 18
US-10-293-418-1690
; Sequence 1690, Application US/10293418
; Publication No. US200302239661
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PR323P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1690
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1690

Query Match      94.3%; Score 83; DB 15; Length 252;
Best Local Similarity 88.2%; Pred. No. 8.1e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 IISYDGSKKYYADSVKG 17
       :|||||
Db      50 VISYDGSKKYYGDSVKG 66

RESULT 19
US-10-292-088-62
; Sequence 62, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
```

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; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-62

Query Match      94.3%; Score 83; DB 15; Length 470;
Best Local Similarity 94.1%; Pred. No. 0.00015;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 IISYDGSKKYYADSVKG 17
       :|||||
Db      69 IISYDGSNKKYYADSVKG 85

RESULT 20
US-09-972-656-48
; Sequence 48, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Tsai, Mei-Mei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 48
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-656-48

Query Match      93.2%; Score 82; DB 10; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 IISYDGSKKYYADSVKG 17
       :|||||
Db      1 VISYDGSNKKYYADSVKG 17

RESULT 21
US-10-384-060-46
; Sequence 46, Application US/10384060
; Publication No. US20030226155A1
; GENERAL INFORMATION:
; APPLICANT: SADEGHI, Homayoun
; APPLICANT: PRIOR, Christopher P.
; APPLICANT: TURNER, Andrew
; TITLE OF INVENTION: MODIFIED TRANSFERRIN-ANTIBODY FUSION PROTEINS
; FILE REFERENCE: 54710-5004-US
; CURRENT APPLICATION NUMBER: US/10/384,060
; CURRENT FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: US 10/231,494
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/406,977
; PRIOR FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: 33 CDR2 sequence
US-10-384-060-46
```

Query Match 93.2%; Score 82; DB 15; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 IISYDGSKKYYADSVKG 17
:|||||:|||||:
DB 1 VISYDGSNNKYADSVKG 17

RESULT 22
US-10-399-701-6
; Sequence 6, Application US/10399701
; Publication No. US20040022791A1
; GENERAL INFORMATION:
; APPLICANT: ASAT AG
; TITLE OF INVENTION: Rekombinant anti-GPIIb/IIIa-antibodies as agents for
; TITLE OF INVENTION: Inhibiting angiogenesis
; FILE REFERENCE: 23600PMO_DRAS
; CURRENT APPLICATION NUMBER: US/10/399,701
; PRIOR FILING DATE: 2003-04-21
; PRIORITY APPLICATION NUMBER: 100 57 443.2
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDR2-region of
US-10-399-701-6

Query Match 93.2%; Score 82; DB 15; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 IISYDGSKKYYADSVKG 17
:|||||:|||||:
DB 1 VISYDGSNNKYADSVKG 17

RESULT 23
US-10-396-578-21
; Sequence 21, Application US/10396578
; Publication No. US20040191260A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Yoram
; TITLE OF INVENTION: COMPOSITIONS CAPABLE OF SPECIFICALLY BINDING PARTICULAR HUMAN
; TITLE OF INVENTION: ANTIGEN PRESENTING MOLECULE/PATHOGEN-DERIVED ANTIGEN COMPLEXES
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 25563
; CURRENT APPLICATION NUMBER: US/10/396,578
; CURRENT FILING DATE: 2003-03-26
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 21
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence of complementarity determining region of Fab
US-10-396-578-21

Query Match 93.2%; Score 82; DB 16; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 IISYDGSKKYYADSVKG 17
:|||||:|||||:
DB 1 VISYDGSNNKYADSVKG 17

DB 1 VISYDGSNNKYADSVKG 17

RESULT 24
US-10-396-578-39
; Sequence 39, Application US/10396578
; Publication No. US20040191260A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Yoram
; TITLE OF INVENTION: COMPOSITIONS CAPABLE OF SPECIFICALLY BINDING PARTICULAR HUMAN
; TITLE OF INVENTION: ANTIGEN PRESENTING MOLECULE/PATHOGEN-DERIVED ANTIGEN COMPLEXES
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 25563
; CURRENT APPLICATION NUMBER: US/10/396,578
; CURRENT FILING DATE: 2003-03-26
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 39
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence of complementarity determining region of Fab
US-10-396-578-39

Query Match 93.2%; Score 82; DB 16; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 IISYDGSKKYYADSVKG 17
:|||||:|||||:
DB 1 VISYDGSNNKYADSVKG 17

RESULT 25
US-10-396-578-51
; Sequence 51, Application US/10396578
; Publication No. US20040191260A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Yoram
; TITLE OF INVENTION: COMPOSITIONS CAPABLE OF SPECIFICALLY BINDING PARTICULAR HUMAN
; TITLE OF INVENTION: ANTIGEN PRESENTING MOLECULE/PATHOGEN-DERIVED ANTIGEN COMPLEXES
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 25563
; CURRENT APPLICATION NUMBER: US/10/396,578
; CURRENT FILING DATE: 2003-03-26
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 51
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence of complementarity determining region of Fab
US-10-396-578-51

Query Match 93.2%; Score 82; DB 16; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 IISYDGSKKYYADSVKG 17
:|||||:|||||:
DB 1 VISYDGSNNKYADSVKG 17

RESULT 26
US-10-396-578-81
; Sequence 81, Application US/10396578
; Publication No. US20040191260A1

GENERAL INFORMATION:
APPLICANT: Reiter, Yoram
APPLICANT: Cohen, Cyril J.
TITLE OF INVENTION: COMPOSITIONS CAPABLE OF SPECIFICALLY BINDING PARTICULAR HUMAN
TITLE OF INVENTION: ANTIGEN PRESENTING MOLECULE/PATHOGEN-DERIVED ANTIGEN COMPLEXES
FILE REFERENCE: 25663
CURRENT APPLICATION NUMBER: US/10/396,578
CURRENT FILING DATE: 2003-03-26
NUMBER OF SEQ ID NOS: 97
SOFTWARE: PatentIn version 3.2
SEQ ID NO 81
LENGTH: 17
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Sequence of complementarity determining region of Fab
US-10-396-578-81

Query Match 93.2%; Score 82; DB 16; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
Db 1 VISYDGSNKYYADSVKG 17

RESULT 27
US-10-726-332-114
Sequence 114, Application US/10726332
Publication No. US20050058649A1
GENERAL INFORMATION:
APPLICANT: Gregory M. Landes
APPLICANT: Mary Haak-Frendescho
APPLICANT: Ling Chen
APPLICANT: Yen-Wah R. Lee
APPLICANT: Weina Liang
APPLICANT: Xiao-Feng
APPLICANT: Xiao-Chi Jia
APPLICANT: Mark R. Nocentini
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PHOSPHOLIPASE A2
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: ABGENIX.072A
CURRENT APPLICATION NUMBER: US/10/726,332
CURRENT FILING DATE: 2003-12-02
PRIOR APPLICATION NUMBER: n/a
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 222
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 114
LENGTH: 17
TYPE: PRT
ORGANISM: Homo sapiens
US-10-726-332-114

Query Match 93.2%; Score 82; DB 17; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
Db 1 VISYDGSNKYYADSVKG 17

RESULT 28
US-10-269-711-47
Sequence 47, Application US/10269711
Publication No. US20040071694A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: DeVries, Peter J.

APPLICANT: Reilly, Edward B.
APPLICANT: Ostrow, Dave
APPLICANT: Weller, James
APPLICANT: Green, Larry
TITLE OF INVENTION: ERYTHROPOIETIN RECEPTOR BINDING
TITLE OF INVENTION: ANTIBODIES
FILE REFERENCE: 6989.US.01
CURRENT APPLICATION NUMBER: US/10/269,711
CURRENT FILING DATE: 2002-10-14
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 47
LENGTH: 41
TYPE: PRT
ORGANISM: Homo sapiens
US-10-269-711-47

Query Match 93.2%; Score 82; DB 15; Length 41;
Best Local Similarity 88.2%; Pred. No. 1.8e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
Db 11 VISYDGSNKYYADSVKG 27

RESULT 29
US-10-269-711-48
Sequence 48, Application US/10269711
Publication No. US20040071694A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: DeVries, Peter J.
APPLICANT: Ostrow, Dave
APPLICANT: Weller, James
APPLICANT: Green, Larry
TITLE OF INVENTION: ERYTHROPOIETIN RECEPTOR BINDING
TITLE OF INVENTION: ANTIBODIES
FILE REFERENCE: 6989.US.01
CURRENT APPLICATION NUMBER: US/10/269,711
CURRENT FILING DATE: 2002-10-14
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 48
LENGTH: 41
TYPE: PRT
ORGANISM: Homo sapiens
US-10-269-711-48

Query Match 93.2%; Score 82; DB 15; Length 41;
Best Local Similarity 88.2%; Pred. No. 1.8e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
Db 11 VISYDGSNKYYADSVKG 27

RESULT 30
US-10-684-109-59
Sequence 59, Application US/10684109
Publication No. US20040175379A1
GENERAL INFORMATION:
APPLICANT: DeVries, Peter J.
APPLICANT: Green, Larry L.
APPLICANT: Ostrow, David H.
APPLICANT: Reilly, Edward B.
APPLICANT: Weller, James
TITLE OF INVENTION: Erythropoietin Receptor Binding
TITLE OF INVENTION: Antibodies
FILE REFERENCE: 6989.US.02
CURRENT APPLICATION NUMBER: US/10/684,109

; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 10/269,711
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatSeq for Windows Version 4.0
; SEQ ID NO 59
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-109-59

Query Match 93.2%; Score 82; DB 16; Length 41;
Best Local Similarity 88.2%; Pred. No. 1.8e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 11 VISYDGNKYYADSVKG 27

RESULT 31
US-10-078-958-7
; Sequence 7, Application US/10078958
; Publication No. US20030070185A1
; GENERAL INFORMATION:
; APPLICANT: JAKOBOVITS, AVA
; APPLICANT: KUCHERLAPATI, RAJU
; APPLICANT: KLAPHOLZ, SUSAN
; APPLICANT: MENDEL, MICHAEL J.
; APPLICANT: GREEN, LARRY
; TITLE OF INVENTION: TRANSGENIC MAMMALS HAVING HUMAN Ig LOCI INCLUDING
; TITLE OF INVENTION: PLURAL VH AND VK REGIONS AND ANTIBODIES PRODUCED
; TITLE OF INVENTION: THEREFROM
; FILE REFERENCE: CELL 4.18 CON
; CURRENT APPLICATION NUMBER: US/10/078,958
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 08/759,620
; PRIOR FILING DATE: 1996-12-03
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 83
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD.RES
; LOCATION: (22)
; OTHER INFORMATION: Variable amino acid
US-10-078-958-7

Query Match 93.2%; Score 82; DB 14; Length 83;
Best Local Similarity 88.2%; Pred. No. 3.7e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 35 VISYDGNKYYADSVKG 51

RESULT 32
US-10-884-830-653
; Sequence 653, Application US/10884830
; Publication No. US20050004354A1
; GENERAL INFORMATION:
; APPLICANT: Jochen, Salfeld et al.
; TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
; FILE REFERENCE: BEI-093CP
; CURRENT APPLICATION NUMBER: US/10/884,830
; CURRENT FILING DATE: 2004-07-01
; PRIOR APPLICATION NUMBER: US/09/534,717
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/126,603
; PRIOR FILING DATE: March 25, 1999

; NUMBER OF SEQ ID NOS: 675
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 653
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-884-830-653

Query Match 93.2%; Score 82; DB 16; Length 95;
Best Local Similarity 88.2%; Pred. No. 4.2e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGNKYYADSVKG 66

RESULT 33
US-09-948-939-15
; Sequence 15, Application US/09948939
; Publication No. US20020086014A1
; GENERAL INFORMATION:
; APPLICANT: Korman, Alan J.
; APPLICANT: Haik, Edward L.
; APPLICANT: Lomborg, Nils
; APPLICANT: Medarex, Inc.
; TITLE OF INVENTION: Human CTLA-4 Antibodies and Their Uses
; FILE REFERENCE: 014643-010520US
; CURRENT APPLICATION NUMBER: US/09/948,939
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/150,452
; PRIOR FILING DATE: 1999-08-24
; PRIOR APPLICATION NUMBER: 09/644,668
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: heavy chain variable region predicted sequence for
US-09-948-939-15

Query Match 93.2%; Score 82; DB 9; Length 98;
Best Local Similarity 88.2%; Pred. No. 4.4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGNKYYADSVKG 66

RESULT 34
US-10-194-975-23
; Sequence 23, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-23

Query Match 93.2%; Score 82; DB 14; Length 98;
Best Local Similarity 88.2%; Pred. No. 4.4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 35
US-10-194-975-24
; Sequence 24, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-24

Query Match 93.2%; Score 82; DB 14; Length 98;
Best Local Similarity 88.2%; Pred. No. 4.4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 36
US-10-194-975-25
; Sequence 25, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-975-25

Query Match 93.2%; Score 82; DB 14; Length 98;
Best Local Similarity 88.2%; Pred. No. 4.4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 37
US-10-308-817-63
; Sequence 63, Application US/10308817
; Publication No. US20030219861A1
; GENERAL INFORMATION:

; APPLICANT: Rother, Russell
; APPLICANT: Wu, Dayang
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 1087-37
; CURRENT APPLICATION NUMBER: US/10/308,817
; CURRENT FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 98
; TYPE: PRT
; ORGANISM: human
US-10-308-817-63

Query Match 93.2%; Score 82; DB 15; Length 98;
Best Local Similarity 88.2%; Pred. No. 4.4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 38
US-10-308-817-64
; Sequence 64, Application US/10308817
; Publication No. US20030219861A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; APPLICANT: Wu, Dayang
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 1087-37
; CURRENT APPLICATION NUMBER: US/10/308,817
; CURRENT FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 98
; TYPE: PRT
; ORGANISM: human
US-10-308-817-64

Query Match 93.2%; Score 82; DB 15; Length 98;
Best Local Similarity 88.2%; Pred. No. 4.4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 39
US-10-308-817-65
; Sequence 65, Application US/10308817
; Publication No. US20030219861A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; APPLICANT: Wu, Dayang
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 1087-37
; CURRENT APPLICATION NUMBER: US/10/308,817
; CURRENT FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 65
; LENGTH: 98
; TYPE: PRT
; ORGANISM: human
US-10-308-817-65

Query Match 93.2%; Score 82; DB 15; Length 98;
Best Local Similarity 88.2%; Pred. No. 4.4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 40
US-10-032-037B-74
; Sequence 74, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 74
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-74

Query March 93.2%; Score 82; DB 15; Length 98;
Best Local Similarity 88.2%; Pred. No. 4.4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNKYYADSVKG 66

Search completed: March 31, 2005, 12:46:07
Job time : 96.0938 secs

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OM protein - protein search, using sw model

Run on: March 31, 2005, 11:51:19 ; Search time 24.1719 Seconds
(without alignments)
67.669 Million cell updates/sec

Title: US-10-614-959-11

Perfect score: 88

Sequence: 1 IISYDGSNKYYADSVKG 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	82	93.2	94	2	PL0120
2	82	93.2	97	2	S44115
3	82	93.2	98	2	PL0116
4	82	93.2	98	2	S29546
5	82	93.2	109	2	PH1646
6	82	93.2	109	2	PH1644
7	82	93.2	111	2	PH1643
8	82	93.2	111	2	PH1645
9	82	93.2	113	2	S38490
10	82	93.2	114	2	S46390
11	82	93.2	114	2	S46392
12	82	93.2	117	2	S36270
13	82	93.2	118	2	S31677
14	82	93.2	118	2	S31116
15	82	93.2	119	2	F36005
16	82	93.2	120	2	S31112
17	82	93.2	121	2	S19666
18	82	93.2	121	2	G36005
19	82	93.2	122	2	E36005
20	82	93.2	122	2	S31119
21	82	93.2	123	2	S38493
22	82	93.2	130	2	PL0098
23	82	93.2	132	2	S31603
24	82	93.2	134	2	S31679
25	82	93.2	139	2	S31674
26	82	93.2	137	2	S31701
27	82	93.2	137	2	PH1642
28	82	93.2	137	2	PH1642
29	82	93.2	137	2	PH1642

30	75	85.2	122	2	S31117	Ig heavy chain - h
31	75	85.2	128	2	S48797	Ig heavy chain v r
32	75	85.2	133	2	A49028	Ig heavy chain v-i
33	75	85.2	133	2	S31510	Ig heavy chain - h
34	75	85.2	133	2	S29543	Ig heavy chain v r
35	74	84.1	117	2	S36259	Ig heavy chain v r
36	74	84.1	118	2	PH1662	Ig heavy chain v-i
37	74	84.1	122	1	M3HUM	Ig heavy chain v-i
38	74	84.1	134	2	S31688	Ig heavy chain v r
39	74	84.1	135	2	S31598	Ig heavy chain v r
40	74	84.1	140	2	S70442	Ig heavy chain pre
41	73	83.0	151	2	A60943	Ig heavy chain pre
42	72	81.8	115	2	S36284	Ig heavy chain v r
43	72	81.8	121	2	PH1661	Ig heavy chain v r
44	71	80.7	118	2	PH1660	Ig heavy chain v r
45	69	78.4	76	2	S31592	Ig heavy chain v r

ALIGNMENTS

RESULT 1

PL0120
Ig heavy chain V-III region (TD-Vo) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004

C:Accession: PL0120

R:Bird, J.; Galili, N.; Link, M.; Stites, D.; Sklar, J.

J. Exp. Med. 168, 229-245, 1988

A:Title: Continuing rearrangement but absence of somatic hypermutation in immunoglobulin

A:Reference number: PL0116; PMID:88286083; PMID:2840480

A:Accession: PL0120

A:Molecule type: mRNA

A:Residues: 1-94 <BIR>

A:Cross-references: UNIPROT:Q8WTK1; UNIPROT:Q9UJ93

A:Experimental source: B cells from patient TD with acute lymphoblastic leukemia, ALL

A>Note: The sequence shows the V region (TD-Vo) from a nonproductive DNA rearrangement f

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: acute lymphoblastic leukemia; heterotetramer; immunoglobulin

F:31-35/Region: complementarity-determining 1

F:49-65/Region: complementarity-determining 2

Query Match 93.2%; Score 82; DB 2; Length 94;

Best Local Similarity 88.2%; Pred. No. 7.2e-06;

Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSNKYYADSVKG 17

Db 50 VISYDGSNKYYADSVKG 66

RESULT 2

S44115
Ig heavy chain V region - human

C:Species: Homo sapiens (man)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001

C:Accession: S44115

R:Howkins, R.E.; Zhu, D.; Owecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.

Submitted to the EMBL Data Library, March 1994

A:Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable r

A:Reference number: S44105

A:Accession: S44115

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-97 <HAM>

A:Cross-references: EMBL:Z31384; NID:G47269; PIDN:CAA83259.1; PID:G940526

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 93.2%; Score 82; DB 2; Length 97;

Best Local Similarity 88.2%; Pred. No. 7.5e-06;

Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 3
PL0116
Ig heavy chain V-III region (AM-Vx) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 23-Jul-1999
C/Accession: PL0116; S26892
R/Bird, J.; Gallili, N.; Link, M.; Stiles, D.; Sklar, J.
J. Exp. Med. 168, 229-245, 1988
A/Title: Continuing rearrangement but absence of somatic hypermutation in immunoglobulin A/Reference number: PL0116; MUID:88286083; PMID:2840480
A/Accession: PL0116
A/Molecule type: mRNA
A/Residues: 1-98 <BIR>
A/Experimental source: B cells from patient AM with acute lymphoblastic leukemia, ALL
A/Note: the sequence shows the V region (AM-Vx) from a nonproductive DNA rearrangement
R/Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A/Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V A/Reference number: S26885; MUID:93021117; PMID:1404388
A/Accession: S26892
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-98 <TOM>
A/Cross-references: EMBL:Z12349; NID:G32918; PIDN:CAA78219.1; PID:G32919
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: acute lymphoblastic leukemia; heterotetramer; immunoglobulin
F/15-98/Domain: immunoglobulin homology <IMM>
F/31-35/Region: complementarity-determining 1
F/49-65/Region: complementarity-determining 2

Query Match 93.2%; Score 82; DB 2; Length 98;
Best Local Similarity 88.2%; Pred. No. 7.5e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 4
S29546
Ig heavy chain V region (COS-8 / DF-46) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 07-Jan-1994 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
C/Accession: S29546; S26888
R/Tomlinson, M.; Walter, G.; Cook, G.P.; Winter, G.
submitted to the EMBL Data Library, October 1992
A/Reference number: S29543
A/Accession: S29546
A/Molecule type: DNA
A/Residues: 1-98 <TOM>
A/Cross-references: EMBL:Z17394; NID:G32843; PIDN:CAA78997.1; PID:G32844
A/Note: designated COS-8
R/Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A/Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V A/Reference number: S26885; MUID:93021117; PMID:1404388
A/Accession: S26888
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-98 <TOM>
A/Cross-references: EMBL:Z12346; NID:G32912; PIDN:CAA78216.1; PID:G32913
A/Note: designated DF-46
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 93.2%; Score 82; DB 2; Length 98;

Best Local Similarity 88.2%; Pred. No. 7.5e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 5
PH1646
Ig heavy chain V region (clone 6H12) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C/Accession: PH1646
R/Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A/Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphyloc A/Reference number: PH1642; MUID:93301610; PMID:8315388
A/Accession: PH1646
A/Molecule type: mRNA
A/Residues: 1-109 <HIL>
A/Cross-references: UNIPROT:Q8WUK1
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/7-90/Domain: immunoglobulin homology <IMM>

Query Match 93.2%; Score 82; DB 2; Length 109;
Best Local Similarity 88.2%; Pred. No. 8.4e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 42 VISYDGSNKYYADSVKG 58

RESULT 6
PH1644
Ig heavy chain V region (clone 5D11) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C/Accession: PH1644
R/Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A/Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphyloc A/Reference number: PH1642; MUID:93301610; PMID:8315388
A/Accession: PH1644
A/Molecule type: mRNA
A/Residues: 1-109 <HIL>
A/Cross-references: UNIPROT:Q9YU93
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/7-90/Domain: immunoglobulin homology <IMM>

Query Match 93.2%; Score 82; DB 2; Length 109;
Best Local Similarity 88.2%; Pred. No. 8.4e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 42 VISYDGSNKYYADSVKG 58

RESULT 7
PH1643
Ig heavy chain V region (clone 6H7) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C/Accession: PH1643
R/Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A/Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphyloc A/Reference number: PH1642; MUID:93301610; PMID:8315388
A/Accession: PH1643

A:Molecule type: mRNA
A:Residues: 1-111 <HIL>
A:Cross-references: UNIPROT:Q8WTK1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-90/Domain: immunoglobulin homology <IMM>

Query Match 93.2%; Score 82; DB 2; Length 111;
Best Local Similarity 88.2%; Pred. No. 8.6e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 42 VISYDGSNKYYADSVKG 58

RESULT 8

PH1645
Ig heavy chain V region (clone 6C8) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C:Accession: PH1645
R:Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylo
A:Reference number: PH1642; MUID:93301610; PMID:8315388
A:Accession: PH1645
A:Molecule type: mRNA
A:Residues: 1-111 <HIL>
A:Cross-references: UNIPROT:Q8WTK1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 93.2%; Score 82; DB 2; Length 111;
Best Local Similarity 88.2%; Pred. No. 8.6e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 42 VISYDGSNKYYADSVKG 58

RESULT 9

S38490
Ig heavy chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S38490
R:Markes, J.D.; Ouehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, S
submitted to the EMBL Data Library, June 1993
A:Description: Human antibody fragments specific for human blood group antigens from a F
A:Reference number: S38488
A:Accession: S38490
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-113 <MAR>
A:Cross-references: EMBL:Z23030, NID:g414027, PIN:CAA80565.1; PID:g414028
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 93.2%; Score 82; DB 2; Length 113;
Best Local Similarity 88.2%; Pred. No. 8.7e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 10
S46390

Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C:Accession: S46390
R:Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A:Title: In vitro assembly of repertoires of antibody chains on the surface of phage by
A:Reference number: S46390; MUID:94254092; PMID:8196048
A:Accession: S46390
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-114 <FIG>
A:Cross-references: EMBL:Z31686, NID:g509782, PIDN:CAA83491.1; PID:g1335143
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 93.2%; Score 82; DB 2; Length 114;
Best Local Similarity 88.2%; Pred. No. 8.8e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 11

S46392
Ig heavy chain V region (VH-28) - human
C:Species: Homo sapiens (man)
C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C:Accession: S46392
R:Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A:Title: In vitro assembly of repertoires of antibody chains on the surface of phage by
A:Reference number: S46390; MUID:94254092; PMID:8196048
A:Accession: S46392
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-114 <FIG>
A:Cross-references: EMBL:Z31688, NID:g499906, PIDN:CAA83493.1; PID:g1335145
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 93.2%; Score 82; DB 2; Length 114;
Best Local Similarity 88.2%; Pred. No. 8.8e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 12

S36270
Ig heavy chain V region (clone alpha-TNF-E1) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C:Accession: S36270
R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A:Title: Human anti-self antibodies with high specificity from phage display libraries.
A:Reference number: S36256; MUID:93176448; PMID:7679990
A:Accession: S36270
A:Status: Preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-117 <GRI>
A:Cross-references: EMBL:Z18839, NID:g33118, PIDN:CAA79291.1; PID:g939898
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 93.2%; Score 82; DB 2; Length 117;
Best Local Similarity 88.2%; Pred. No. 9e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 13
S31677
Ig heavy chain V region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S31677
R/CuSinker, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelie, C.
submitted to the EMBL Data Library, June 1992
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the
A/Reference number: S31585
A/Accession: S31677
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-118 <CU>
A/Cross-references: EMBL:Z14172; NID:G31009; PIDN:CA478541.1; PID:G31010
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

Query Match 93.2%; Score 82; DB 2; Length 118;
Best Local Similarity 88.2%; Pred. No. 9.1e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 14
S31116
Ig heavy chain - human
C/Species: Homo sapiens (man)
C/Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C/Accession: S31116
R/Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Eur. J. Immunol. 22, 247-251, 1992
A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complement
A/Reference number: S31104; MUID:92111633; PMID:1730252
A/Accession: S31116
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: mRNA
A/Residues: 1-118 <RAA>
A/Cross-references: UNIPROT:Q8WUK1; EMBL:X62966
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 93.2%; Score 82; DB 2; Length 118;
Best Local Similarity 88.2%; Pred. No. 9.1e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 15
F36005
Ig heavy chain V region (M49) - human
C/Species: Homo sapiens (man)
C/Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 09-Jul-2004
C/Accession: F36005
R/Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990

A/Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A/Reference number: A36005; MUID:90349571; PMID:2117273
A/Accession: F36005
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-119 <SCH>
A/Cross-references: UNIPROT:Q8WUK1; GB:M34026
C/Genetics:
A/Gene: GDB:IGH@; IGHDI1
A/Cross-references: GDB:118731; OMIM:146910
A/Map position: 14q32.33-14q32.33
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 93.2%; Score 82; DB 2; Length 119;
Best Local Similarity 88.2%; Pred. No. 9.2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 16
S31112
Ig heavy chain - human
C/Species: Homo sapiens (man)
C/Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C/Accession: S31112
R/Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Eur. J. Immunol. 22, 247-251, 1992
A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third compleme
A/Reference number: S31104; MUID:92111633; PMID:1730252
A/Accession: S31112
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: mRNA
A/Residues: 1-120 <RAA>
A/Cross-references: EMBL:X62961
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 93.2%; Score 82; DB 2; Length 120;
Best Local Similarity 88.2%; Pred. No. 9.3e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 17
S19666
Ig heavy chain V region (VH3DH4) - human
C/Species: Homo sapiens (man)
C/Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C/Accession: S19666
R/Marks, J.D.; Hoogenboom, H.R.; Bonmert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter,
J. Mol. Biol. 222, 581-597, 1991
A/Title: By-passing immunization. Human antibodies from V-gene libraries displayed on ph
A/Reference number: S19663; MUID:92085276; PMID:1748994
A/Accession: S19666
A/Molecule type: mRNA
A/Residues: 1-121 <MAR>
A/Cross-references: EMBL:X61646; NID:G37688; PIDN:CA43827.1; PID:G1335369
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 93.2%; Score 82; DB 2; Length 121;
Best Local Similarity 88.2%; Pred. No. 9.3e-06;

Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 18
G36005
Ig heavy chain V region (M74) - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 09-Jul-2004
C:Accession: G36005
R:Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A:Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A:Reference number: A36005; MUID:90349571; PMID:2117273
A:Accession: G36005
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-121 <SCH>
A:Cross-references: UNIPROT:Q8WUK1; GB:M34031
C:Genetics:
A:Gene: GDB:IGH@; IGHDI1
A:Cross-references: GDB:118731; OMTM:146910
A:Map position: 14q32.33-14q32.33
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 93.2%; Score 82; DB 2; Length 121;
Best Local Similarity 88.2%; Pred. No. 9.3e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 19
E36005
Ig heavy chain V region (M72) - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
C:Accession: E36005
R:Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A:Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A:Reference number: A36005; MUID:90349571; PMID:2117273
A:Accession: E36005
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-122 <SCH>
A:Cross-references: GB:M34030
C:Genetics:
A:Gene: GDB:IGH@; IGHDI1
A:Cross-references: GDB:118731; OMTM:146910
A:Map position: 14q32.33-14q32.33
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 93.2%; Score 82; DB 2; Length 122;
Best Local Similarity 88.2%; Pred. No. 9.4e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 20
S31119

Ig heavy chain - human
C:Species: Homo sapiens (man)
C:Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C:Accession: S31119
R:Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Eur. J. Immunol. 22, 247-251, 1992
A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complement
A:Reference number: S31104; MUID:92111633; PMID:1730252
A:Accession: S31119
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-122 <RA>
A:Cross-references: UNIPROT:Q8WUK1; EMBL:X62970
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 93.2%; Score 82; DB 2; Length 122;
Best Local Similarity 88.2%; Pred. No. 9.4e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 21
S38493
Ig heavy chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S38493
R:Matks, J.D.; Ouehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, S
submitted to the EMBL Data Library, June 1993
A:Description: Human antibody fragments specific for human blood group antigens from a p
A:Reference number: S38488
A:Accession: S38493
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-123 <MAR>
A:Cross-references: EMBL:Z23036; NID:9414033; PIDN:CA80571.1; PID:9414034
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 93.2%; Score 82; DB 2; Length 123;
Best Local Similarity 88.2%; Pred. No. 9.5e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 22
P10098
Ig heavy chain precursor V-III region (FL2-2) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C:Accession: P10098
R:Nickerson, K.G.; Berman, J.; Glickman, E.; Chessa, L.; Alt, F.W.
J. Exp. Med. 169, 1391-1403, 1989
A:Title: Early human IgH gene assembly in Epstein-Barr virus-transformed fetal B cell li
A:Reference number: P10098; MUID:89176893; PMID:2538551
A:Accession: P10098
A:Molecule type: DNA
A:Residues: 1-130 <NIC>
A:Cross-references: UNIPROT:Q8WUK1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:17-120/Product: Ig heavy chain V-III region FL2-2 #status predicted <MAT>

F:32-115/Domain: immunoglobulin homology <IMM>

Query Match 93.2%; Score 82; DB 2; Length 130;
Best Local Similarity 88.2%; Pred. No. 1e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 67 VISYDGSNKYYADSVKG 83

RESULT 23

S31603

Ig heavy chain V region - human

C/Species: Homo sapiens (man)

C/Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C/Accession: S31603

R/Chislier: A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.

A/Description: Mechanisms that generate human immunoglobulin diversity operate from the

A/Reference number: S31585

A/Accession: S31603

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-132 <CUI>

A/Cross-references: EMBL:Z14168; NID:G30999; PIDN:CA78537.1; PID:G31000

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F:30-113/Domain: immunoglobulin homology <IMM>

Query Match 93.2%; Score 82; DB 2; Length 132;
Best Local Similarity 88.2%; Pred. No. 1e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 65 VISYDGSNKYYADSVKG 81

RESULT 24

S31679

Ig heavy chain V region - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C/Accession: S31679

R/Chislier: A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.

A/Description: Mechanisms that generate human immunoglobulin diversity operate from the

A/Reference number: S31585

A/Accession: S31679

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-134 <CUI>

A/Cross-references: EMBL:Z14203; NID:G30965; PIDN:CA78572.1; PID:G30966

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 93.2%; Score 82; DB 2; Length 134;
Best Local Similarity 88.2%; Pred. No. 1e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 69 VISYDGSNKYYADSVKG 85

RESULT 25

S31674

Ig heavy chain V region - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C/Accession: S31674

R/Chislier: A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.

A/Description: Mechanisms that generate human immunoglobulin diversity operate from the

A/Reference number: S31585

A/Accession: S31674

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-139 <CUI>

A/Cross-references: EMBL:Z14204; NID:G30967; PIDN:CA78573.1; PID:G30968

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 93.2%; Score 82; DB 2; Length 139;
Best Local Similarity 88.2%; Pred. No. 1.1e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 69 VISYDGSNKYYADSVKG 85

RESULT 26

S31701

Ig heavy chain V region - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C/Accession: S31701

R/Chislier: A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.

A/Description: Mechanisms that generate human immunoglobulin diversity operate from the

A/Reference number: S31585

A/Accession: S31701

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-137 <CUI>

A/Cross-references: EMBL:Z14177; NID:G31020; PIDN:CA78546.1; PID:G31021

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 87.5%; Score 77; DB 2; Length 137;
Best Local Similarity 82.4%; Pred. No. 6.5e-05;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 69 VISYDGSNKYYADSVKG 85

RESULT 27

PH1642

Ig heavy chain V region (clone 5A10) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004

C/Accession: PH1642

R/Hillson, J.L.; Karr, N.S.; Oppiger, I.R.; Mannik, M.; Sasseo, E.H.

J. Exp. Med. 178, 331-336, 1993

A/Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphyloc

A/Reference number: PH1642; MUID:93301610; PMID:8315388

A/Accession: PH1642

A/Molecule type: mRNA

A/Residues: 1-108 <HIL>

A/Cross-references: UNIPROT:Q8WUK1

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 85.2%; Score 75; DB 2; Length 108;
Best Local Similarity 82.4%; Pred. No. 0.00011;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17

Db 42 VIWYDGSNKYYADSVKG 58

RESULT 28

S46391
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C:Accession: S46391
R:Fitgin, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A:Title: In vitro assembly of repertoires of antibody chains on the surface of phage by
A:Reference number: S46390; MUID:94254092; PMID:8196048
A:Accession: S46391
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-114 <FIG>
A:Cross-references: EMBL:Z31687; NID:G509784; PIDN:CA83492.1; PID:G1335144
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 85.2%; Score 75; DB 2; Length 114;
Best Local Similarity 82.4%; Pred. No. 0.00011;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 IISYDGSKKYYADSVKG 17
: ||||| |||||
Db 50 VIWYDGSNKYYADSVKG 66

RESULT 29

S31111
Ig heavy chain - human
C:Species: Homo sapiens (man)
C:Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C:Accession: S31111
R:Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurmat
Eur. J. Immunol. 22, 247-251, 1992
A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complement
A:Reference number: S31104; MUID:92111633; PMID:1730252
A:Accession: S31111
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-119 <RAA>
A:Cross-references: EMBL:X62959
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 85.2%; Score 75; DB 2; Length 119;
Best Local Similarity 82.4%; Pred. No. 0.00012;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 IISYDGSKKYYADSVKG 17
: ||||| |||||
Db 50 VIWYDGSNKYYADSVKG 66

RESULT 30

S31117
Ig heavy chain - human
C:Species: Homo sapiens (man)
C:Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C:Accession: S31117
R:Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurmat
Eur. J. Immunol. 22, 247-251, 1992
A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complement
A:Reference number: S31104; MUID:92111633; PMID:1730252
A:Accession: S31117
A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: mRNA
A:Residues: 1-122 <RAA>
A:Cross-references: EMBL:X62967
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 85.2%; Score 75; DB 2; Length 122;
Best Local Similarity 82.4%; Pred. No. 0.00012;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 IISYDGSKKYYADSVKG 17
: ||||| |||||
Db 50 VIWYDGSNKYYADSVKG 66

RESULT 31

S48797
Ig heavy chain V region (anti-Sm, VH3/Dxp4/JH6) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Sep-1998 #text_change 23-Jul-1999
C:Accession: S48797; S26893
R:Mamoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data Library, October 1994
A:Description: Molecular characterization of natural human anti-Sm autoantibodies.
A:Reference number: S48797
A:Accession: S48797
A:Molecule type: mRNA
A:Residues: 1-128 <MAH>
A:Cross-references: EMBL:Z46379; NID:G587147; PIDN:CA86512.1; PID:G1340168
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline VH sequences reveals about fifty groups of V
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26893
A:Molecule type: DNA
A:Residues: 1-98 <TOM>
A:Cross-references: EMBL:Z12350; NID:G32922; PIDN:CA87820.1; PID:G32923
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 85.2%; Score 75; DB 2; Length 128;
Best Local Similarity 82.4%; Pred. No. 0.00013;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 IISYDGSKKYYADSVKG 17
: ||||| |||||
Db 50 VIWYDGSNKYYADSVKG 66

RESULT 32

A49028
Ig heavy chain V-II region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C:Accession: A49028
R:Timmers, E.; Kenter, M.; Thompson, A.; Kraakman, M.E.; Berman, J.E.; Alt, F.W.; Schuurmat
Eur. J. Immunol. 21, 2355-2363, 1991
A:Title: Diversity of immunoglobulin heavy chain gene segment rearrangement in B lymphob
A:Reference number: A49028; MUID:92008140; PMID:1915549
A:Accession: A49028
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-133 <TIM>
A:Cross-references: GB:564471; NID:G236904; PIDN:AA820011.1; PID:G236905
A:Experimental source: X-linked agammaglobulinemia patients; B lymphoblastoid cell lines
A>Note: sequence extracted from NCBI backbone (NCBI:64471, NCBI:64470)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 85.2%; Score 75; DB 2; Length 133;
Best Local Similarity 82.4%; Pred. No. 0.00013;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Db 50 IISYDGSKKYVADSVKG 66

RESULT 33
Ig heavy chain - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C:Accession: S31510
R:Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
submitted to the EMBL Data Library, December 1992
A:Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto
A:Reference number: S31509
A:Accession: S31510
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-133 <CH>
A:Cross-references: EMBL:X69865; NID:G33092; PIDN:CAA9499.1; PID:G33093
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 85.2%; Score 75; DB 2; Length 133;
Best Local Similarity 87.5%; Pred. No. 0.00013;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Db 62 IISYDGSNEKYVADSVKG 77

RESULT 34
Ig heavy chain V region (COS 3) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-Jan-1994 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
C:Accession: S29543
R:Tomlinson, M.; Walter, G.; Cook, G.P.; Winter, G.
submitted to the EMBL Data Library, October 1992
A:Reference number: S29543
A:Accession: S29543
A:Molecule type: DNA
A:Residues: 1-98 <TOM>
A:Cross-references: EMBL:Z17389; NID:G32835; PIDN:CAA78994.1; PID:G32836
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 84.1%; Score 74; DB 2; Length 98;
Best Local Similarity 87.5%; Pred. No. 0.00014;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 51 IRYDGSNKYVADSVKG 66

RESULT 35
Ig heavy chain V region (clone alpha-TNF-A1) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C:Accession: S36259
R:Griffiths, A.D.; Malmqvist, M.; Marke, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A:Title: Human anti-self antibodies with high specificity from phage display libraries.
A:Reference number: S36256; MUID:93178448; PMID:7679990

A:Accession: S36259
A:Status: Preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-117 <GR1>
A:Cross-references: EMBL:Z18850; NID:G33123; PIDN:CAA79302.1; PID:G939902
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 84.1%; Score 74; DB 2; Length 117;
Best Local Similarity 87.5%; Pred. No. 0.00017;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 51 IRYDGSNKYVADSVKG 66

RESULT 36
Ig heavy chain V region (clone TS2) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C:Accession: PH1662
R:Hillson, J.L.; Karr, N.S.; Oppiger, I.R.; Mannik, M.; Saseo, E.H.
J. Exp. Med. 178, 331-336, 1993
A:Title: The structural basis of germ-line-encoded VH3 immunoglobulin binding to staphyloc
A:Reference number: PH1642; MUID:93301610; PMID:8315388
A:Accession: PH1662
A:Molecule type: mRNA
A:Residues: 1-118 <HIL>
A:Experimental source: B cell
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 84.1%; Score 74; DB 2; Length 118;
Best Local Similarity 76.5%; Pred. No. 0.00017;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Db 42 VISYDGSNEKYVADSVKG 58

RESULT 37
Ig heavy chain V-III region (Cam) - human (tentative sequence)
C:Species: Homo sapiens (man)
C:Date: 31-Aug-1980 #sequence_revision 23-Oct-1981 #text_change 09-Jul-2004
C:Accession: A02051
R:Lehman, D.W.; Putnam, F.W.
Proc. Natl. Acad. Sci. U.S.A. 77, 3239-3243, 1980
A:Title: Amino acid sequence of the variable region of a human mu chain: location of a pc
A:Reference number: A02051; MUID:81013859; PMID:6774332
A:Accession: A02051
A:Molecule type: protein
A:Residues: 1-122 <LEH>
A:Cross-references: UNIPROT:P01768
C:Comment: This mu chain was isolated from the plasma of a patient with macroglobulinemia;
C:Genetics:
A:Gene: GDB:IGHV@
A:Cross-references: GDB:128528; OMIM:147070
A:Map position: 14q32.33-14q32.33
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin; pyroglyutamic acid
F:15-98/Domain: immunoglobulin homology <IMM>
F:1/Modified site: pyridone carboxylic acid (Gln) #status experimental
F:22-96/Disulfide bonds: #status predicted

Query Match 84.1%; Score 74; DB 1; Length 122;
Best Local Similarity 70.6%; Pred. No. 0.00017;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYGBBKYYABSVKG 66

RESULT 38

S31598
Ig heavy chain V region - human
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S31598
R/Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the
A/Reference number: S31585
A/Accession: S31598
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-134 <CUI>
A/Cross-references: EMBL:Z14174; NID:G31013; PIDN:CAA78543.1; PID:G31014
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/31-114/Domain: immunoglobulin homology <IMM>

Query Match 84.1%; Score 74; DB 2; Length 134;
Best Local Similarity 87.5%; Pred. No. 0.00019;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISYDGSKKYYADSVKG 17
:|||||
Db 67 IRYDGSNRYADSVKG 82

RESULT 39

S31598
Ig heavy chain V region - human
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S31598
R/Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the
A/Reference number: S31585
A/Accession: S31598
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-135 <CUI>
A/Cross-references: EMBL:Z14170; NID:G31001; PIDN:CAA78539.1; PID:G31002
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/31-114/Domain: immunoglobulin homology <IMM>

Query Match 84.1%; Score 74; DB 2; Length 135;
Best Local Similarity 87.5%; Pred. No. 0.00019;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISYDGSKKYYADSVKG 17
:|||||
Db 67 IRYDGSNRYADSVKG 82

RESULT 40

S70442
Ig heavy chain precursor V region (mu) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C/Accession: S70442
R/Cuisinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelle, C.
Mol. Immunol. 29, 1363-1373, 1992
A/Title: Igm kappa/lambda EBV human B cell clone: an early step of differentiation of fe
A/Reference number: S70442; MUID:93024508; PMID:1383695
A/Accession: S70442

A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-140 <CUI>
A/Cross-references: UNIPROT:Q8WUK1
C/Superfamily: immunoglobulin V region; immunoglobulin homology
F/34-117/Domain: immunoglobulin homology <IMM>

Query Match 84.1%; Score 74; DB 2; Length 140;
Best Local Similarity 87.5%; Pred. No. 0.0002;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ISYDGSKKYYADSVKG 17
:|||||
Db 70 IRYDGSNRYADSVKG 85

Search completed: March 31, 2005, 12:11:13
Job time : 24.1719 secs

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OM protein - protein search, using sw model

Run on: March 31, 2005, 11:42:54 ; Search time 112.891 Seconds
(without alignments)
77.113 Million cell updates/sec

Title: US-10-614-959-11
Perfect score: 88
Sequence: 1 IISYDGSKKYYADSVKG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	82	93.2	116	2 Q9UL93	Q9UL93 homo sapien
2	82	93.2	240	2 Q65ZC9	Q65ZC9 homo sapien
3	82	93.2	613	2 Q8WUK1	Q8WUK1 homo sapien
4	74	84.1	113	2 Q9UL90	Q9UL90 homo sapien
5	74	84.1	122	1 HV3G_HUMAN	P01768 homo sapien
6	71	80.7	417	2 Q6N093	Q6N093 homo sapien
7	70	79.5	493	2 Q68CN4	Q68CN4 homo sapien
8	69	78.4	147	2 Q9Y509	Q9Y509 homo sapien
9	67	76.1	482	2 Q7Z351	Q7Z351 homo sapien
10	67	76.1	493	2 Q8KCL6	Q8KCL6 homo sapien
11	66	75.0	122	2 Q9UL84	Q9UL84 homo sapien
12	65	73.9	119	1 HV3L_HUMAN	P01773 homo sapien
13	64	72.7	95	2 Q9ULB6	Q9ULB6 homo sapien
14	64	72.7	122	1 HV3H_HUMAN	P01769 homo sapien
15	64	72.7	470	2 Q6RJA4	Q6RJA4 homo sapien
16	64	72.7	478	2 Q6P181	Q6P181 homo sapien
17	63	71.6	119	1 HV3I_HUMAN	P01770 homo sapien
18	63	71.6	614	2 Q6DDQ7	Q6DDQ7 xenopus lae
19	62	70.5	121	1 HV3J_HUMAN	P01771 homo sapien
20	62	70.5	519	2 Q6N092	Q6N092 homo sapien
21	61	69.3	121	2 Q9UL71	Q9UL71 homo sapien
22	61	69.3	544	2 Q6RJ95	Q6RJ95 homo sapien
23	60	68.2	118	2 Q9UL72	Q9UL72 homo sapien
24	56	63.6	116	1 HV05_CARAU	Q9UL81 carassius a
25	56	63.6	126	1 HV3K_HUMAN	P01772 homo sapien
26	55	62.5	593	2 Q6INM5	Q6INM5 xenopus lae
27	55	62.5	481	2 Q6N097	Q6N097 homo sapien
28	53	60.2	464	2 Q6MZU6	Q6MZU6 homo sapien
29	53	60.2	597	2 Q96BB9	Q96BB9 homo sapien
30	52.5	57.7	122	1 HV3A_HUMAN	P01762 homo sapien
31	52	59.1	115	1 HV3F_HUMAN	P01767 homo sapien

32	52	59.1	466	2 Q6IN78	Q6IN78 homo sapien
33	52	59.1	475	2 Q6MZ06	Q6MZ06 homo sapien
34	52	59.1	493	2 Q6GMX2	Q6GMX2 homo sapien
35	50	56.8	114	1 HV3B_HUMAN	P01763 homo sapien
36	50	56.8	119	2 Q920E7	Q920E7 mus musculi
37	50	56.8	196	2 Q65ZL8	Q65ZL8 mus musculi
38	50	56.8	585	2 Q6GPK4	Q6GPK4 xenopus lae
39	49	55.7	71	2 Q9GJ71	Q9GJ71 salmo trutt
40	49	55.7	87	2 Q9AV03	Q9AV03 oryza sativ
41	49	55.7	98	1 HV57_MOUSE	P18528 mus musculi
42	49	55.7	117	1 HV3C_HUMAN	P01764 homo sapien
43	49	55.7	480	2 Q6N094	Q6N094 homo sapien
44	49	55.7	1048	1 YC81_METTA	Q58677 methanococc
45	48.5	55.1	247	2 Q9VZF9	Q9VZF9 drosophila

ALIGNMENTS

```

RESULT 1
Q9UL93      PRELIMINARY;      PRT;      116 AA.
ID   Q9UL93
AC   Q9UL93;
DT   01-MAY-2000 (TREMBLrel. 13, Created)
DT   01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE   01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE   Myosin-reactive immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX   NCBI_TaxId=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.N.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035021; RAD56257.1; -.
DR   PIR; P01644; P01644.
DR   HSSP; P01772; 2PB4.
DR   InterPro; IPR007110; IG-like.
DR   InterPro; IPR003596; IG_v.
DR   SMART; SM00406; IGV; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER
FT   NON_TER
SQ   SEQUENCE 116 AA; 12434 MW; 0DA0348154D6061 CRC64;

Query Match      93.2%; Score 82; DB 2; Length 116;
Best Local Similarity 88.2%; Pred. No. 1e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 IISYDGSKKYYADSVKG 17
Db      49 VISYDGSNKKYYADSVKG 65

RESULT 2
Q65ZC9      PRELIMINARY;      PRT;      240 AA.
ID   Q65ZC9
AC   Q65ZC9;
DT   25-OCT-2004 (TREMBLrel. 28, Created)
DT   25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE   Single-chain Fv (Fragment).
GN   Name=scFv;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

```

```
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C1q/7;
RX MEDLINE=97362799; PubMed=9219263;
RA Kontermann R.E., Wing M.G., Winter G.;
RT "Complement recruitment using bispecific diabodies.";
RL Nat. Biotechnol. 15:629-631(1997).
DR EMBL, Y13056; CAA73499.1; -.
DR InterPro; IPR003599; IG_v.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00409; IGv_2.
DR SMART; SM00406; IGv_2.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 240 AA; 25569 MW; FDCFD645F64B373 CRC64;

Query Match 93.2%; Score 82; DB 2; Length 240;
Best Local Similarity 88.2%; Pred. No. 2.3e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Cy 1 IISYDGSKKYYADSVKG 17
Db 50 VISYDGSNKYYADSVKG 66

RESULT 3
Q8WUK1 PRELIMINARY; PRT; 613 AA.
ID Q8WUK1
AC Q8WUK1;
DT 01-MAR-2002 (TrEMBLrel. 20; Created)
DT 01-MAR-2002 (TrEMBLrel. 20; Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26; Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Martuna K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodchenko V., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko V., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
RA Jones S.J., Mair M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC020240; AAH20240.1; -.
DR PIR; P36005; P36005.
DR PIR; G36005; G36005.
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DR PIR; PH1642; PH1642.
DR PIR; PH1643; PH1643.
DR PIR; PH1645; PH1645.
DR PIR; PH1646; PH1646.
DR PIR; P10098; P10098.
DR PIR; P10120; P10120.
DR PIR; P10120; P10120.
DR PIR; S15590; S15590.
DR PIR; S31116; S31116.
DR PIR; S31119; S31119.
DR PIR; S70442; S70442.
DR HSSP; P01861; IADO.
DR Pfam; PF07654; C1-set; 4.
DR SMART; SM00406; IGv_1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
SQ SEQUENCE 613 AA; 67295 MW; 60C7F5950671E315 CRC64;

Query Match 93.2%; Score 82; DB 2; Length 613;
Best Local Similarity 88.2%; Pred. No. 6.4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Cy 1 IISYDGSKKYYADSVKG 17
Db 69 VISYDGSNKYYADSVKG 85

RESULT 4
Q9UL90 PRELIMINARY; PRT; 113 AA.
ID Q9UL90
AC Q9UL90;
DT 01-MAY-2000 (TrEMBLrel. 13; Created)
DT 01-MAY-2000 (TrEMBLrel. 13; Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26; Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/cjln.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetuses.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035024; AAD56260.1; -.
DR PIR; S78486; S78486.
DR HSSP; P01772; ZFB4.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGv_1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 113 AA; 12437 MW; ED57PDD19086D07F CRC64;

Query Match 84.1%; Score 74; DB 2; Length 113;
Best Local Similarity 87.5%; Pred. No. 0.00022;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy 2 IISYDGSKKYYADSVKG 17
Db 51 IRYDGSNKYYADSVKG 66

RESULT 5
HV3G HUMAN STANDARD; PRT; 122 AA.
ID HV3G HUMAN
AC P01768;
DT 21-JUL-1986 (Rel. 01; Created)
DT 21-JUL-1986 (Rel. 01; Last sequence update)
```


DR	PROSITE; PS50835; IG LIKE; 3.
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KM	Hypothetical protein.
FT	NON_TER 1
SQ	SEQUENCE 417 AA; 46061 MW; C451E844CFB83C CRC64;
Query Match	
Best Local Similarity 70.6%; Score 71; DB 2; Length 417;	
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;	
Oy	1 IISYDGSKKYYADSVKG 17 ::: ::: :
Dd	22 VIADSGSTOYYADSVRG 38
RESULT 7	
ID	068CM4 PRELIMINARY; PRT; 493 AA.
AC	068CM4;
DT	25-OCT-2004 (TrEMBLrel. 28, Created)
DT	25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT	25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE	Hypothetical protein DKFZp686E23209 (Fragment).
CN	Name=DKFZp686E23209;
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX	NCBI_Taxid=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Rectum tumor;
RG	The German cDNA Consortium;
RA	Bloecher H., Boescher M., Brandt P., Mewes H.W., Weil B., Amid C.,
RA	Osaenger A., Fobo G., Han M., Wiemann S.;
RL	Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR	EMBL; CR499661; CAH18705.1; -.
DR	InterPro; IPRO03599; IG.
DR	InterPro; IPRO07110; IG-like.
DR	InterPro; IPRO03597; IG-cl.
DR	InterPro; IPRO03006; IG_MHC.
DR	InterPro; IPRO03596; IG v.
DR	Pfam; PF07654; Cl-set; 3.
DR	Pfam; PF00047; Ig; 4.
DR	SMART; SM00409; IG; 2.
DR	SMART; SM00407; IGC1; 3.
DR	SMART; SM00406; IGV; 1.
DR	PROSITE; PSS0835; IG LIKE; 4.
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW	Hypothetical protein.
FT	NON_TER 1
SQ	SEQUENCE 493 AA; 54117 MW; A1FAF5ED3FA8AB40 CRC64;
Query Match	
Best Local Similarity 79.5%; Score 70; DB 2; Length 493;	
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;	
Oy	1 IISYDGSKKYYADSVKG 17 ::: ::: :
Dd	92 VISTEGGKOHYADSVKG 108
RESULT 8	
ID	09Y509 PRELIMINARY; PRT; 147 AA.
AC	09Y509;
DT	01-NOV-1999 (TrEMBLrel. 12, Created)
DT	01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	VH3 protein (Fragment).
CN	Name=VH3;
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96071149; PubMed=7475288;
RA Cao J., Vescio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,
R Lichtenstein A.K., Berenson J.R.;
RT "A CD10-positive population of malignant cells is identified in multiple
myeloma using PCR with patient-specific immunoglobulin gene primers";
RL Leukemia 9:1548-1553(1995).
DR EMBL; S80860; AAD14339.1; -.
DR HSSP; P01842; 1AOK.
DR GO; GO:0005887; C:Integral to plasma membrane; NAS.
DR GO; GO:0016066; P:cellular defense response (sensu Vertebrata); NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 147 147
SQ SEQUENCE 147 AA; 15768 MW; 8489FCAA7BC925C CRC64;

Query Match 76.4%; Score 69; DB 2; Length 147;
Best Local Similarity 76.5%; Pred. No. 0.002;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 1 IISYDGSKKYVADSVKG 17
Db 50 LIYDGSSTQYVAGSVKG 66

RESULT 9

Q72351 PRELIMINARY; PRT; 482 AA.
ID Q72351
AC Q72351
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Hypothetical protein DKFZp686N02209.
GN Name=DKFZp686N02209;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RA Bloecher H., Boecher W., Nemes H.W., Weil B., Amid C., Oeanger A.,
RA Pobo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX538118; CAD98026.1; -.
DR HSSP; P01857; 1H2H.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 482 AA; 52852 MW; EDA75F1901D1A034 CRC64;

Query Match 76.1%; Score 67; DB 2; Length 482;
Best Local Similarity 70.6%; Pred. No. 0.016;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 1 IISYDGSKKYVADSVKG 17
Db 69 VIYDGNHKLXSDSVKG 85

RESULT 10
Q8NCL6 PRELIMINARY; PRT; 493 AA.

AC Q8NCL6;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Hypothetical protein FJ910170.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Isegai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hiro Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahara K.,
RA Masuko Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK074651; BAC1114.1; -.
DR HSSP; P01876; 1OW0.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 493 AA; 53224 MW; 12ECD7E094777101 CRC64;

Query Match 76.1%; Score 67; DB 2; Length 493;
Best Local Similarity 70.6%; Pred. No. 0.016;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 1 IISYDGSKKYVADSVKG 17
Db 69 LIWYDGRKTYSDSVKG 85

RESULT 11

Q9UL84 PRELIMINARY; PRT; 122 AA.
ID Q9UL84
AC Q9UL84
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DR (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetuses";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035030; AAD56266.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13579 MW; 36054D41366545B8 CRC64;

Query Match 75.0%; Score 66; DB 2; Length 122;
Best Local Similarity 81.2%; Pred. No. 0.0053;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 ISYDSSKKYVADSVKG 17
| | | | | : | | | | |
Db 51 ISNDGSKNFYADSVKG 66

RESULT 12

HV3L HUMAN STANDARD; PRT; 119 AA.

AC P01773; 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig heavy chain V-II region BUR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_Taxid=9606;

RP SEQUENCE (MYELOMA PROTEIN BUR).
RX MEDLINE=79151016; PubMed=107164;

RA Putnam F.W., Liu Y.-S.V., Low T.L.K.;
RT "Primary structure of a human IgM immunoglobulin. IV. Streptococcal
RT IgM1 protease, digestion, Fab and Fc fragments, and the complete amino
RT acid sequence of the alpha 1 heavy chain.";
RL J. Biol. Chem. 254:2865-2874(1979).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.

DR PIR; A02056; A1H0BR.
DR HSSP; P01772; 2FB4.

DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.

DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

KW Direct protein sequencing; Glycoprotein; Immunoglobulin V region;
KW Pyrolydione carboxylic acid. Ig-like.

FT DOMAIN 1 112
FT MOD_RES 1 1 Pyrolydione carboxylic acid.

FT DISULFID 22 96
FT CARBOHYD 28 28 N-linked (GlcNAc...).

FT NON_TER 119 119
SQ SEQUENCE 119 AA; 12981 MW; 12A709A75344D024 CRC64;

Query Match 73.9%; Score 65; DB 1; Length 119;
Best Local Similarity 70.6%; Pred. No. 0.0076;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 IISYDSSKKYVADSVKG 17
: | | | | | : | | | | |
Db 50 LISYGSBTVYADSVRG 66

RESULT 13

O9ULB6 PRELIMINARY; PRT; 95 AA.

AC O9ULB6; 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Immunoglobulin heavy chain (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_Taxid=9606;

RP SEQUENCE FROM N.A.
RA Tange Y., Kayano H.;

RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB035268; BAA87067.1; -.

DR PIR; PH0872; PH0872.

DR PIR; S36280; S36280.
DR HSSP; P01820; 1G7J.
DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1 1
FT NON_TER 95 95

SQ SEQUENCE 95 AA; 10527 MW; 90A8C6D16D2574A CRC64;

Query Match 72.7%; Score 64; DB 2; Length 95;
Best Local Similarity 75.0%; Pred. No. 0.0087;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 ISYDSSKKYVADSVKG 17
| | | | | : | | | | |
Db 50 IKDSEKTYVADSVKG 65

RESULT 14

HV3H HUMAN STANDARD; PRT; 122 AA.

AC P01769; 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Ig heavy chain V-II region GA.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

NCBI_Taxid=9606;

RP SEQUENCE.
RX MEDLINE=74175307; PubMed=4208843;

RA Florent G., Lehman D., Putnam F.W.;

RT "The switch point in mu heavy chains of human IgM immunoglobulins.";

RL Biochemistry 13:2482-2498(1974).

CC -1- MISCELLANEOUS: This chain was isolated from a Waldenstrom's
CC macroglobulin.

CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.

DR PIR; A02052; M3H0GA.

DR HSSP; P01772; 2FB4.

DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0003823; F:antigen binding; NAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

KW Direct protein sequencing; Immunoglobulin V region;
KW Pyrolydione carboxylic acid. Ig-like.

FT DOMAIN 1 112
FT MOD_RES 1 1 Pyrolydione carboxylic acid.

FT DISULFID 1 1
FT CARBOHYD 122 122
SQ SEQUENCE 122 AA; 13166 MW; 74E5B695E84100A CRC64;

Query Match 72.7%; Score 64; DB 1; Length 122;
Best Local Similarity 64.7%; Pred. No. 0.011;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 IISYDSSKKYVADSVKG 17
: | | | | | : | | | | |
Db 50 VISYGBBZYVADSVKG 66

RESULT 15

O6PJA4 PRELIMINARY; PRT; 470 AA.

AC O6PJA4; 05-JUL-2004 (TREMBlrel. 27, Created)

DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)

DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)

```

DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Dietchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stetpleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Maitra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strauberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018747; AAH18747.1; -
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; IG_1.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IG_C1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
DR Hypothetical protein.
SQ SEQUENCE 470 AA; 51715 MW; 7849556A11FD7D9 CRC64;

Query Match 72.7%; Score 64; DB 2; Length 470;
Best Local Similarity 75.0%; Pred. No. 0.05;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Cy 2 ISYDSSKKYVDSYKG 17
Db 70 IKQDSEKTYVDSYKG 85

RESULT 16
ID Q6P181 PRELIMINARY; PRT; 478 AA.
AC Q6P181;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

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RC TISSUE=Primary B-Cells;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Dietchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stetpleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Maitra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strauberg R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC041037; AAH41037.1; -
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; IG_1.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IG_C1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
DR Hypothetical protein.
SQ SEQUENCE 478 AA; 52666 MW; 17BED38D917970D6 CRC64;

Query Match 72.7%; Score 64; DB 2; Length 478;
Best Local Similarity 75.0%; Pred. No. 0.051;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Cy 2 ISYDSSKKYVDSYKG 17
Db 70 IKQDSEKTYVDSYKG 85

RESULT 17
ID HV31 HUMAN STANDARD; PRT; 119 AA.
AC P01770;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig heavy chain V-III region NIE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=77070269; PubMed=826475;
RA Ponsstingl H., Hilschmann N.;
RT "The rule of antibody structure. The primary structure of a monoclonal
RT IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic
RT peptides of the H-chain, alignment of the tryptic peptides and
RT discussion of the complete structure."
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).

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DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region;
KM Pyroliidone carboxylic acid.
FT DOMAIN 1 112 Ig-like.
FT MOD_RES 1 1 Pyroliidone carboxylic acid.
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13566 MW; 480FC53610EFSDB CRC64;

Query Match
Best Local Similarity 70.5%; Score 62; DB 1; Length 121;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
Db 50 VIVYNGSRTYYGDSVKG 66

RESULT 20
Q6N092 PRELIMINARY; PRT; 519 AA.
ID Q6N092;
AC Q6N092;
DT 05-JUL-2004 (TREMBlrel. 27, Last Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Hypothetical protein DKFZp686K18196 (Fragment).
GN Name=DKFZp686K18196;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human esophagus tumor;
RG The German Human cDNA Consortium;
RA Wandut R., Heubner D., Mewes H.W., Weil B., Amid C., Oesanger A.,
RA Fodo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640624; CAE45778.1; -.
DR HSSP; P01842; IAOK.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003597; IG_cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; CI-set; 2.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IGV; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
FT NON_TER 1 1
SQ SEQUENCE 519 AA; 56423 MW; F839EF7F911EB88D CRC64;

Query Match
Best Local Similarity 70.5%; Score 62; DB 2; Length 519;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 YDGSKKYYADSVKG 17
Db 96 FDGSNNYYADSVKG 109

RESULT 21
Q9UL71 PRELIMINARY; PRT; 121 AA.
ID Q9UL71;
AC Q9UL71;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
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DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035043; AAD56279.1; -.
DR HSSP; P01852; INFJ.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1 1
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13154 MW; 2F045CFAD50736 CRC64;

Query Match
Best Local Similarity 69.3%; Score 61; DB 2; Length 121;
Matches 12; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
Db 50 LISGDGSGTYYADSVKG 66

RESULT 22
Q6P395 PRELIMINARY; PRT; 544 AA.
ID Q6P395;
AC Q6P395;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Hopkins S.F., Zeeberg K.H., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hochkin R.F., Jordan B., Moore T., Max S.I., Wang J., Hsieh F.,
RA Dietchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshtyuk S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McGwan P.J., McKernan K.J., Malek J.A., Gunarene P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulys S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman W., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Maitra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
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RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019046; AAH19046.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; C1-sec; 3.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; Ig_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KM Hypothetical protein.
SQ SEQUENCE 544 AA; 60102 MW; 1895814B2297C668 CRC64;

Query Match 69.3%; Score 61; DB 2; Length 544;
Best Local Similarity 70.6%; Pred. No. 0.19;
Matches 12; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 IISYDSKKYVADSVKG 17
Db 69 VFSYDSDDKYVAAVKG 85

RESULT 23
Q9UL72 PRELIMINARY; PRT; 118 AA.
ID Q9UL72;
AC Q9UL72;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
OX [1]
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Bernex S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035042; AAD56278.1; -.
DR PIR; S21205; S21205.
DR HSSP; P01783; IIGC.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003596; Ig_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 118 AA; 12872 MW; BAD1A5944B2D5CCA CRC64;

Query Match 68.2%; Score 60; DB 2; Length 118;
Best Local Similarity 62.5%; Pred. No. 0.051;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 IISYDSKKYVADSVKG 17
Db 50 VTYSGGSSYVADSVKG 65

RESULT 24
HV05 CARAU STANDARD; PRT; 116 AA.
ID HV05 CARAU
AC P19181;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)

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DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 5A precursor.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88144476; PubMed=3125551;
RA Wilson M.R., Middleton D., Warr G.W.;
RT "Immunoglobulin heavy chain variable region gene evolution: structure
RT and family relationships of two genes and a pseudogene in a teleost
RT fish.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:1566-1570(1988).
DR HSSP; P01783; IIGC.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KM Immunoglobulin V region; Signal.
SQ SEQUENCE 116 AA; 12808 MW; 9C2279E2DF199B12 CRC64;

Query Match 63.6%; Score 56; DB 1; Length 116;
Best Local Similarity 62.5%; Pred. No. 0.24;
Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 IISYDSKKYVADSVKG 17
Db 69 VTYSGGSSYVADSVKG 84

RESULT 25
HV3K HUMAN STANDARD; PRT; 126 AA.
ID HV3K HUMAN
AC P01772;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig heavy chain V-III region KOL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
OX [1]
RN [1]
RP SEQUENCE AND DISULFIDE BONDS.
RX MEDLINE=83289131; PubMed=6884994;
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT "Three-dimensional structure determination of antibodies. Primary
RT structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=81072295; PubMed=7441755;
RA Marquart M., Deisenhofer J., Huber R., Palm W.;
RT "Crystallographic refinement and atomic models of the intact
RT immunoglobulin molecule KOL and its antigen-binding fragment at 3.0 A
RT and 1.0-A resolution.";
RL J. Mol. Biol. 141:369-391(1980).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02055; G1HOKL.
DR PDB; 2FB4; X-ray; H=1-126.
DR PDB; 2IG2; X-ray; H=-.

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DR GO: 0005576; C:extracellular; NAS.
DR GO: 0003823; P:antigen binding; NAS.
DR GO: 0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW 3D-structure; Direct protein sequencing; Immunoglobulin V region;
KW Pyroglutamate carboxylic acid.
FT DOMAIN 1 112 Ig-like.
FT MOD_RES 1 112 Pyroglutamate carboxylic acid.
FT DISULFID 22 96
FT STRAND 105 110
FT STRAND 3 7
FT STRAND 11 12
FT STRAND 14 15
FT STRAND 18 25
FT STRAND 29 31
FT STRAND 34 39
FT STRAND 41 42
FT STRAND 45 51
FT STRAND 53 54
FT STRAND 58 60
FT STRAND 62 64
FT STRAND 65 65
FT STRAND 66 67
FT STRAND 68 73
FT STRAND 74 77
FT STRAND 78 83
FT STRAND 88 90
FT STRAND 92 99
FT STRAND 106 106
FT STRAND 107 108
FT STRAND 109 109
FT STRAND 113 116
FT STRAND 120 124
FT NON_TER 126 126
SQ SEQUENCE 126 AA; 13718 MW; EAD71B52B16F8776 CRC64;

Query Match 63.6%; Score 56; DB 1; Length 126;
Best Local Similarity 70.6%; Pred. No. 0.26;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
Db 50 IIMDDGSDQHYADSVKG 66

RESULT 26
Q6INM5 PRELIMINARY; PRT; 593 AA.
ID Q6INM5;
AC Q6INM5;
DT 05-JUL-2004 (TREMblrel. 27, Created)
DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)
DE MG659066 protein.
GN Name=MG659066;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stepieton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

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RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loguigliano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Myers R.M., Buterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smallos D.E., Schermer A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RL [2]
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative."
RT Dev. Dyn. 225:384-391(2002).
RL [3]
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Klein S., Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC072253; AAH72253.1; -.
DR HSSP; P01842; IAOK.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003597; Ig_c1.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR InterPro: IPR001680; WD40.
DR Pfam; PF07654; C1-set; 4.
DR SMART; SM00409; Ig; 4.
DR SMART; SM00407; IgC1; 4.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 4.
DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN 1.
SQ SEQUENCE 593 AA; 65874 MW; BB314FF921E12FC CRC64;

Query Match 63.6%; Score 56; DB 2; Length 593;
Best Local Similarity 68.8%; Pred. No. 1.4;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 ISYDGSKKYYADSVKG 17
Db 68 INPDGSGTYADSVKG 83

RESULT 27
Q6N097 PRELIMINARY; PRT; 481 AA.
ID Q6N097;
AC Q6N097;
DT 05-JUL-2004 (TREMblrel. 27, Created)
DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMblrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686H20196.
GN Name=DKFZp686H20196;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human esophagus tumor;
RG The German Human cDNA Consortium;
RA Wandut R., Heubner D., Mewes H.W., Weill B., Amid C., Oanger A.,
RA Fodor G., Han W., Wiemann S.;

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RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640619; CA645773.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KM Hypothetical protein.
SQ SEQUENCE 481 AA; 52759 MW; 4722009E64BDF988 CRC64;

Query Match 62.5%; Score 55; DB 2; Length 481;
Best Local Similarity 68.8%; Pred. No. 1.6;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 ISYDGSKKYYADSVKG 17
Db 70 ISFGSGSKYYARSVKG 85

RESULT 28
ID Q6MB9 PRELIMINARY; PRT; 464 AA.
AC Q6MB9;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686C15213.
GN Name=DKFZp686C15213;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RA Bloecher H., Boecher M., Mewes H.W., Weill B., Amid C., Oeanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640874; CA645931.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KM Hypothetical protein.
SQ SEQUENCE 464 AA; 51099 MW; 2FCA72C66E8A0ABC CRC64;

Query Match 60.2%; Score 53; DB 2; Length 464;
Best Local Similarity 73.3%; Pred. No. 3.4;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 SYDGSKKYYADSVKG 17
Db 72 SRGSGYEVYADSVKG 86

RESULT 29
Q96BB9

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ID Q96BB9 PRELIMINARY; PRT; 597 AA.
AC Q96BB9;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE IGH protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straubeberg R.L., Fubngold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Wotley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalski U., Smallos D.E., Scherch A., Schein J.E.,
RA Jones S.J., Maira M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Straubeberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC015760; AAH15760.1; -.
DR PIR; S05271; S05271.
DR PIR; S24260; S24260.
DR HSSP; P01861; IADQ.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 4.
DR SMART; SM00406; IGV; 1.
DR SMART; PF07654; C1-set; 3.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8CE263D9 CRC64;

Query Match 60.2%; Score 53; DB 2; Length 597;
Best Local Similarity 68.8%; Pred. No. 4.5;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ISYDGSKKYYADSVKG 17
Db 70 ISFGSGSKYYARSVKG 85

RESULT 30
ID HV3A HUMAN STANDARD; PRT; 122 AA.
AC HV3A HUMAN;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig heavy chain V-II region TRO.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

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OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE (MYELOMA PROTEIN TRO).
 RX MEDLINE=76023781; PubMed=809331;
 RA Kratzin H., Altevogt P., Ruban E., Kortt A., Starescuk K.,
 RA Hilschmann N.;
 RT "The primary structure of a monoclonal IgA-immunoglobulin (IgA Tro),
 RT II. The amino acid sequence of the H-chain, alpha-type, subgroup III;
 RT structure of the complete IgA-molecule.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 356:1337-1342(1975).
 CC -1- MISCELLANEOUS: The sequence of the C region is also given.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR: A02045; A1HTR.
 DR HSSP; P01783; 11GC.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KM Direct protein sequencing; Immunoglobulin V region.
 FT DOMAIN 1 111 Ig-like.
 FT NON_TER 115 115
 SQ SEQUENCE 122 AA; 13472 MW; 2821A11DA04D80F9 CRC64;
 FT MOD_RES 1 108 Ig-like.
 FT NON_TER 1 122 Pyroglutamate carboxylic acid.
 SQ SEQUENCE 122 AA; 13472 MW; 2821A11DA04D80F9 CRC64;
 Query Match 59.1%; Score 52.5; DB 1; Length 122;
 Best Local Similarity 63.2%; Pred. No. 0.96;
 Matches 12; Conservative 1; Mismatches 3; Indels 3; Gaps 1;
 Qy 2 ISY---DGSKRYADSVKG 17
 Db 48 VSYIGSGSGLTYADSVKG 66
 RESULT 31
 HV3F_HUMAN STANDARD; PRT; 115 AA.
 AC P01767;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig heavy chain V-III region BJT.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=78137069; PubMed=416441;
 RA Torano A., Putnam F.W.;
 RT "Complete amino acid sequence of the alpha 2 heavy chain of a human
 RT IgA2 immunoglobulin of the A2m (2) allotype.";
 RL Proc. Natl. Acad. Sci. U.S.A. 75:966-969(1978).
 CC -1- MISCELLANEOUS: The sequence of the alpha-2, A2m(2) allotype, C
 CC region of this myeloma protein is also given.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR: A02050; A2HUBU.
 DR HSSP; P01783; 11GC.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KM Direct protein sequencing; Immunoglobulin V region.
 FT DOMAIN 1 111 Ig-like.
 FT NON_TER 115 115

SO SEQUENCE 115 AA; 12379 MW; 208876A7DF52DCFA CRC64;
 Query Match 59.1%; Score 52; DB 1; Length 115;
 Best Local Similarity 71.4%; Pred. No. 1.1;
 Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Qy 4 YDGSKRYADSVKG 17
 Db 52 YRGGTYADSVKG 65
 RESULT 32
 Q6INT8 PRELIMINARY; PRT; 466 AA.
 ID Q6INT8;
 AC Q6INT8;
 DT 05-JUL-2004 (TRENDEL. 27, Created)
 DT 05-JUL-2004 (TRENDEL. 27, Last sequence update)
 DT 05-JUL-2004 (TRENDEL. 27, Last annotation update)
 DE IGHG1 protein.
 GN Name=IGHG1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Peripheral Nervous System;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huylk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallos D.B., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Peripheral Nervous System;
 RA Strausberg R.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC072419; AAH72419.1; -.
 DR HSSP; P01861; IADQ.
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003597; Ig_C1.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam; PF0654; C1-sect; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGC1; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 2
 SO SEQUENCE 466 AA; 50853 MW; 53EB0BCDEB81076E CRC64;
 Query Match 59.1%; Score 52; DB 2; Length 466;
 Best Local Similarity 62.5%; Pred. No. 5;
 Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 Qy 2 ISYDGSKRYADSVKG 17

Db 69 VLYTGATYADVSKG 84

RESULT 33

Q6MZ06 PRELIMINARY; PRT; 475 AA.
AC Q6MZ06;
DT 05-JUL-2004 (TRENBLREL. 27, Created)
DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLREL. 27, Last annotation update)
DE Hypothetical protein DKFP686G1190.
GN Name=DKFP686G1190;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human esophagus tumor;
RG The German Human cDNA Consortium;
RA Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A., Robo G., Han M., Wiemann S.;
RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640947; CAE45972.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; IG. 1.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; CI-sec; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 52043 MW; B7EAE255A26F4B8E CRC64;

Query Match 59.1%; Score 52; DB 2; Length 475;
Best Local Similarity 68.8%; Pred. No. 5.1;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ISYDSKKYADVSKG 17
Db 70 ISSGVNTYADVSKG 85

RESULT 34

Q6GMX2 PRELIMINARY; PRT; 493 AA.
AC Q6GMX2;
DT 05-JUL-2004 (TRENBLREL. 27, Created)
DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLREL. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Dietchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stetson M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carinci P., Prange C., Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska J., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Maira M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strauberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073771; AAH73771.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; CI-sec; 2.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGcl; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 493 AA; 52865 MW; 55B99305B286203 CRC64;

Query Match 59.1%; Score 52; DB 2; Length 493;
Best Local Similarity 68.8%; Pred. No. 5.4;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ISYDSKKYADVSKG 17
Db 70 INSDGSTYADVSKG 85

RESULT 35

HV3B HUMAN STANDARD; PRT; 114 AA.
ID HV3B_HUMAN
AC P01763;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig heavy chain V-II region WEA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=83273707; PubMed=6410398;
RA Goni F., Frangione B.;
RT "Amino acid sequence of the Fv region of a human monoclonal IgM
RT in Klebsiella polysaccharides K30 and K33.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
CC -I- MISCELLANEOUS: This chain was obtained from a monoclonal antibody
CC against 3,4-pyruvylated galactose and isolated from a patient with
CC Waldenstrom's macroglobulinemia.
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC PIR; A02046; M3HWE.
DR HSSP; P01772; 2FP4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003596; IG_v.

DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Ig; 1.
DR PROSITE: PS50835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region;
KW Pyrolydione carboxylic acid.
FT DOMAIN 1 112 Ig-like.
FT MOD_RES 1 112 Pyrolydione carboxylic acid.
FT NON_TER 1 114
SQ SEQUENCE 114 AA; 12256 MW; DB8294FBA18A07B7 CRC64;

Query Match 56.8%; Score 50; DB 1; Length 114;
Best Local Similarity 68.8%; Pred. No. 2.3;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ISYDGSKKYVADSVKG 17
Db 51 IGGSGSYTYYPDSYVG 66

RESULT 36
Q920E7 PRELIMINARY; PRT; 119 AA.
ID Q920E7
AC Q920E7;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Pterin-mimicking anti-idiotope heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF307937; AL09421.1; -
DR PIR: C25913; C25913.
DR HSSP: P01783; 11GC.
DR SMART: SM00406; Ig; 1.
DR PROSITE: PS50835; IG LIKE; 1.
FT NON_TER 1 119
FT NON_TER 1 119
SQ SEQUENCE 119 AA; 13025 MW; FEE904044381CA7C CRC64;

Query Match 56.8%; Score 50; DB 2; Length 119;
Best Local Similarity 68.8%; Pred. No. 2.5;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ISYDGSKKYVADSVKG 17
Db 51 IGGSGSYTYYPDSYVG 66

RESULT 37
O65ZL8 PRELIMINARY; PRT; 196 AA.
ID O65ZL8
AC O65ZL8;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE VH7183-DSP2-JH3-CH1 protein (Fragment).
GN Name=VH7183-DSP2-JH3-CH1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=95362300; PubMed=7635518;
RA Komori T., Sugiyama H.;
RT "An aberrant splicing using a 3' cryptic splice site within the CH1

RT exon induces truncated mu-chain production.";
RL Immunology 85:166-170(1995).
DR EMBL: S79401; AAB35023.2; -
DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00409; Ig; 1.
DR SMART: SM00406; Ig; 1.
DR PROSITE: PS50835; IG LIKE; 1.
FT NON_TER 196 196
SQ SEQUENCE 196 AA; 21429 MW; 12A381018944B268 CRC64;

Query Match 56.8%; Score 50; DB 2; Length 196;
Best Local Similarity 68.8%; Pred. No. 4.2;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ISYDGSKKYVADSVKG 17
Db 70 IGGSGSYTYYPDSYVG 85

RESULT 38
O6GPX4 PRELIMINARY; PRT; 585 AA.
ID O6GPX4
AC O6GPX4;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
RA Datchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buttefield Y.S.,
RA Krzywinski M.I., Skalka U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX Klein S., Strausberg R.;
RT Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

```

DR EMBL; BC072981; AAT72981.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003597; IG_CL.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; CI-sec; 4.
DR Pfam; PF00047; IG; 3.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IGcl; 4.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
DR Hypothetical protein.
KW SEQUENCE 585 AA; 64853 MW; 05A3D91B29E566A3 CRC64;
SQ
Query Match 56.8%; Score 50; DB 2; Length 585;
Best Local Similarity 71.4%; Pred. No. 14;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 YDGSKKYVADSVKG 17
Db 71 YDASKINVADSLKG 84

RESULT 39
09GJ71 PRELIMINARY; PRT; 71 AA.
ID 09GJ71;
AC 09GJ71;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE MHC class II alpha chain (Fragment).
GN Name=atr-DA;
OS Salmo trutta (Brown trout).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8032;
RN [1]
RP SEQUENCE FROM N.A.
RA Stet R.J.M., Jordan W.C.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ293950; CAC08187.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001003; MHC_II_alpha.
DR Pfam; PF00993; MHC_II_alpha; 1.
FT NON_TER 1
FT NON_TER 71
SQ SEQUENCE 71 AA; 7699 MW; 0E3D9764E397FF72 CRC64;

Query Match 55.7%; Score 49; DB 2; Length 71;
Best Local Similarity 61.5%; Pred. No. 2.1;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 5 DGSKKYVADSVKG 17
Db 14 DGEKWIADPIKG 26

RESULT 40
09AV03 PRELIMINARY; PRT; 87 AA.
ID 09AV03;
AC 09AV03; Q7XDS;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein OS:JNBA0026012.3.
GN ORFNames=OSJNBA0026012.3;
OS Oryza sativa (Japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

```

```

OC Euphorbiaceae; Oryzaeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Burr P.C., Hsiao J.,
RA Zisman V., Pai G., Bowman C.L., Fujii C.Y., Vanaken S.E.,
RA Bowman C.L., Craven B., Utterback T.R., Khalak H., Feldblum T.V.,
RA Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
RN Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RL [2]
RP SEQUENCE FROM N.A.
RA Buell R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA The Rice Chromosome 10 Sequencing Consortium;
RT "In-depth view of structure, activity, and evolution of rice
RT chromosome 10."
RL Science 300:1566-1569 (2003).
RN [4]
RP SEQUENCE FROM N.A.
RA Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC078829; AAK13161.1; -.
DR EMBL; AB017105; AAP54276.1; -.
DR Gramene; Q7XDS; -.
DR Gramene; Q9AV03; -.
KW Hypothetical protein.
SQ SEQUENCE 87 AA; 10264 MW; B9FE244022D4E718 CRC64;

Query Match 55.7%; Score 49; DB 2; Length 87;
Best Local Similarity 60.0%; Pred. No. 2.6;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 ISYDGSKKYVADSVK 16
Db 9 ISYDGSKKYVADSVK 23

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Search completed: March 31, 2005, 12:09:38
Job time : 114.057 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 31, 2005, 11:42:18 ; Search time 85.25 Seconds
(without alignments)
49.905 Million cell updates/sec

Title: US-10-614-959-12
Perfect score: 50
Sequence: 1 ASINAPARVLDY 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_16Dec04:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	50	100.0	11 3 AAY79070	Aay79070 Anti-fact
2	46	92.0	11 3 AAY79077	Aay79077 Anti-fact
3	37	74.0	408 8 ADJ48827	Adj48827 Oil-aseoc
4	36	72.0	58 4 AAOL3448	Aaol3448 Human pol
5	36	72.0	652 8 ADS26132	Ads26132 Bacterial
6	36	72.0	652 8 ADS25655	Ads25655 Bacterial
7	36	72.0	655 8 ADS25373	Ads25373 Bacterial
8	36	72.0	656 8 ADS22602	Ads22602 Bacterial
9	35	70.0	708 5 ABB48560	Abb48560 Listeria
10	34	68.0	157 3 AAG18510	Aag18510 Zea mays
11	34	68.0	159 3 AAG18509	Aag18509 Zea mays
12	34	68.0	180 3 AAY37904	Aay37904 Amino aci
13	34	68.0	231 8 ADS28058	Ads28058 Bacterial
14	34	68.0	237 3 AAG20306	Aag20306 Arabidops
15	34	68.0	237 3 AAG51887	Aag51887 Arabidops
16	34	68.0	278 1 AAP80850	Aap80850 Sequence
17	34	68.0	279 1 AAP80274	Aap80274 Amino aci
18	34	68.0	279 2 AAR54838	Aar54838 Thermitas
19	34	68.0	279 2 AAM00768	Aam00768 Thermitas
20	34	68.0	279 2 AAM00769	Aam00769 Thermitas
21	34	68.0	279 2 AAM00774	Aam00774 Thermitas
22	34	68.0	279 2 AAM00798	Aam00798 Thermitas
23	34	68.0	279 2 AAM00770	Aam00770 Thermitas
24	34	68.0	279 2 AAM00775	Aam00775 Thermitas
25	34	68.0	279 2 AAM00780	Aam00780 Thermitas

26	34	68.0	279 2 AAM00783	Aam00783 Thermitas
27	34	68.0	279 2 AAM00792	Aam00792 Thermitas
28	34	68.0	279 2 AAM00772	Aam00772 Thermitas
29	34	68.0	279 2 AAM00784	Aam00784 Thermitas
30	34	68.0	279 2 AAM00793	Aam00793 Thermitas
31	34	68.0	279 2 AAM00796	Aam00796 Thermitas
32	34	68.0	279 2 AAM00794	Aam00794 Thermitas
33	34	68.0	279 2 AAM00785	Aam00785 Thermitas
34	34	68.0	279 2 AAM00787	Aam00787 Thermitas
35	34	68.0	279 2 AAM00789	Aam00789 Thermitas
36	34	68.0	279 2 AAM00799	Aam00799 Thermitas
37	34	68.0	279 2 AAM00803	Aam00803 Thermitas
38	34	68.0	279 2 AAM00767	Aam00767 Thermitas
39	34	68.0	279 2 AAM00771	Aam00771 Thermitas
40	34	68.0	279 2 AAM00801	Aam00801 Thermitas
41	34	68.0	279 2 AAM00790	Aam00790 Thermitas
42	34	68.0	279 2 AAM00788	Aam00788 Thermitas
43	34	68.0	279 2 AAM00797	Aam00797 Thermitas
44	34	68.0	279 2 AAM00800	Aam00800 Thermitas
45	34	68.0	279 2	

ALIGNMENTS

RESULT 1	
AY79070	
ID AAY79070 standard; peptide; 11 AA.	
XX	
AC AAY79070;	
XX	
DT 12-JUN-2000 (first entry)	
XX	
DE Anti-factor IX/IXa antibody H chain V domain CDR3 amino acid sequence.	
XX	
KW Complementarity determining region 3; CDR3; antibody; Gla domain;	
KW factor IX/IXa; blood coagulation; deep venous thrombosis;	
KW arterial thrombosis; unstable angina; post myocardial infarction;	
KW coronary artery bypass graft; CABG; stroke; tumour growth; metastasis;	
KW percutaneous transluminal coronary angioplasty; PTCA; inflammation;	
KW septic shock; hypotension; adult respiratory distress syndrome; ARDS;	
KW arterial fibrillation; disseminated intravascular coagulopathy; DIC.	
XX	
OS Homo sapiens.	
XX	
PN WO200012562-A1.	
XX	
PD 09-MAR-2000.	
XX	
PF 26-AUG-1999; 99WO-US019453.	
XX	
PR 28-AUG-1998; 98US-0098233P.	
XX	
PR 03-MAR-1999; 99US-0122767P.	
XX	
PA (GETH) GENENTECH INC.	
XX	
PI Adams CW, Devaux B, Baton DL, Hase PE, Judice JK, Kirchhofer D;	
PI Suggest S;	
XX	
DR WPI; 2000-256595/22.	
XX	
PT Novel human anti-Factor IX/IXa antibodies against IX/IXa gamma-	
PT carboxyglutamic acid domains useful as anti-coagulant in thrombosis,	
PT stroke, and post myocardial infarction.	
XX	
PS Claim 2; Fig 2; 84pp; English.	
XX	
CC This sequence represents a complementarity determining region 3 (CDR3) of	
CC the heavy chain variable domain of a human anti-factor IX/IXa Gla domain	
CC antibody. Factor IXa is a vitamin K dependent plasma serine protease that	
CC participates in the blood coagulation pathways. The Gla domain of factor	
CC IXa and its zymogen factor IX contains important structural determinants	
CC for interaction with high affinity binding sites on vascular endothelial	
CC	

CC cells and platelets. Compositions comprising the antibodies are used for
 CC the treatment or prophylaxis of thrombotic or coagulopathic diseases or
 CC disorders in a mammal for which inhibiting a FIX/IXa mediated event is
 CC indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable
 CC angina, post myocardial infarction, post surgical thrombosis, coronary
 CC artery bypass graft (CABG), percutaneous transluminal coronary
 CC angioplasty (PTCA), stroke, tumour growth, invasion or metastasis,
 CC inflammation, septic shock, hypotension, adult respiratory distress
 CC syndrome (ARDS), arterial fibrillation and disseminated intravascular
 CC coagulopathy (DIC)

XX
 SQ Sequence 11 AA;

Query Match 100.0%; Score 50; DB 3; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.003;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASIAARVLDY 11
 Db 1 ASIAARVLDY 11

RESULT 2
 AAY79077
 ID AAY79077 standard; peptide; 11 AA.
 AC AAY79077;
 XX
 XX 12-JUN-2000 (first entry)
 XX
 XX Anti-factor IX/IXa antibody H chain V domain CDR3 amino acid sequence.
 XX
 XX Complementarily determining region 3; CDR3; antibody; Gla domain;
 XX factor IX/IXa; blood coagulation; deep venous thrombosis;
 XX arterial thrombosis; unstable angina; post myocardial infarction;
 XX coronary artery bypass graft; CABG; stroke; tumour growth; metastasis;
 XX percutaneous transluminal coronary angioplasty; PTCA; inflammation;
 XX septic shock; hypotension; adult respiratory distress syndrome; ARDS;
 XX arterial fibrillation; disseminated intravascular coagulopathy; DIC.

XX
 OS Homo sapiens.
 XX
 XX WO200012562-A1.
 XX
 XX 09-MAR-2000.
 XX
 XX 26-AUG-1999; 99WO-US019453.
 XX
 XX 28-AUG-1998; 98US-0098233P.
 XX
 XX 03-MAR-1999; 99US-0122767P.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX
 PI Adams CW, Devaux B, Eaton DL, Hase PE, Justice JK, Kirchofer D;
 PI Suggest S;
 XX
 XX WPI; 2000-256595/22.
 XX
 XX Novel human anti-Factor IX/IXa antibodies against IX/IXa gamma-
 PT carboxylutamic acid domains useful as anti-coagulant in thrombosis,
 PT stroke, and post myocardial infarction.
 PT
 XX
 XX Claim 2; Fig 2; 84pp; English.

XX This sequence represents a complementarity determining region 3 (CDR3) of
 CC the heavy chain variable domain of a human anti-factor IX/IXa Gla domain
 CC antibody. Factor IXa is a vitamin K dependent plasma serine protease that
 CC participates in the blood coagulation pathways. The Gla domain of factor
 CC IXa and its zymogen factor IX contains important structural determinants
 CC for interaction with high affinity binding sites on vascular endothelial
 CC cells and platelets. Compositions comprising the antibodies are used for
 CC the treatment or prophylaxis of thrombotic or coagulopathic diseases or
 CC disorders in a mammal for which inhibiting a FIX/IXa mediated event is

CC indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable
 CC angina, post myocardial infarction, post surgical thrombosis, coronary
 CC artery bypass graft (CABG), percutaneous transluminal coronary
 CC angioplasty (PTCA), stroke, tumour growth, invasion or metastasis,
 CC inflammation, septic shock, hypotension, adult respiratory distress
 CC syndrome (ARDS), arterial fibrillation and disseminated intravascular
 CC coagulopathy (DIC)

XX
 SQ Sequence 11 AA;

Query Match 92.0%; Score 46; DB 3; Length 11;
 Best Local Similarity 90.9%; Pred. No. 0.019;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ASIAARVLDY 11
 Db 1 ASIAARVLDY 11

RESULT 3
 ADJ48827
 ID ADJ48827 standard; protein; 408 AA.
 AC ADJ48827;
 XX
 XX 06-MAY-2004 (first entry)
 XX
 XX O11-associated gene related protein #327.
 XX
 XX O11-associated gene; transgenic; enhanced seed oil; vegetable oil.
 XX
 XX Unidentified.
 XX
 XX US2004025202-A1.
 XX
 XX 05-FEB-2004.
 XX
 XX 14-MAR-2003; 2003US-00389566.
 XX
 XX 15-MAR-2002; 2002US-0365301P.
 XX
 XX 26-JUN-2002; 2002US-0391786P.
 XX
 XX 26-JUN-2002; 2002US-0392018P.
 XX
 XX (LAURIE C C.
 XX (RAVA/) RAVANELLO M.
 XX (SAVA/) SAVAGE T.
 XX (LEDE/) LEDEAUX J R.
 XX (ROGE/) ROGERS J A.
 XX
 XX Laurie CC, Ravanello M, Savage T, Ledeaux JR, Rogers JA;
 XX
 XX WPI; 2004-142683/14.
 XX
 XX Novel recombinant DNA construct comprising a promoter functional in
 PT plants operably linked to an oil-associated gene for producing transgenic
 PT plant seed.
 PT
 XX
 XX Example 3; SEQ ID NO 831; 22pp; English.

XX The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in plants operably linked to an oil-associated gene.
 CC The construct is useful for transgenic plant seed which has in its genome
 CC the construct, that is functional in the plant to transcribe the oil-
 CC associated gene. The transgenic plant seed grows into a plant having
 CC enhanced seed oil as compared to wild type. The construct is useful for
 CC producing hybrid maize seed. The transgenic plant seed is useful for
 CC producing vegetable oil. The present sequence represents the amino acid
 CC sequence of an oil-associated gene related protein.

XX
 SQ Sequence 408 AA;

Query Match 74.0%; Score 37; DB 8; Length 408;
 Best Local Similarity 80.0%; Pred. No. 62;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASIAARVLDY 10
||:|||||
Db 275 ASIAAARALD 284

RESULT 4
AAO13448 standard; protein; 58 AA.
XX AAO13448;
AC AAO13448;
XX 06-NOV-2001 (first entry)
XX DE Human polypeptide SEQ ID NO 27340.
XX KM Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX KM vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX KM tissue growth factor; immunomodulatory; cancer; leukaemia;
XX KM nervous system disorders; arthritis; inflammation.
XX OS Homo sapiens.
XX PN MO200164835-A2.
XX PD 07-SEP-2001.
XX PF 26-FEB-2001; 2001WO-US004927.
XX PR 28-FEB-2000; 2000US-00515126.
XX PR 18-MAY-2000; 2000US-00577409.
XX PA (HYSE-) HYSEQ INC.
XX PI Tang YT, Liu C, Drmanac RT;
XX DR WPI; 2001-514838/56.
XX DR N-PSDB; AAI93379.
XX PT Isolated nucleic acids and polypeptides, useful for preventing diagnosing
XX PT and treating e.g. leukemia, inflammation and immune disorders.
XX PS Claim 20; SEQ ID NO 27340; 1399pp + Sequence listing; English.
XX CC The invention relates to human polynucleotides (AA179941-AA193841) and
XX CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
XX CC cytokine, cell proliferation or cell differentiation or which may induce
XX CC production of other cytokines in other cell populations. The
XX CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
XX CC peptide therapy. The polypeptides have various cytokine-like activities,
XX CC e.g. stem cell growth factor activity, haematopoiesis regulating
XX CC activity, tissue growth factor activity, immunomodulatory activity and
XX CC activin/inhibin activity and may be useful in the diagnosis and/or
XX CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
XX CC inflammation. Note: The sequence data for this patent did not form part
XX CC of the printed specification, but was obtained in electronic format
XX CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 58 AA;
QY Query Match 72.0%; Score 36; DB 4; Length 58;
Db Best Local Similarity 70.0%; Pred. No. 12;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

2 SIAARVLDY 11
||:|||||
12 SVAQARVLEY 21

RESULT 5
ADS26132 standard; protein; 652 AA.
ID ADS26132

XX AC ADS26132;
XX XX 02-DEC-2004 (first entry)
XX DT Bacterial polypeptide #15165.
XX DE
XX XX Recombinant DNA construct; transformed plant; improved plant property;
XX KM cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
XX KM pathogen tolerance; pest tolerance; plant disease resistance;
XX KM cell cycle pathway modification; plant growth regulator;
XX KM homologous recombination; seed oil yield; protein yield; carbohydrate;
XX KM nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
XX KM bacterial polypeptide.
XX OS Bacteria.
XX PN US2003233675-A1.
XX XX 18-DEC-2003.
XX PD 20-FEB-2003; 2003US-00369493.
XX PF 21-FEB-2002; 2002US-0360039P.
XX PR (CAOY/) CAO Y.
XX PA (HINK/) HINKLE G J.
XX PA (SLAT/) SLATER S C.
XX PA (CHEN/) CHEN X.
XX PA (GOLD/) GOLDMAN B S.
XX PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX DR WPI; 2004-061375/06.
XX PT New recombinant DNA construct comprising a promoter positioned to provide
XX PT for expression of a polynucleotide encoding a polypeptide from a
XX PT microbial source, useful for producing plants with improved properties.
XX PS Claim 1; SEQ ID NO 15165; 122pp; English.
XX CC The invention relates to a recombinant DNA construct comprising a
XX CC promoter functional in a plant cell, where the promoter is positioned to
XX CC provide for expression of a polynucleotide encoding a polypeptide from a
XX CC microbial source. The invention also relates to a transformed plant
XX CC comprising the recombinant DNA construct and a method of producing a
XX CC transformed plant having an improved property. The plant is a crop plant
XX CC such as maize or soybean. The method of producing a transformed plant
XX CC having an improved property comprises transforming a plant with the
XX CC recombinant DNA construct and growing the transformed plant, where the
XX CC polynucleotide or polypeptide is useful for improving plant properties.
XX CC The recombinant DNA construct is useful for producing plants with
XX CC improved plant properties, e.g. improved cold, heat or drought tolerance,
XX CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
XX CC increased resistance to plant disease, better growth rate by modification
XX CC of the cell cycle pathway with plant growth regulators, increased rate of
XX CC homologous recombination, modified seed oil or protein yield and/or
XX CC content, improved yield by modification of carbohydrate, nitrogen or
XX CC phosphorus use and/or uptake, by modification of photosynthesis or by
XX CC providing improved plant growth and development under at least one stress
XX CC condition, improved lignin production or improved galactomannan
XX CC production. This sequence represents a bacterial polypeptide used in the
XX CC scope of the invention. Note: The sequence data for this patent did not
XX CC form part of the printed specification but was obtained in electronic
XX CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX SQ Sequence 652 AA;
QY Query Match 72.0%; Score 36; DB 8; Length 652;
Db Best Local Similarity 63.6%; Pred. No. 1.6e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

1 ASIAARVLDY 11

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Db      255 AATMAARAIDY 265
      ||:|||||:||||
RESULT 6
ID      ADS25655
      ADS25655 standard; protein; 652 AA.
XX
AC      ADS25655;
XX
DT      02-DEC-2004 (first entry)
XX
DE      Bacterial polypeptide #14688.
XX
KW      Recombinant DNA construct; transformed plant; improved plant property;
KW      cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW      pathogen tolerance; pest tolerance; plant disease resistance;
KW      cell cycle pathway modification; plant growth regulator;
KW      homologous recombination; seed oil yield; protein yield; carbohydrate;
KW      nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW      bacterial polypeptide..
XX
OS      Bacteria.
XX
PN      US2003233675-A1.
XX
PD      18-DEC-2003.
XX
PF      20-FEB-2003; 2003US-00369493.
XX
PR      21-FEB-2002; 2002US-0360039P.
XX
PA      (CAOY/) CAO Y.
PA      (HINK/) HINKLE G J.
PA      (SLAT/) SLATER S C.
PA      (CHEN/) CHEN X.
PA      (GOLD/) GOLDMAN B S.
XX
PI      Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX
WI      WPI; 2004-061375/06.
XX
PT      New recombinant DNA construct comprising a promoter positioned to provide
PT      for expression of a polynucleotide encoding a polypeptide from a
PT      microbial source, useful for producing plants with improved properties.
XX
PS      Claim 1; SEQ ID NO 14688; 122pp; English.
XX
CC      The invention relates to a recombinant DNA construct comprising a
CC      promoter functional in a plant cell, where the promoter is positioned to
CC      provide for expression of a polynucleotide encoding a polypeptide from a
CC      microbial source. The invention also relates to a transformed plant
CC      comprising the recombinant DNA construct and a method of producing a
CC      transformed plant having an improved property. The plant is a crop plant
CC      such as maize or soybean. The method of producing a transformed plant
CC      having an improved property comprises transforming a plant with the
CC      recombinant DNA construct and growing the transformed plant, where the
CC      polynucleotide or polypeptide is useful for improving plant properties.
CC      The recombinant DNA construct is useful for producing plants with
CC      improved plant properties, e.g. improved cold, heat or drought tolerance,
CC      tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC      increased resistance to plant disease, better growth rate by modification
CC      of the cell cycle pathway with plant growth regulators, increased rate of
CC      homologous recombination, modified seed oil or protein yield and/or
CC      content, improved yield by modification of carbohydrate, nitrogen or
CC      phosphorus use and/or uptake, by modification of photosynthesis or by
CC      providing improved plant growth and development under at least one stress
CC      condition, improved lignin production or improved galactomannan
CC      production. This sequence represents a bacterial polypeptide used in the
CC      scope of the invention. Note: The sequence data for this patent did not
CC      form part of the printed specification but was obtained in electronic
CC      format from USPTO at seqdata.uspto.gov/sequence.html.
XX

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SQ      Sequence 652 AA;
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      Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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Db      255 AATMAARAIDY 265
      ||:|||||:||||
RESULT 7
ID      ADS25373
      ADS25373 standard; protein; 655 AA.
XX
AC      ADS25373;
XX
DT      02-DEC-2004 (first entry)
XX
DE      Bacterial polypeptide #14406.
XX
KW      Recombinant DNA construct; transformed plant; improved plant property;
KW      cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW      pathogen tolerance; pest tolerance; plant disease resistance;
KW      cell cycle pathway modification; plant growth regulator;
KW      homologous recombination; seed oil yield; protein yield; carbohydrate;
KW      nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW      bacterial polypeptide.
XX
OS      Bacteria.
XX
PN      US2003233675-A1.
XX
PD      18-DEC-2003.
XX
PF      20-FEB-2003; 2003US-00369493.
XX
PR      21-FEB-2002; 2002US-0360039P.
XX
PA      (CAOY/) CAO Y.
PA      (HINK/) HINKLE G J.
PA      (SLAT/) SLATER S C.
PA      (CHEN/) CHEN X.
PA      (GOLD/) GOLDMAN B S.
XX
PI      Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX
WI      WPI; 2004-061375/06.
XX
PT      New recombinant DNA construct comprising a promoter positioned to provide
PT      for expression of a polynucleotide encoding a polypeptide from a
PT      microbial source, useful for producing plants with improved properties.
XX
PS      Claim 1; SEQ ID NO 14406; 122pp; English.
XX
CC      The invention relates to a recombinant DNA construct comprising a
CC      promoter functional in a plant cell, where the promoter is positioned to
CC      provide for expression of a polynucleotide encoding a polypeptide from a
CC      microbial source. The invention also relates to a transformed plant
CC      comprising the recombinant DNA construct and a method of producing a
CC      transformed plant having an improved property. The plant is a crop plant
CC      such as maize or soybean. The method of producing a transformed plant
CC      having an improved property comprises transforming a plant with the
CC      recombinant DNA construct and growing the transformed plant, where the
CC      polynucleotide or polypeptide is useful for improving plant properties.
CC      The recombinant DNA construct is useful for producing plants with
CC      improved plant properties, e.g. improved cold, heat or drought tolerance,
CC      tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC      increased resistance to plant disease, better growth rate by modification
CC      of the cell cycle pathway with plant growth regulators, increased rate of
CC      homologous recombination, modified seed oil or protein yield and/or
CC      content, improved yield by modification of carbohydrate, nitrogen or
CC      phosphorus use and/or uptake, by modification of photosynthesis or by
XX

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CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.

CC
XX
SQ Sequence 655 AA;

QY Query Match 72.0%; Score 36; DB 8; Length 655;
Best Local Similarity 63.6%; Pred. No. 1.6e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

DB 1 ASIAAARVLDY 11
255 AATMAARAIDY 265

RESULT 8
ID ADS22602 standard; protein; 656 AA.

AC ADS22602;
XX
DT 02-DEC-2004 (first entry)
XX
DE Bacterial polypeptide #11635.

XX
KW Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.

XX
OS Bacteria.

XX
PN US200323675-A1.

XX
PD 18-DEC-2003.

XX
PF 20-FEB-2003; 2003US-00369493.

XX
PR 21-FEB-2002; 2002US-0360039P.

XX
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.

XX
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX
DR WPI; 2004-061375/06.

XX
PT New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.

XX
PS Claim 1; SEQ ID NO 11635; 122pp; English.

XX
CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with

CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.

CC
XX
SQ Sequence 656 AA;

QY Query Match 72.0%; Score 36; DB 8; Length 656;
Best Local Similarity 63.6%; Pred. No. 1.7e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

DB 1 ASIAAARVLDY 11
255 AATMAARAIDY 265

RESULT 9
ID ABB48560 standard; protein; 708 AA.

AC ABB48560;
XX
DT 05-FEB-2002 (first entry)
XX
DE Listeria monocytogenes protein #1264.

XX
KW Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
KW vitamin B12; bacterial infection; disease.

XX
OS Listeria monocytogenes.

XX
PN WO200177335-A2.

XX
PD 18-OCT-2001.

XX
PF 11-APR-2001; 2001WO-FR001118.

XX
PR 11-APR-2000; 2000FR-00004629.

XX
PA (INSP) INST PASTEUR.

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PI Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P;
PI Dussurget O, Chetoui F, Medjari H, Glaser P, Kunst F, Cossart P;
PI Daniels U, Goebel W, Kreft U, Kuhn M, Ng B, Vazquez-Boland JA;
PI Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A;
PI Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L;
PI Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;
PI Madueno E, De Pablos B, Wehland U, Kaerst U, Entian K, Hauf U;
PI Rose M, Voss H;
XX
DR WPI; 2002-010914/01.

XX
PT Genomic sequence for Listeria monocytogenes, useful e.g. for treatment
PT and prevention of Listeria and related bacterial infections, and related
PT polypeptides.

XX
PS Claim 6; SEQ ID NO 1265; 192pp; French.

XX
CC The present invention relates to the genome sequence of Listeria
CC monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of
CC it are useful for selecting probes and primers for detecting genes in L.
CC monocytogenes and related organisms, and for studying genetic
CC polymorphisms and other genomes. The present sequence is a protein
CC encoded by the genome sequence of the present invention. Proteins

CC expressed from the genome sequence are useful for raising specific
CC antibodies, identification of *L. monocytogenes* and related organisms, and
CC for biosynthesis and biodegradation, especially biosynthesis of Vitamin
CC B12. The genome sequence and proteins encoded by it are also useful for
CC selecting compounds that regulate gene expression and cell replication
CC and modulate *L. monocytogenes*-related diseases. In addition, the genome
CC sequence and proteins encoded by it are useful in pharmaceutical and
CC vaccines compositions for the treatment or prevention of infections by *L.*
CC *monocytogenes* and related organisms. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 708 AA:

QY 4 AAARVLDY 11
Db 697 AAARIDY 704
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Query Match 70.0%; Score 35; DB 5; Length 708;
Best Local Similarity 75.0%; Pred. No. 2.9e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

RESULT 10
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ID AAG18510 standard; protein, 157 AA.
XX
AC AAG18510;
XX
DT 17-OCT-2000 (first entry)
XX
DE Zea mays protein fragment SEQ ID NO: 19948.
XX
KM Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence; corn.
XX
OS Zea mays subsp. mays.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301339.
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PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
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Query Match 68.0%; Score 34; DB 3; Length 157;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AARVDY 11
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Db 117 AARVDY 123

RESULT 11
AAG18509
ID AAG18509 strand; protein; 159 AA.
XX
AC AAG18509;
XX
DT 17-OCT-2000 (first entry)
XX
DE Zea mays protein fragment SEQ ID NO: 19947.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence; corn.
OS Zea mays subsp. mays.
XX
PN EP103405-A2.
XX
PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-00301439.
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XX KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX OS Arabidopsis thaliana.
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PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 68.0%; Score 34; DB 3; Length 217;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 AARVLDY 11
|||||
Db 8 AARVLDY 14

RESULT 16

ID AAP80850 standard; protein: 278 AA.

AC AAP80850;

DT 25-MAR-2003 (revised)

DT 31-OCT-2002 (revised)

DT 10-SEP-1990 (first entry)

XX

DE Sequence of subtilisin thermilase.
 XX Serine protease TW3; proteinase K; subtilisin thermilase.
 XX Unidentified.
 OS WO8807581-A.
 XX
 XX 06-OCT-1988.
 PD
 XX 28-MAR-1988; 88WO-US001040.
 PF
 XX 03-APR-1987; 87US-00035816.
 PR
 XX (AMGE-) AMGEN.
 PA
 XX Samal BB, Strabinsky Y;
 PI
 XX WPI; 1988-292865/41.
 DR
 XX
 XX New purified serine protease - isolated from culture medium of fungus
 PT Triticichum album or produced by recombinant DNA techniques.
 PS
 XX Disclosure; Fig 9a-9c; 74pp; English.
 PS
 XX Fig. 9 represents a comparison of the AA sequences of protease TW3 with
 CC those of proteinase K, subtilisin novo, subtilisin Carlsberg, subtilisin
 CC DY and thermilase. The AA sequence of the mature TW3 protein as
 CC determined from the nucleotide sequence has approximately 90% homology
 CC with that of proteinase K. There are certain positions where the TW3 AA
 CC sequence resembles that in subtilisin, but not to proteinase K. For
 CC example, at positions 143, a methionine residue occurs in all subtilisins
 CC as well as in protease TW3, while a leucine residue is present at that
 CC position in proteinase K. Similarly at position 219, an alanine residue
 CC is present in protease TW3 and subtilisin, but not in proteinase K. In
 CC addition, the AA fragment, Ser-Thr-, is absent from proteinase K while
 CC being present in the other enzymes (see AAP80847-49 and AAP80851) at
 CC position 226 and 227. Purified serine protease (SP), can be used in
 CC detergents and cleansers or spot removers, as a depilatory in tanning and
 CC also in the food industry for the prepn. of protein hydrolysates and in
 CC serology for the detection of incomplete antibodies. (Updated on 31-OCT-
 CC 2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PR
 CC field.) (Updated on 25-MAR-2003 to correct PA field.)
 CC
 XX
 SQ Sequence 278 AA;
 Query Match 68.0%; Score 34; DB 1; Length 278;
 Best Local Similarity 80.0%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ASIAARVLD 10
 DB 96 ASILAVRLD 105
 RESULT 17
 AAP80274
 ID AAP80274 standard; protein; 279 AA.
 AC AAP80274;
 XX
 XX 27-AUG-2003 (revised)
 DT 10-SEP-1990 (first entry)
 DT
 XX Amino acid sequence of Bacillus thermilase subtilisin.
 DE Enzyme mutant; catalytic function; Bacillus thermilase subtilisin.
 XX
 XX Bacillus sp.
 OS
 XX WO8807578-A.
 PN
 XX 06-OCT-1988.
 PD

XX 30-MAR-1988; 88WO-US001078.
 PF
 XX 02-APR-1987; 87US-00034085.
 PR
 XX (GERTH) GENENTECH INC.
 PA
 XX Wells JA, Carter PJ;
 PI
 XX WPI; 1988-292862/41.
 DR
 XX
 XX Enzyme mutants with modified catalytic functional gp. - react with
 PT modified substrates which contain moiety to complement catalytic
 PT functionality.
 PS
 XX Disclosure; Fig 3b; 90pp; English.
 PS
 XX The patent is for a novel enzyme mutant (EM), not found in nature,
 CC derived by the replacement or modification, in a precursor enzyme, of at
 CC least one catalytic gp. of an amino acid residue which when in contact
 CC with a selected region of a polypeptide substrate, functions
 CC catalytically. The precursor enzyme may be, eg oxido-reductases,
 CC transferases, hydrolases, lyases, isomerases or ligases. EM have a
 CC catalytic preference for substrates which provide the replaced or
 CC modified functional gp. or its equivalent such that the substrate
 CC together with the enzyme mutant assists in its own catalysis. In Fig 3b
 CC B. amyloliquefaciens subtilisin and thermilase are aligned to compare
 CC conserved residues. (Updated on 27-AUG-2003 to correct OS field.)
 CC
 XX
 SQ Sequence 279 AA;
 Query Match 68.0%; Score 34; DB 1; Length 279;
 Best Local Similarity 80.0%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ASIAARVLD 10
 DB 96 ASILAVRLD 105
 RESULT 18
 AAR54838
 ID AAR54838 standard; protein; 279 AA.
 AC AAR54838;
 XX
 XX 27-AUG-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 11-JAN-1995 (first entry)
 DT
 XX Thermilase (p229X).
 DE
 XX Subtilisin; mutant; variant; enzyme; protease; substrate; thermilase.
 XX
 XX Thermoactinomyces vulgaris.
 OS
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 229 /label= Ala, Leu, Met, Gln, Val, Ser
 FT /note= "pref. Ala"
 FT
 XX US5316941-A.
 PD 31-MAY-1994.
 PD
 XX 29-APR-1992; 92US-00876818.
 PF
 XX 06-JAN-1989; 89US-00294340.
 PR
 XX (GEMV) GENENCOR INC.
 PA
 XX Graycar TP, Bott RR, Estell DA, Caldwell RM;
 PI
 XX

DR WPI; 1994-176274/21.
XX
FT New DNA encoding subtilisin mutated at position - producing protease with
PT altered substrate specificity and reactivity.
XX
PS Disclosure; Fig 3b; 13pp; English.
XX
CC DNA encoding subtilisin in which the amino acid equiv. to Pro(225) of B.
CC amyloliquefactors subtilisin has been replaced by Ala, Leu, Met, Gln, Val
CC or Ser (pref. Ala) is claimed. Compared with wild-type subtilisin, the
CC variants have different catalytic and/or Michaelis constants, i.e.
CC different substrate reactivity and/or specificity. partic. at least a 2-
CC fold increase or decrease in the kcat/Km ratio. Changing Pro to Ala gives
CC a mutant enzyme with greater activity for ester as opposed to amide
CC substrates. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 27-
CC AUG-2003 to correct OS field.)
XX
SQ Sequence 279 AA;

Query Match 68.0%; Score 34; DB 2; Length 279;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASIAARVLD 10
||| |||
Db 96 ASIAARVLD 105

RESULT 19
AAW00768
ID AAW00768 standard; protein; 279 AA.
XX
AC AAW00768;
XX
DT 20-NOV-1996 (first entry)
XX
DE Thermilase G206N.
XX
KW Thermilase; hydrolysis; enzyme; protease; Bacillus thermilase; hygiene;
KW subtilisin; cleaning composition; proteinaceous stain removal;
KW hard surface cleaning; dishwashing composition; oral cleaning;
KW denture cleaning; contact lens cleaning; fabric cleaner.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FH 66..73
FT /note= "loop 1"
FT 103..115
FT /note= "loop 2"
FT 134..141
FT /note= "loop 3"
FT 162..171
FT /note= "loop 4"
FT 191..195
FT /note= "loop 5"
FT Region 204..224
FT /note= "loop 6"
FT Misc-difference 206
FT /note= "G206N"
XX
XX W09628558-A1.
XX
XX 19-SEP-1996.
XX
XX 06-MAR-1996; 96WO-US003009.
XX
XX 09-MAR-1995; 95US-00401573.
XX
XX (PROC) PROCTER & GAMBLE CO.
XX
XX Brode PF, Barnett BL, Rubingh DN;
XX

DR WPI; 1996-433830/43.
XX
XX New thermilase variants, partic. for cleaning compns. - having amino
PT acid substns. to provide decreased adsorption to and increased hydrolysis
PT of bound substrates.
XX
XX Example 7; Page 7; 159pp; English.
XX
CC AAW00766-W00803 represent thermilase variants of the invention.
CC Thermilase is a protease. These sequences are based on the wild type
CC Bacillus thermilase subtilisin sequence, which is specified but not given
CC in the specification (there are no sequences given in their entirety in
CC the specification). The variant sequences have one or more substitutions
CC in one or more of the six loop regions of the thermilase sequence. The
CC loop regions play a significant role in the adsorption of the enzyme
CC molecule to a surface-bound peptide. The amino acids of the loop regions,
CC make contact with any surface to which the molecule is exposed. The
CC proximity of the loop regions to the active site and binding pocket of
CC the thermilase in the catalytically productive adsorption of the enzyme
CC to the surface bound molecule. Mutations in the loop regions will
CC therefore have a significant effect on this adsorption. The thermilase
CC variants can be used in cleaning compositions for proteinaceous stain
CC removal. The variants can be used in hard surface cleaning compositions,
CC dishwashing compositions, oral cleaning compositions, denture cleaning
CC compositions, contact lens cleaning compositions, and fabric cleaners.
CC These sequences have decreased adsorption to insoluble substrates,
CC thereby increasing mobility and increasing hydrolysis of the substrates
XX
SQ Sequence 279 AA;

Query Match 68.0%; Score 34; DB 2; Length 279;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASIAARVLD 10
||| |||
Db 96 ASIAARVLD 105

RESULT 20
AAW00769
ID AAW00769 standard; protein; 279 AA.
XX
AC AAW00769;
XX
DT 20-NOV-1996 (first entry)
XX
DE Thermilase T11N.
XX
KW Thermilase; hydrolysis; enzyme; protease; Bacillus thermilase; hygiene;
KW subtilisin; cleaning composition; proteinaceous stain removal;
KW hard surface cleaning; dishwashing composition; oral cleaning;
KW denture cleaning; contact lens cleaning; fabric cleaner.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FH 66..73
FT /note= "loop 1"
FT 103..115
FT /note= "loop 2"
FT 111
FT Misc-difference 111
FT /note= "T11N"
FT 134..141
FT /note= "loop 3"
FT 162..171
FT /note= "loop 4"
FT 191..195
FT /note= "loop 5"
FT Region 204..224
FT /note= "loop 6"
XX
XX W09628558-A1.
XX

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XX 19-SEP-1996.
PD 06-MAR-1996; 96WO-US003009.
XX 09-MAR-1995; 95US-00401573.
XX (PROC ) PROCTER & GAMBLE CO.
XX Brode PF, Barnett BL, Rubingh DN;
XX WPI; 1996-433830/43.
XX
XX New thermatase variants, partic. for cleaning compsns. - having amino
XX acid substrns. to provide decreased adsorption to and increased hydrolysis
XX of bound substrates.
XX
XX Example 13; Page ?, 159pp; English.
XX
XX AAM00766-W00803 represent thermatase variants of the invention.
XX Thermatase is a protease. These sequences are based on the wild type
XX Bacillus thermatase subtilisin sequence, which is specified but not given
XX in the specification (there are no sequences given in their entirety in
XX the specification). The variant sequences have one or more substitutions
XX in one or more of the six loop regions of the thermatase sequence. The
XX loop regions play a significant role in the adsorption of the enzyme
XX molecule to a surface-bound peptide. The amino acids of the loop regions,
XX make contact with any surface to which the molecule is exposed. The
XX proximity of the loop regions to the active site and binding pocket of
XX the thermatase in the catalytically productive adsorption of the enzyme
XX to the surface bound molecule. Mutations in the loop regions will
XX therefore have a significant effect on this adsorption. The thermatase
XX variants can be used in cleaning compositions for proteinaceous stain
XX removal. The variants can be used in hard surface cleaning compositions,
XX dishwashing compositions, oral cleaning compositions, denture cleaning
XX compositions, contact lens cleaning compositions, and fabric cleaners.
XX These sequences have decreased adsorption to insoluble substrates,
XX thereby increasing mobility and increasing hydrolysis of the substrates
XX
XX SQ Sequence 279 AA;
XX
XX Query Match 68.0%; Score 34; DB 2; Length 279;
XX Best Local Similarity 80.0%; Pred. No. 1.7e+02;
XX Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1 ASIAARVLD 10
XX 96 ASIAVRVLD 105
XX
XX DB
XX
XX RESULT 21
XX ID AAM00774 standard; protein; 279 AA.
XX AC AAM00774;
XX
XX 20-NOV-1996 (first entry)
XX
XX Thermatase Y210G, T212P, P214G, S222D.
XX
XX Thermatase; hydrolysis; enzyme; protease; Bacillus thermatase; hygiene;
XX subtilisin; cleaning composition; proteinaceous stain removal;
XX hard surface cleaning; dishwashing composition; oral cleaning;
XX denture cleaning; contact lens cleaning; fabric cleaner.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX FT 66..73
XX FT /note= "loop 1"
XX FT 103..115
XX FT /note= "loop 2"
XX FT 134..141
XX FT Region

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FT /note= "loop 3"
FT 162..171
FT /note= "loop 4"
FT 191..195
FT /note= "loop 5"
FT 204..224
FT /note= "loop 6"
FT Misc-difference 210
FT /note= "Y210G"
FT Misc-difference 212
FT /note= "T212P"
FT Misc-difference 214
FT /note= "P214G"
FT Misc-difference 222
FT /note= "S222D"
XX
XX W09628558-A1.
XX
XX 19-SEP-1996.
XX
XX 06-MAR-1996; 96WO-US003009.
XX
XX 09-MAR-1995; 95US-00401573.
XX (PROC ) PROCTER & GAMBLE CO.
XX
XX Brode PF, Barnett BL, Rubingh DN;
XX WPI; 1996-433830/43.
XX
XX New thermatase variants, partic. for cleaning compsns. - having amino
XX acid substrns. to provide decreased adsorption to and increased hydrolysis
XX of bound substrates.
XX
XX Example 25; Page ?, 159pp; English.
XX
XX AAM00766-W00803 represent thermatase variants of the invention.
XX Thermatase is a protease. These sequences are based on the wild type
XX Bacillus thermatase subtilisin sequence, which is specified but not given
XX in the specification (there are no sequences given in their entirety in
XX the specification). The variant sequences have one or more substitutions
XX in one or more of the six loop regions of the thermatase sequence. The
XX loop regions play a significant role in the adsorption of the enzyme
XX molecule to a surface-bound peptide. The amino acids of the loop regions,
XX make contact with any surface to which the molecule is exposed. The
XX proximity of the loop regions to the active site and binding pocket of
XX the thermatase in the catalytically productive adsorption of the enzyme
XX to the surface bound molecule. Mutations in the loop regions will
XX therefore have a significant effect on this adsorption. The thermatase
XX variants can be used in cleaning compositions for proteinaceous stain
XX removal. The variants can be used in hard surface cleaning compositions,
XX dishwashing compositions, oral cleaning compositions, denture cleaning
XX compositions, contact lens cleaning compositions, and fabric cleaners.
XX These sequences have decreased adsorption to insoluble substrates,
XX thereby increasing mobility and increasing hydrolysis of the substrates
XX
XX SQ Sequence 279 AA;
XX
XX Query Match 68.0%; Score 34; DB 2; Length 279;
XX Best Local Similarity 80.0%; Pred. No. 1.7e+02;
XX Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1 ASIAARVLD 10
XX 96 ASIAVRVLD 105
XX
XX DB
XX
XX RESULT 22
XX ID AAM00798 standard; protein; 279 AA.
XX AC AAM00798;
XX

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DT 20-NOV-1996 (first entry)
 XX Thermiltase Y218A.
 XX Thermiltase; hydrolysis; enzyme; protease; Bacillus thermiltase; hygiene;
 KW subtilisin; cleaning composition; proteinaceous stain removal;
 KW hard surface cleaning; dishwashing composition; oral cleaning;
 KW denture cleaning; contact lens cleaning; fabric cleaner.
 XX Synthetic.
 OS
 XX
 XX Key Location/Qualifiers
 FT Region 66..73
 FT /note= "loop 1"
 FT Region 103..115
 FT /note= "loop 2"
 FT Region 134..141
 FT /note= "loop 3"
 FT Region 162..171
 FT /note= "loop 4"
 FT Region 191..195
 FT /note= "loop 5"
 FT Region 204..224
 FT /note= "loop 6"
 FT Misc-difference 218
 FT /note= "Y218A"
 FT
 XX WO9628558-A1.
 PN 19-SEP-1996.
 XX
 XX 06-MAR-1996; 96WO-US003009.
 XX
 XX 09-MAR-1995; 95US-00401573.
 XX
 XX (PROC) PROCTER & GAMBLE CO.
 PA
 XX Brode PF, Barnett BL, Rubingh DN;
 PI
 XX WPI; 1996-433830/43.
 DR
 XX New thermiltase variants, partic. for cleaning compns. - having amino
 PT acid substns. to provide decreased adsorption to and increased hydrolysis
 PT of bound substrates.
 PT
 XX Example 71; Page ?; 159pp; English.
 PS
 XX AAM00766-W00803 represent thermiltase variants of the invention.
 CC Thermiltase is a protease. These sequences are based on the wild type
 CC Bacillus thermiltase subtilisin sequence, which is specified but not given
 CC in the specification (there are no sequences given in their entirety in
 CC the specification). The variant sequences have one or more substitutions
 CC in one or more of the six loop regions of the thermiltase sequence. The
 CC loop regions play a significant role in the adsorption of the enzyme
 CC molecule to a surface-bound peptide. The amino acids of the loop regions,
 CC make contact with any surface to which the molecule is exposed. The
 CC proximity of the loop regions to the active site and binding pocket of
 CC the thermiltase in the catalytically productive adsorption of the enzyme
 CC to the surface bound molecule. Mutations in the loop regions will
 CC therefore have a significant effect on this adsorption. The thermiltase
 CC variants can be used in cleaning compositions for proteinaceous stain
 CC removal. The variants can be used in hard surface cleaning compositions,
 CC dishwashing compositions, oral cleaning compositions, denture cleaning
 CC compositions, contact lens cleaning compositions, and fabric cleaners.
 CC These sequences have decreased adsorption to insoluble substrates,
 CC thereby increasing mobility and increasing hydrolysis of the substrates
 CC
 XX Sequence 279 AA;
 SO
 Query Match 68.0%; Score 34; DB 2; Length 279;
 Best Local Similarity 80.0%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAARVLD 10
 |||||
 Db 96 ASIILAVRVD 105
 RESULT 23
 AAM00770
 ID AAM00770 standard; protein; 279 AA.
 XX
 XX AAM00770;
 AC
 XX 20-NOV-1996 (first entry)
 DT
 XX Thermiltase T217G + S222E.
 DE
 XX Thermiltase; hydrolysis; enzyme; protease; Bacillus thermiltase; hygiene;
 KW subtilisin; cleaning composition; proteinaceous stain removal;
 KW hard surface cleaning; dishwashing composition; oral cleaning;
 KW denture cleaning; contact lens cleaning; fabric cleaner.
 XX Synthetic.
 OS
 XX
 XX Key Location/Qualifiers
 FT Region 66..73
 FT /note= "loop 1"
 FT Region 103..115
 FT /note= "loop 2"
 FT Region 134..141
 FT /note= "loop 3"
 FT Region 162..171
 FT /note= "loop 4"
 FT Region 191..195
 FT /note= "loop 5"
 FT Region 204..224
 FT /note= "loop 6"
 FT Misc-difference 217
 FT /note= "T217G"
 FT Misc-difference 222
 FT /note= "S222E"
 FT
 XX WO9628558-A1.
 PN 19-SEP-1996.
 XX
 XX 06-MAR-1996; 96WO-US003009.
 XX
 XX 09-MAR-1995; 95US-00401573.
 XX
 XX (PROC) PROCTER & GAMBLE CO.
 PA
 XX Brode PF, Barnett BL, Rubingh DN;
 PI
 XX WPI; 1996-433830/43.
 DR
 XX New thermiltase variants, partic. for cleaning compns. - having amino
 PT acid substns. to provide decreased adsorption to and increased hydrolysis
 PT of bound substrates.
 PT
 XX Example 13; Page ?; 159pp; English.
 PS
 XX AAM00766-W00803 represent thermiltase variants of the invention.
 CC Thermiltase is a protease. These sequences are based on the wild type
 CC Bacillus thermiltase subtilisin sequence, which is specified but not given
 CC in the specification (there are no sequences given in their entirety in
 CC the specification). The variant sequences have one or more substitutions
 CC in one or more of the six loop regions of the thermiltase sequence. The
 CC loop regions play a significant role in the adsorption of the enzyme
 CC molecule to a surface-bound peptide. The amino acids of the loop regions,
 CC make contact with any surface to which the molecule is exposed. The
 CC proximity of the loop regions to the active site and binding pocket of
 CC the thermiltase in the catalytically productive adsorption of the enzyme
 CC to the surface bound molecule. Mutations in the loop regions will
 CC therefore have a significant effect on this adsorption. The thermiltase

CC variants can be used in cleaning compositions for proteinaceous stain removal. The variants can be used in hard surface cleaning compositions, dishwashing compositions, oral cleaning compositions, denture cleaning compositions, contact lens cleaning compositions, and fabric cleaners. CC These sequences have decreased adsorption to insoluble substrates, CC thereby increasing mobility and increasing hydrolysis of the substrates SQ Sequence 279 AA;

Query Match 68.0%; Score 34; DB 2; Length 279;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASIAARVLD 10
||| |||
96 ASILAVRLD 105

Db 96 ASILAVRLD 105

RESULT 24
AAW00775
ID AAW00775 standard; protein; 279 AA.
AC AAW00775;
XX 20-NOV-1996 (first entry)
DT Thermilase T195P.
XX Thermilase T195P.
XX Thermilase; hydrolysis; enzyme; protease; Bacillus thermilase; hygiene;
KW subtilisin; cleaning composition; proteinaceous stain removal;
KM hard surface cleaning; dishwashing composition; oral cleaning;
XX denture cleaning; contact lens cleaning; fabric cleaner.
XX Synthetic.

XX Key Location/Qualifiers
XX Region 66..73
FT /note= "loop 1"
FT 103..115
FT /note= "loop 2"
FT 134..141
FT /note= "loop 3"
FT 162..171
FT /note= "loop 4"
FT 191..195
FT /note= "loop 5"
FT Misc-difference 195
FT /note= "T195P"
FT 204..224
FT Region /note= "loop 6"
XX W09628558-A1.
XX 19-SEP-1996.
XX
XX PD
XX
XX PF 06-MAR-1996; 96WO-US003009.
XX
XX PR 09-MAR-1995; 95US-00401573.
XX (PROC) PROCTER & GAMBLE CO.
XX
XX PA Brode PF, Barnett BL, Rudinigh DN;
XX
XX PI WPI; 1996-433830/43.
XX
XX New thermilase variants, partic. for cleaning compns. - having amino
XX acid substs. to provide decreased adsorption to and increased hydrolysis
XX of bound substrates.
XX
XX Example 29; Page 7; 159pp; English.
XX
XX AAW00766-W00803 represent thermilase variants of the invention.
XX Thermilase is a protease. These sequences are based on the wild type

CC Bacillus thermilase subtilisin sequence, which is specified but not given in the specification (there are no sequences given in their entirety in the specification). The variant sequences have one or more substitutions in one or more of the six loop regions of the thermilase sequence. The CC loop regions play a significant role in the adsorption of the enzyme molecule to a surface-bound peptide. The amino acids of the loop regions, CC make contact with any surface to which the molecule is exposed. The CC proximity of the loop regions to the active site and binding pocket of the thermilase in the catalytically productive adsorption of the enzyme CC to the surface bound molecule. Mutations in the loop regions will therefore have a significant effect on this adsorption. The thermilase CC variants can be used in cleaning compositions for proteinaceous stain removal. The variants can be used in hard surface cleaning compositions, dishwashing compositions, oral cleaning compositions, denture cleaning compositions, contact lens cleaning compositions, and fabric cleaners. CC These sequences have decreased adsorption to insoluble substrates, CC thereby increasing mobility and increasing hydrolysis of the substrates SQ Sequence 279 AA;

Query Match 68.0%; Score 34; DB 2; Length 279;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASIAARVLD 10
||| |||
96 ASILAVRLD 105

Db 96 ASILAVRLD 105

RESULT 25
AAW00780
ID AAW00780 standard; protein; 279 AA.
AC AAW00780;
XX 20-NOV-1996 (first entry)
DT Thermilase Y213S, T217G, G223E.
XX Thermilase Y213S, T217G, G223E.
XX
XX Key Location/Qualifiers
XX Region 66..73
FT /note= "loop 1"
FT 103..115
FT /note= "loop 2"
FT 134..141
FT /note= "loop 3"
FT 162..171
FT /note= "loop 4"
FT 191..195
FT /note= "loop 5"
FT 204..224
FT Region /note= "loop 6"
FT Misc-difference 213
FT /note= "Y213S"
FT Misc-difference 217
FT /note= "T217G"
FT Misc-difference 223
FT /note= "G223E"
XX W09628558-A1.
XX 19-SEP-1996.
XX
XX PD
XX
XX PF 06-MAR-1996; 96WO-US003009.
XX
XX PR 09-MAR-1995; 95US-00401573.

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XX (PROC ) PROCTER & GAMBLE CO.
PA Brode PF, Barnett BL, Rubingh DN;
XX WPI; 1996-433830/43.
XX New thermaltase variants, partic. for cleaning compans. - having amino
PT acid substns. to provide decreased adsorption to and increased hydrolysis
PT of bound substrates.
XX
XX Example 37; Page 7; 159pp; English.
XX
XX AAM00766-W00803 represent thermaltase variants of the invention.
CC Thermaltase is a protease. These sequences are based on the wild type
CC Bacillus thermaltase subtilisin sequence, which is specified but not given
CC in the specification (there are no sequences given in their entirety in
CC the specification). The variant sequences have one or more substitutions
CC in one or more of the six loop regions of the thermaltase sequence. The
CC loop regions play a significant role in the adsorption of the enzyme
CC molecule to a surface-bound peptide. The amino acids of the loop regions,
CC make contact with any surface to which the molecule is exposed. The
CC proximity of the loop regions to the active site and binding pocket of
CC the thermaltase in the catalytically productive adsorption of the enzyme
CC to the surface bound molecule. Mutations in the loop regions will
CC therefore have a significant effect on this adsorption. The thermaltase
CC variants can be used in cleaning compositions for proteinaceous stain
CC removal. The variants can be used in hard surface cleaning compositions,
CC dishwashing compositions, oral cleaning compositions, denture cleaning
CC compositions, contact lens cleaning compositions, and fabric cleaners.
CC These sequences have decreased adsorption to insoluble substrates,
CC thereby increasing mobility and increasing hydrolysis of the substrates
XX
SQ Sequence 279 AA;
XX
XX Query Match 68.0%; Score 34; DB 2; Length 279;
XX Best Local Similarity 80.0%; Pred. No. 1.7e+02;
XX Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1 ASIAAARVLD 10
XX |||||
XX 96 ASIAAARVLD 105
XX
XX RESULT 26
XX AAM00783 ID AAM00783 standard; protein; 279 AA.
XX
XX AC AAM00783;
XX
XX DT 20-NOV-1996 (first entry)
XX
XX DE Thermaltase N66S, S70E, G72N.
XX
XX KM Thermaltase; hydrolysis; enzyme; protease; Bacillus thermaltase; hygiene;
XX subtilisin; cleaning composition; proteinaceous stain removal;
XX hard surface cleaning; dishwashing composition; oral cleaning;
XX denture cleaning; contact lens cleaning; fabric cleaner.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX FH Region 66..73
XX FT /note= "loop 1"
XX FT Misc-difference 66
XX FT /note= "specified as N66S, but the mutation should
XX FT actually be Q66S, as elsewhere in the specification
XX FT residue 66 is specified as Q"
XX FT Misc-difference 70
XX FT /note= "specified as S70E, but the mutation should
XX FT actually be G70E, as elsewhere in the specification
XX FT residue 70 is specified as G"
XX FT Misc-difference 72

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FT FT /note= "G72N"
FT FT 103..115
FT FT /note= "loop 2"
FT FT Region 134..141
FT FT /note= "loop 3"
FT FT Region 162..171
FT FT /note= "loop 4"
FT FT Region 191..195
FT FT /note= "loop 5"
FT FT Region 204..224
FT FT /note= "loop 6"
XX
XX W09628558-A1.
XX
XX PD 19-SEP-1996.
XX
XX PD 06-MAR-1996; 96WO-US003009.
XX
XX PR 09-MAR-1995; 95US-00401573.
XX
XX (PROC ) PROCTER & GAMBLE CO.
XX
XX PI Brode PF, Barnett BL, Rubingh DN;
XX WPI; 1996-433830/43.
XX
XX DR New thermaltase variants, partic. for cleaning compans. - having amino
XX PT acid substns. to provide decreased adsorption to and increased hydrolysis
XX PT of bound substrates.
XX
XX PS Example 45; Page 7; 159pp; English.
XX
XX CC AAM00766-W00803 represent thermaltase variants of the invention.
XX CC Thermaltase is a protease. These sequences are based on the wild type
XX CC Bacillus thermaltase subtilisin sequence, which is specified but not given
XX CC in the specification (there are no sequences given in their entirety in
XX CC the specification). The variant sequences have one or more substitutions
XX CC in one or more of the six loop regions of the thermaltase sequence. The
XX CC loop regions play a significant role in the adsorption of the enzyme
XX CC molecule to a surface-bound peptide. The amino acids of the loop regions,
XX CC make contact with any surface to which the molecule is exposed. The
XX CC proximity of the loop regions to the active site and binding pocket of
XX CC the thermaltase in the catalytically productive adsorption of the enzyme
XX CC to the surface bound molecule. Mutations in the loop regions will
XX CC therefore have a significant effect on this adsorption. The thermaltase
XX CC variants can be used in cleaning compositions for proteinaceous stain
XX CC removal. The variants can be used in hard surface cleaning compositions,
XX CC dishwashing compositions, oral cleaning compositions, denture cleaning,
XX CC compositions, contact lens cleaning compositions, and fabric cleaners.
XX CC These sequences have decreased adsorption to insoluble substrates,
XX CC thereby increasing mobility and increasing hydrolysis of the substrates
XX
XX SQ Sequence 279 AA;
XX
XX XX Query Match 68.0%; Score 34; DB 2; Length 279;
XX XX Best Local Similarity 80.0%; Pred. No. 1.7e+02;
XX XX Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX XX 1 ASIAAARVLD 10
XX XX |||||
XX XX 96 ASIAAARVLD 105
XX
XX XX RESULT 27
XX XX AAM00792 ID AAM00792 standard; protein; 279 AA.
XX XX
XX XX AC AAM00792;
XX XX
XX XX DT 20-NOV-1996 (first entry)
XX XX
XX XX DE Thermaltase I209A, A219P.
XX

```


CC variants can be used in cleaning compositions for proteinaceous stain removal. The variants can be used in hard surface cleaning compositions, CC dishwashing compositions, oral cleaning compositions, denture cleaning compositions, contact lens cleaning compositions, and fabric cleaners. CC These sequences have decreased adsorption to insoluble substrates. CC thereby increasing mobility and increasing hydrolysis of the substrates

XX Sequence 279 AA;

Query Match 68.0%; Score 34; DB 2; Length 279;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAPARVLD 10
||| |||
96 ASIAPARVLD 105

Db 96 ASIAPARVLD 105

RESULT 29
AAW00784 standard; protein; 279 AA.

XX AAW00784;
AC AAW00784;
DT 20-NOV-1996 (first entry)
XX Thermolase S109E, T113G.
XX Thermolase; hydrolysis; enzyme; protease; Bacillus thermolase; hygiene;
KM subtilisin; cleaning composition; proteinaceous stain removal;
KW hard surface cleaning; dishwashing composition; oral cleaning;
KM denture cleaning; contact lens cleaning; fabric cleaner.
XX Synthetic.
OS Synthetic.
XX Key Location/Qualifiers
FH Region 66..73
FT /note= "loop 1"
FT 103..115
FT /note= "loop 2"
FT Misc-difference 109
FT /note= "S109E"
FT Misc-difference 113
FT /note= "T113G"
FT Region 134..141
FT /note= "loop 3"
FT Region 162..171
FT /note= "loop 4"
FT Region 191..195
FT /note= "loop 5"
FT Region 204..224
FT /note= "loop 6"
XX W09628558-A1.
XX 19-SEP-1996.
XX 06-MAR-1996; 96WO-US003009.
XX 09-MAR-1995; 95US-00401573.
XX (PROC) PROCTER & GAMBLE CO.
XX Brode PF, Barnett BL, Rubingh DN;
XX WPI; 1996-433830/43.
XX New thermolase variants, partic. for cleaning compns. - having amino
PT acid subens. to provide decreased adsorption to and increased hydrolysis
XX of bound substrates.
PS Example 46; Page 7; 159pp; English.
XX

CC AAW00766-W00803 represent thermolase variants of the invention.
CC Thermolase is a protease. These sequences are based on the wild type
CC Bacillus thermolase subtilisin sequence, which is specified but not given
CC in the specification (there are no sequences given in their entirety in
CC the specification). The variant sequences have one or more substitutions
CC in one or more of the six loop regions of the thermolase sequence. The
CC loop regions play a significant role in the adsorption of the enzyme
CC molecule to a surface-bound peptide. The amino acids of the loop regions,
CC make contact with any surface to which the molecule is exposed. The
CC proximity of the loop regions to the active site and binding pocket of
CC the thermolase in the catalytically productive adsorption of the enzyme
CC to the surface bound molecule. Mutations in the loop regions will
CC therefore have a significant effect on this adsorption. The thermolase
CC variants can be used in cleaning compositions for proteinaceous stain
CC removal. The variants can be used in hard surface cleaning compositions,
CC dishwashing compositions, oral cleaning compositions, denture cleaning
CC compositions, contact lens cleaning compositions, and fabric cleaners.
CC These sequences have decreased adsorption to insoluble substrates.
CC thereby increasing mobility and increasing hydrolysis of the substrates

XX Sequence 279 AA;

Query Match 68.0%; Score 34; DB 2; Length 279;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAPARVLD 10
||| |||
96 ASIAPARVLD 105

Db 96 ASIAPARVLD 105

RESULT 30
AAW00793 standard; protein; 279 AA.

XX AAW00793;
AC AAW00793;
DT 20-NOV-1996 (first entry)
XX Thermolase L216N.
XX Thermolase; hydrolysis; enzyme; protease; Bacillus thermolase; hygiene;
KM subtilisin; cleaning composition; proteinaceous stain removal;
KW hard surface cleaning; dishwashing composition; oral cleaning;
KM denture cleaning; contact lens cleaning; fabric cleaner.
XX Synthetic.
OS Synthetic.
XX Key Location/Qualifiers
FH Region 66..73
FT /note= "loop 1"
FT 103..115
FT /note= "loop 2"
FT Region 134..141
FT /note= "loop 3"
FT Region 162..171
FT /note= "loop 4"
FT Region 191..195
FT /note= "loop 5"
FT Region 204..224
FT /note= "loop 6"
XX Misc-difference 216
FT /note= "specified as L216E, but the mutation should
FT actually be S216E, as elsewhere in the specification
FT residue 216 is specified as S"
XX W09628558-A1.
XX 19-SEP-1996.
XX 06-MAR-1996; 96WO-US003009.
XX 09-MAR-1995; 95US-00401573.
XX

XX (PROC) PROCTER & GAMBLE CO.
 PA Brode PF, Barnett BL, Rubingh DN;
 PI WPI; 1996-433830/43.
 XX
 DR New thermaltase variants, partic. for cleaning compns. - having amino
 PT acid substns. to provide decreased adsorption to and increased hydrolysis
 PT of bound substrates.
 XX
 PS Example 60; Page 7; 159pp; English.
 PS
 CC AAM00766-W00803 represent thermaltase variants of the invention.
 CC Thermaltase is a protease. These sequences are based on the wild type
 CC Bacillus thermaltase subtilisin sequence, which is specified but not given
 CC in the specification (there are no sequences given in their entirety in
 CC the specification). The variant sequences have one or more substitutions
 CC in one or more of the six loop regions of the thermaltase sequence. The
 CC loop regions play a significant role in the adsorption of the enzyme
 CC molecule to a surface-bound peptide. The amino acids of the loop regions,
 CC make contact with any surface to which the molecule is exposed. The
 CC proximity of the loop regions to the active site and binding pocket of
 CC the thermaltase in the catalytically productive adsorption of the enzyme
 CC to the surface bound molecule. Mutations in the loop regions will
 CC therefore have a significant effect on this adsorption. The thermaltase
 CC variants can be used in cleaning compositions for proteinaceous stain
 CC removal. The variants can be used in hard surface cleaning compositions,
 CC dishwashing compositions, oral cleaning compositions, denture cleaning
 CC compositions, contact lens cleaning compositions, and fabric cleaners.
 CC These sequences have decreased adsorption to insoluble substrates,
 CC thereby increasing mobility and increasing hydrolysis of the substrates
 XX
 SQ Sequence 279 AA;
 SQ
 Query Match 68.0%; Score 34; DB 2; Length 279;
 Best Local Similarity 80.0%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ASIAARVLD 10
 Db 96 ASIAARVLD 105
 Db
 RESULT 31
 AAM00796
 ID AAM00796 standard; protein; 279 AA.
 XX
 AC AAM00796;
 XX
 DT 20-NOV-1996 (first entry)
 XX
 DE Thermaltase S109E.
 XX
 KW Thermaltase; hydrolysis; enzyme; protease; Bacillus thermaltase; hygiene;
 KW subtilisin; cleaning composition; proteinaceous stain removal;
 KW hard surface cleaning; dishwashing composition; oral cleaning;
 KW denture cleaning; contact lens cleaning; fabric cleaner.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Region 66..73
 FT /note= "loop 1"
 FT Region 103..115
 FT /note= "loop 2"
 FT Misc-difference 109
 FT /note= "S109E"
 FT Region 134..141
 FT /note= "loop 3"
 FT Region 162..171
 FT /note= "loop 4"
 FT Region 191..195
 FT

FT /note= "loop 5"
 FT Region 204..224
 FT /note= "loop 6"
 XX
 XX W09628558-AI.
 XX
 XX 19-SEP-1996.
 XX
 XX PD
 XX 06-MAR-1996; 96WO-US003009.
 XX
 XX PR 09-MAR-1995; 95US-00401573.
 XX
 PA (PROC) PROCTER & GAMBLE CO.
 PI Brode PF, Barnett BL, Rubingh DN;
 XX
 DR WPI; 1996-433830/43.
 XX
 CC New thermaltase variants, partic. for cleaning compns. - having amino
 CC acid substns. to provide decreased adsorption to and increased hydrolysis
 CC of bound substrates.
 CC
 PS Example 67; Page 7; 159pp; English.
 PS
 CC AAM00766-W00803 represent thermaltase variants of the invention.
 CC Thermaltase is a protease. These sequences are based on the wild type
 CC Bacillus thermaltase subtilisin sequence, which is specified but not given
 CC in the specification (there are no sequences given in their entirety in
 CC the specification). The variant sequences have one or more substitutions
 CC in one or more of the six loop regions of the thermaltase sequence. The
 CC loop regions play a significant role in the adsorption of the enzyme
 CC molecule to a surface-bound peptide. The amino acids of the loop regions,
 CC make contact with any surface to which the molecule is exposed. The
 CC proximity of the loop regions to the active site and binding pocket of
 CC the thermaltase in the catalytically productive adsorption of the enzyme
 CC to the surface bound molecule. Mutations in the loop regions will
 CC therefore have a significant effect on this adsorption. The thermaltase
 CC variants can be used in cleaning compositions for proteinaceous stain
 CC removal. The variants can be used in hard surface cleaning compositions,
 CC dishwashing compositions, oral cleaning compositions, denture cleaning
 CC compositions, contact lens cleaning compositions, and fabric cleaners.
 CC These sequences have decreased adsorption to insoluble substrates,
 CC thereby increasing mobility and increasing hydrolysis of the substrates
 XX
 SQ Sequence 279 AA;
 SQ
 Query Match 68.0%; Score 34; DB 2; Length 279;
 Best Local Similarity 80.0%; Pred. No. 1.7e+02;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ASIAARVLD 10
 Db 96 ASIAARVLD 105
 Db
 RESULT 32
 AAM00794
 ID AAM00794 standard; protein; 279 AA.
 XX
 AC AAM00794;
 XX
 DT 20-NOV-1996 (first entry)
 XX
 DE Thermaltase W112C, T217G.
 XX
 KW Thermaltase; hydrolysis; enzyme; protease; Bacillus thermaltase; hygiene;
 KW subtilisin; cleaning composition; proteinaceous stain removal;
 KW hard surface cleaning; dishwashing composition; oral cleaning;
 KW denture cleaning; contact lens cleaning; fabric cleaner.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Region 66..73
 FT /note= "loop 1"
 FT Region 103..115
 FT /note= "loop 2"
 FT Misc-difference 109
 FT /note= "S109E"
 FT Region 134..141
 FT /note= "loop 3"
 FT Region 162..171
 FT /note= "loop 4"
 FT Region 191..195
 FT

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FT Region 66. .73
FT /note= "loop 1"
FT 103. .115
FT Region
FT /note= "loop 2"
FT Misc-difference 112
FT /note= "W112C"
FT Region 134. .141
FT /note= "loop 3"
FT Region 162. .171
FT /note= "loop 4"
FT Region 191. .195
FT /note= "loop 5"
FT Region 204. .224
FT /note= "loop 6"
FT Misc-difference 217
FT /note= "T217G"
FT
FT W09628558-A1.
FT
FT 19-SEP-1996.
FT
FT 06-MAR-1996; 96WO-US003009.
FT
FT 09-MAR-1995; 95US-00401573.
FT
FT (PROC ) PROCTER & GAMBLE CO.
FT
FT Brode PF, Barnett BL, Rubingh DN;
FT
FT WPI, 1996-433030/43.
FT
FT New thermitase variants, partic. for cleaning compans. - having amino
PT acid substns. to provide decreased adsorption to and increased hydrolysis
PT of bound substrates.
XX
XX Example 63, Page 7; 159pp; English.
XX
XX AAM0076-W00803 represent thermitase variants of the invention.
CC Thermitase is a procase. These sequences are based on the wild type
CC Bacillus thermatase subtilisin sequence, which is specified but not given
CC in the specification (there are no sequences given in their entirety in
CC the specification). The variant sequences have one or more substitutions
CC in one or more of the six loop regions of the thermitase sequence. The
CC loop regions play a significant role in the adsorption of the enzyme
CC molecule to a surface-bound peptide. The amino acids of the loop regions,
CC make contact with any surface to which the molecule is exposed. The
CC proximity of the loop regions to the active site and binding pocket of
CC the thermitase in the catalytically productive adsorption of the enzyme
CC to the surface bound molecule. Mutations in the loop regions will
CC therefore have a significant effect on this adsorption. The thermitase
CC variants can be used in cleaning compositions for proteinaceous stain
CC removal. The variants can be used in hard surface cleaning compositions,
CC dishwashing compositions, oral cleaning compositions, denture cleaning
CC compositions, contract lens cleaning compositions, and fabric cleaners.
CC These sequences have decreased adsorption to insoluble substrates,
CC thereby increasing mobility and increasing hydrolysis of the substrates
CC
XX Sequence 279 AA;
SQ
Query Match 68.0%; Score 34; DB 2; Length 279;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0
OY 1 ASIAARVTD 10
DB 96 ASIILAVRVD 105

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XX	20-NOV-1996	(first entry)
DT		
XX		
XX	Thermilase W208F, Y213M, T215P, S220E, T224G.	
DE		
XX		
KW	Thermilase: hydrolysis; enzyme: protease; Bacillus thermilase: hygiene;	
KW	subtilisin; cleaning composition; protease: stain removal;	
KW	hard surface cleaning; dishwashing composition; oral cleaning;	
KW	denture cleaning; contact lens cleaning; fabric cleaner.	
XX		
OS	Synthetic.	
XX		
PH	Key	Location/Qualifiers
FT	Region	66..73
FT		/note= "loop 1"
FT	Region	103..115
FT		/note= "loop 2"
FT	Region	134..141
FT		/note= "loop 3"
FT	Region	162..171
FT		/note= "loop 4"
FT	Region	191..195
FT		/note= "loop 5"
FT	Region	204..224
FT		/note= "loop 6"
FT	Misc-difference	208
FT		/note= "W208F"
FT	Misc-difference	213
FT		/note= "Y213M"
FT	Misc-difference	215
FT		/note= "T215P"
FT	Misc-difference	220
FT		/note= "S220E"
FT	Misc-difference	224
FT		/note= "T224G"
XX		
EN	W09628558-A1.	
XX		
PD	19-SEP-1996.	
XX		
PE	06-MAR-1996;	96WO-US003009.
XX		
XX	09-MAR-1995;	95US-00401573.
PR		
XX	(PROC) PROCTER & GAMBLE CO.	
PA		
PI	Brode PF, Barnett BL, Rudin DN;	
XX		
DR	WPI; 1996-433830/43.	
XX		
XX	New thermilase variants, partic. for cleaning compns. - having amino	
PT	acid substns. to provide decreased adsorption to and increased hydrolysis	
PT	of bound substrates.	
XX		
PS	Example 29; Page 7; 159pp; English.	
XX		
XX	AAW00766-000803 represent thermilase variants of the invention.	
CC	Thermilase is a protease. These sequences are based on the wild type	
CC	Bacillus thermilase subtilisin sequence, which is specified but not given	
CC	in the specification) (there are no sequences given in their entirety in	
CC	the specification) . The variant sequences have one or more substitutions	
CC	in one or more of the six loop regions of the thermilase sequence. The	
CC	loop regions play a significant role in the adsorption of the enzyme	
CC	molecule to a surface-bound peptide. The amino acids of the loop regions,	
CC	make contact with any surface to which the molecule is exposed. The	
CC	proximity of the loop regions to the active site and binding pocket of	
CC	the thermilase in the catalytically productive adsorption of the enzyme	
CC	to the surface bound molecule. Mutations in the loop regions will	
CC	therefore have a significant effect on this adsorption. The thermilase	
CC	variants can be used in cleaning compositions for proteaceous stain	
CC	removal. The variants can be used in hard surface cleaning compositions,	
CC	dishwashing compositions, oral cleaning compositions, denture cleaning	
CC	compositions, contact lens cleaning compositions, and fabric cleaners.	
CC		

CC These sequences have decreased adsorption to insoluble substrates,
CC thereby increasing mobility and increasing hydrolysis of the substrates
XX
SQ Sequence 279 AA;

Query Match 68.0%; Score 34; DB 2; Length 279;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ASIAARVLD 10
||| |||
Db 96 ASIAARVLD 105

RESULT 34
AAW00785
ID AAW00785 standard; protein; 279 AA.

XX AAW00785;

XX 20-NOV-1996 (first entry)

XX Thermittase G135Q, V138D, G139S.

XX Thermittase; hydrolysis; enzyme; protease; Bacillus thermittase; hygiene;
KW subtilisin; cleaning composition; proteinaceous stain removal;
KW hard surface cleaning; dishwashing composition; oral cleaning;
KW denture cleaning; contact lens cleaning; fabric cleaner.

XX Synthetic.

XX Key Location/Qualifiers

FT Region 66..73

FT Region /note= "loop 1"

FT Region 103..115

FT Region /note= "loop 2"

FT Region 134..141

FT Region /note= "loop 3"

FT Misc-difference 135

FT Misc-difference 138 /note= "G135Q"

FT Misc-difference 139 /note= "V138D"

FT Misc-difference 139 /note= "G139S"

FT Region 162..171

FT Region /note= "loop 4"

FT Region 191..195

FT Region /note= "loop 5"

FT Region 204..224

FT Region /note= "loop 6"

XX W09628558-A1.

XX 19-SEP-1996.

XX 06-MAR-1996; 96WO-US003009.

XX 09-MAR-1995; 95US-00401573.

XX (PROC) PROCTER & GAMBLE CO.

XX Brode PF, Barnett BL, Rubingh DN;

XX WPI; 1996-433830/43.

XX New thermittase variants, partic. for cleaning compns. - having amino
PT acid substns. to provide decreased adsorption to and increased hydrolysis
PT of bound substrates.

XX Example 47; Page 7; 159pp; English.

XX AAW00766-W00803 represent thermittase variants of the invention.

CC Thermittase is a protease. These sequences are based on the wild type

CC Bacillus thermittase subtilisin sequence, which is specified but not given
CC in the specification (there are no sequences given in their entirety in
CC the specification). The variant sequences have one or more substitutions
CC in one or more of the six loop regions of the thermittase sequence. The
CC loop regions play a significant role in the adsorption of the enzyme
CC molecule to a surface-bound peptide. The amino acids of the loop regions,
CC make contact with any surface to which the molecule is exposed. The
CC proximity of the loop regions to the active site and binding pocket of
CC the thermittase in the catalytically productive adsorption of the enzyme
CC to the surface bound molecule. Mutations in the loop regions will
CC therefore have a significant effect on this adsorption. The thermittase
CC variants can be used in cleaning compositions for proteinaceous stain
CC removal. The variants can be used in hard surface cleaning compositions,
CC dishwashing compositions, oral cleaning compositions, denture cleaning
CC compositions, contact lens cleaning compositions, and fabric cleaners.
CC These sequences have decreased adsorption to insoluble substrates,
CC thereby increasing mobility and increasing hydrolysis of the substrates

XX Sequence 279 AA;

Query Match 68.0%; Score 34; DB 2; Length 279;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ASIAARVLD 10
||| |||
Db 96 ASIAARVLD 105

RESULT 35

AAW00787
ID AAW00787 standard; protein; 279 AA.

XX AAW00787;

XX 20-NOV-1996 (first entry)

XX Thermittase S191E, S192D, F193D, T195P.

XX Thermittase; hydrolysis; enzyme; protease; Bacillus thermittase; hygiene;
KW subtilisin; cleaning composition; proteinaceous stain removal;
KW hard surface cleaning; dishwashing composition; oral cleaning;
KW denture cleaning; contact lens cleaning; fabric cleaner.

XX Synthetic.

XX Key Location/Qualifiers

FT Region 66..73

FT Region /note= "loop 1"

FT Region 103..115

FT Region /note= "loop 2"

FT Region 134..141

FT Region /note= "loop 3"

FT Region 162..171

FT Region /note= "loop 4"

FT Region 191..195

FT Region /note= "loop 5"

FT Misc-difference 191 /note= "S191E"

FT Misc-difference 192 /note= "S192D"

FT Misc-difference 193 /note= "F193D"

FT Misc-difference 195 /note= "T195P"

FT Region 204..224

FT Region /note= "loop 6"

XX W09628558-A1.

XX 19-SEP-1996.

XX 06-MAR-1996; 96WO-US003009.

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XX 09-MAR-1995; 95US-00401573.
PR (PROC ) PROCTER & GAMBLE CO.
XX Brode PF, Barnett BL, Rubingh DN;
XX WPI, 1996-433830/43.
XX
XX New thermatase variants, partic. for cleaning compns. - having amino
XX acid substsns. to provide decreased adsorption to and increased hydrolysis
XX of bound substrates.
XX
XX Example 48; Page 7; 159pp; English.
XX
XX AAM00766-W00803 represent thermatase variants of the invention.
XX Thermatase is a protease. These sequences are based on the wild type
XX Bacillus thermatase subtilisin sequence, which is specified but not given
XX in the specification (there are no sequences given in their entirety in
XX the specification). The variant sequences have one or more substitutions
XX in one or more of the six loop regions of the thermatase sequence. The
XX loop regions play a significant role in the adsorption of the enzyme
XX molecule to a surface-bound peptide. The amino acids of the loop regions,
XX make contact with any surface to which the molecule is exposed. The
XX proximity of the loop regions to the active site and binding pocket of
XX the thermatase in the catalytically productive adsorption of the enzyme
XX to the surface bound molecule. Mutations in the loop regions will
XX therefore have a significant effect on this adsorption. The thermatase
XX variants can be used in cleaning compositions for proteinaceous stain
XX removal. The variants can be used in hard surface cleaning compositions,
XX dishwashing compositions, oral cleaning compositions, denture cleaning
XX compositions, contact lens cleaning compositions, and fabric cleaners.
XX These sequences have decreased adsorption to insoluble substrates,
XX thereby increasing mobility and increasing hydrolysis of the substrates
XX
XX Sequence 279 AA;
XX
XX Query March 68.0%; Score 34; DB 2; Length 279;
XX Best Local Similarity 80.0%; Pred. No. 1.7e+02;
XX Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1 ASIAAARVLD 10
XX 96 ASIILAVRLD 105
XX
XX RESULT 36
XX AAM00789 standard; protein; 279 AA.
XX
XX AAM00789;
XX
XX 20-NOV-1996 (first entry)
XX
XX Thermatase N68D, V138D, A164G, A168E, T217G.
XX
XX Thermatase; hydrolysis; enzyme; protease; Bacillus thermatase; hygiene;
XX subtilisin; cleaning composition; proteinaceous stain removal;
XX hard surface cleaning; dishwashing composition; oral cleaning;
XX denture cleaning; contact lens cleaning; fabric cleaner.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Region 66..73
XX /note= "loop 1"
XX
XX Misc-difference 68
XX /note= "specified as N68D, but the mutation should
XX actually be G68D, as elsewhere in the specification
XX residue 68 is specified as G"
XX 103..115
XX /note= "loop 2"
XX 134..141
XX Region
XX

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FT /note= "loop 3"
FT Misc-difference 138
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FT Region 162..171
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FT /note= "A168E"
FT Region 191..195
FT /note= "loop 5"
FT Region 204..224
FT /note= "loop 6"
FT Misc-difference 217
FT /note= "T217G"
FT
XX
XX W09628558-A1.
XX
XX 19-SEP-1996.
XX
XX 06-MAR-1996; 96WO-US003009.
XX
XX 09-MAR-1995; 95US-00401573.
XX
XX (PROC ) PROCTER & GAMBLE CO.
XX
XX Brode PF, Barnett BL, Rubingh DN;
XX WPI, 1996-433830/43.
XX
XX New thermatase variants, partic. for cleaning compns. - having amino
XX acid substsns. to provide decreased adsorption to and increased hydrolysis
XX of bound substrates.
XX
XX Example 53; Page 7; 159pp; English.
XX
XX AAM00766-W00803 represent thermatase variants of the invention.
XX Thermatase is a protease. These sequences are based on the wild type
XX Bacillus thermatase subtilisin sequence, which is specified but not given
XX in the specification (there are no sequences given in their entirety in
XX the specification). The variant sequences have one or more substitutions
XX in one or more of the six loop regions of the thermatase sequence. The
XX loop regions play a significant role in the adsorption of the enzyme
XX molecule to a surface-bound peptide. The amino acids of the loop regions,
XX make contact with any surface to which the molecule is exposed. The
XX proximity of the loop regions to the active site and binding pocket of
XX the thermatase in the catalytically productive adsorption of the enzyme
XX to the surface bound molecule. Mutations in the loop regions will
XX therefore have a significant effect on this adsorption. The thermatase
XX variants can be used in cleaning compositions for proteinaceous stain
XX removal. The variants can be used in hard surface cleaning compositions,
XX dishwashing compositions, oral cleaning compositions, denture cleaning
XX compositions, contact lens cleaning compositions, and fabric cleaners.
XX These sequences have decreased adsorption to insoluble substrates,
XX thereby increasing mobility and increasing hydrolysis of the substrates
XX
XX Sequence 279 AA;
XX
XX Query March 68.0%; Score 34; DB 2; Length 279;
XX Best Local Similarity 80.0%; Pred. No. 1.7e+02;
XX Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1 ASIAAARVLD 10
XX 96 ASIILAVRLD 105
XX
XX RESULT 37
XX AAM00799 standard; protein; 279 AA.
XX
XX AAM00799;
XX

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DT 20-NOV-1996 (first entry)
 XX Thermiltase A164H, S220E.
 XX
 KW Thermiltase; hydrolysis; enzyme; protease; Bacillus thermiltase; hygiene;
 KW subtilisin; cleaning composition; proteinaceous stain removal;
 KW hard surface cleaning; dishwashing composition; oral cleaning;
 KW denture cleaning; contact lens cleaning; fabric cleaner.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FH Region 66..73
 FT /note= "loop 1"
 FT 103..115
 FT Region /note= "loop 2"
 FT 134..141
 FT Region /note= "loop 3"
 FT 162..171
 FT /note= "loop 4"
 FT Misc-difference 164
 FT /note= "A164H"
 FT Region 191..195
 FT /note= "loop 5"
 FT 204..224
 FT Region /note= "loop 6"
 FT Misc-difference 220
 FT /note= "S220E"
 XX
 XX WO9628558-A1.
 XX 19-SEP-1996.
 XX
 PD 06-MAR-1996; 96WO-US003009.
 XX
 XX 09-MAR-1995; 95US-00401573.
 XX
 XX (PROC) PROCTER & GAMBLE CO.
 XX
 PI Brode PF, Barnett BL, Rubingh DN;
 XX
 DR WPI; 1996-433830/43.
 XX
 PT New thermiltase variants, partic. for cleaning compns. - having amino
 PT acid substrs. to provide decreased adsorption to and increased hydrolysis
 PT of bound substrates.
 XX
 XX Example 75; Page ?; 159pp; English.
 XX
 CC AAM00766-W00803 represent thermiltase variants of the invention.
 CC Thermiltase is a protease. These sequences are based on the wild type
 CC Bacillus thermiltase subtilisin sequence, which is specified but not given
 CC in the specification (there are no sequences given in their entirety in
 CC the specification). The variant sequences have one or more substitutions
 CC in one or more of the six loop regions of the thermiltase sequence. The
 CC loop regions play a significant role in the adsorption of the enzyme
 CC molecule to a surface-bound peptide. The amino acids of the loop regions,
 CC make contact with any surface to which the molecule is exposed. The
 CC proximity of the loop regions to the active site and binding pocket of
 CC the thermiltase in the catalytically productive adsorption of the enzyme
 CC to the surface bound molecule. Mutations in the loop regions will
 CC therefore have a significant effect on this adsorption. The thermiltase
 CC variants can be used in cleaning compositions for proteinaceous stain
 CC removal. The variants can be used in hard surface cleaning compositions,
 CC dishwashing compositions, oral cleaning compositions, denture cleaning
 CC compositions, contact lens cleaning compositions, and fabric cleaners.
 CC These sequences have decreased adsorption to insoluble substrates,
 CC thereby increasing mobility and increasing hydrolysis of the substrates
 CC
 XX Sequence 279 AA;
 SQ
 Query Match 68.0%; Score 34; DB 2; Length 279;
 Best Local Similarity 80.0%; Pred. No. 1.7e+02;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 1 ASIAARVLD 10
 ||| |||
 Db 96 ASIIVARVLD 105
 RESULT 38
 AAM00803
 ID AAM00803 standard; protein; 279 AA.
 XX
 AC AAM00803;
 DT 20-NOV-1996 (first entry)
 XX
 DE Thermiltase L221Q.
 XX
 KW Thermiltase; hydrolysis; enzyme; protease; Bacillus thermiltase; hygiene;
 KW subtilisin; cleaning composition; proteinaceous stain removal;
 KW hard surface cleaning; dishwashing composition; oral cleaning;
 KW denture cleaning; contact lens cleaning; fabric cleaner.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FH Region 66..73
 FT /note= "loop 1"
 FT 103..115
 FT Region /note= "loop 2"
 FT 134..141
 FT Region /note= "loop 3"
 FT 162..171
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 FT Region 191..195
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 FT 204..224
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 XX WO9628558-A1.
 XX 19-SEP-1996.
 XX
 PD 06-MAR-1996; 96WO-US003009.
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 XX 09-MAR-1995; 95US-00401573.
 XX
 XX (PROC) PROCTER & GAMBLE CO.
 XX
 PI Brode PF, Barnett BL, Rubingh DN;
 XX
 DR WPI; 1996-433830/43.
 XX
 PT New thermiltase variants, partic. for cleaning compns. - having amino
 PT acid substrs. to provide decreased adsorption to and increased hydrolysis
 PT of bound substrates.
 XX
 XX Example 91; Page ?; 159pp; English.
 XX
 CC AAM00766-W00803 represent thermiltase variants of the invention.
 CC Thermiltase is a protease. These sequences are based on the wild type
 CC Bacillus thermiltase subtilisin sequence, which is specified but not given
 CC in the specification (there are no sequences given in their entirety in
 CC the specification). The variant sequences have one or more substitutions
 CC in one or more of the six loop regions of the thermiltase sequence. The
 CC loop regions play a significant role in the adsorption of the enzyme
 CC molecule to a surface-bound peptide. The amino acids of the loop regions,
 CC make contact with any surface to which the molecule is exposed. The
 CC proximity of the loop regions to the active site and binding pocket of
 CC the thermiltase in the catalytically productive adsorption of the enzyme
 CC to the surface bound molecule. Mutations in the loop regions will
 CC therefore have a significant effect on this adsorption. The thermiltase

CC variants can be used in cleaning compositions for proteinaceous stain removal. The variants can be used in hard surface cleaning compositions, dishwashing compositions, oral cleaning compositions, denture cleaning compositions, contact lens cleaning compositions, and fabric cleaners. These sequences have decreased adsorption to insoluble substrates, thereby increasing mobility and increasing hydrolysis of the substrates

XX Sequence 279 AA;

Query Match 68.0%; Score 34; DB 2; Length 279;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAARVLD 10
DB 96 ASIAAVRVD 105

RESULT 39
AAW00767
ID AAW00767 standard; protein; 279 AA.
AC AAW00767;
XX 20-NOV-1996 (first entry)
DT Thermaltase Q66N.
XX Thermaltase; hydrolysis; enzyme; protease; Bacillus thermaltase; hygiene;
KM subtilisin; cleaning composition; proteinaceous stain removal;
KW hard surface cleaning; dishwashing composition; oral cleaning;
KW denture cleaning; contact lens cleaning; fabric cleaner.
XX Synthetic.
OS
XX
FH Key Location/Qualifiers
FT 66..73
FT /note= "loop 1"
FT Misc-difference 66
FT /note= "Q66N"
FT 103..115
FT /note= "loop 2"
FT 134..141
FT /note= "loop 3"
FT 162..171
FT /note= "loop 4"
FT 191..195
FT /note= "loop 5"
FT 204..224
FT /note= "loop 6"
XX
XX W09628558-A1.
XX 19-SEP-1996.
XX
XX 06-MAR-1996; 96WO-US003009.
XX
XX 09-MAR-1995; 95US-00401573.
XX
XX (PROC) PROCTER & GAMBLE CO.
XX
XX Brode PF, Barnett BL, Rubingh DN;
XX
XX WPI; 1996-433830/43.
XX
XX New thermaltase variants, partic. for cleaning compns. - having amino
PT acid subunits, to provide decreased adsorption to and increased hydrolysis
PT of bound substrates.
XX
XX Example 7; Page 7; 159pp; English.
XX
XX AAW00766-W00803 represent thermaltase variants of the invention.
CC Thermaltase is a protease. These sequences are based on the wild type

CC Bacillus thermaltase subtilisin sequence, which is specified but not given in the specification (there are no sequences given in their entirety in the specification). The variant sequences have one or more substitutions in one or more of the six loop regions of the thermaltase sequence. The loop regions play a significant role in the adsorption of the enzyme molecule to a surface-bound peptide. The amino acids of the loop regions, make contact with any surface to which the molecule is exposed. The proximity of the loop regions to the active site and binding pocket of the thermaltase in the catalytically productive adsorption of the enzyme to the surface bound molecule. Mutations in the loop regions will therefore have a significant effect on this adsorption. The thermaltase variants can be used in cleaning compositions for proteinaceous stain removal. The variants can be used in hard surface cleaning compositions, dishwashing compositions, oral cleaning compositions, denture cleaning compositions, contact lens cleaning compositions, and fabric cleaners. These sequences have decreased adsorption to insoluble substrates, thereby increasing mobility and increasing hydrolysis of the substrates

XX Sequence 279 AA;

Query Match 68.0%; Score 34; DB 2; Length 279;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAARVLD 10
DB 96 ASIAAVRVD 105

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ID AAW00771 standard; protein; 279 AA.
AC AAW00771;
XX 20-NOV-1996 (first entry)
DT Thermaltase G139N.
XX Thermaltase; hydrolysis; enzyme; protease; Bacillus thermaltase; hygiene;
KM subtilisin; cleaning composition; proteinaceous stain removal;
KW hard surface cleaning; dishwashing composition; oral cleaning;
KW denture cleaning; contact lens cleaning; fabric cleaner.
XX Synthetic.
OS
XX
FH Key Location/Qualifiers
FT 66..73
FT /note= "loop 1"
FT 103..115
FT /note= "loop 2"
FT 134..141
FT /note= "loop 3"
FT Misc-difference 139
FT /note= "G139N"
FT 162..171
FT /note= "loop 4"
FT 191..195
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FT 204..224
FT /note= "loop 6"
XX
XX W09628558-A1.
XX 19-SEP-1996.
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XX 06-MAR-1996; 96WO-US003009.
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XX 09-MAR-1995; 95US-00401573.
XX
XX (PROC) PROCTER & GAMBLE CO.
XX
XX Brode PF, Barnett BL, Rubingh DN;

XX WPI; 1996-433830/43.

DR New thermilase variants, partic. for cleaning compsns. - having amino
XX acid suberns. to provide decreased adsorption to and increased hydrolysis
PT of bound substrates.

XX Example 19; Page ?; 159pp; English.

XX AAW00766-W00803 represent thermilase variants of the invention.
XX Thermilase is a protease. These sequences are based on the wild type
CC Bacillus thermilase subtilisin sequence, which is specified but not given
CC in the specification (there are no sequences given in their entirety in
CC the specification). The variant sequences have one or more substitutions
CC in one or more of the six loop regions of the thermilase sequence. The
CC loop regions play a significant role in the adsorption of the enzyme
CC molecule to a surface-bound peptide. The amino acids of the loop regions,
CC make contact with any surface to which the molecule is exposed. The
CC proximity of the loop regions to the active site and binding pocket of
CC the thermilase in the catalytically productive adsorption of the enzyme
CC to the surface bound molecule. Mutations in the loop regions will
CC therefore have a significant effect on this adsorption. The thermilase
CC variants can be used in cleaning compositions for proteinaceous stain
CC removal. The variants can be used in hard surface cleaning compositions,
CC dishwashing compositions, oral cleaning compositions, denture cleaning
CC compositions, contact lens cleaning compositions, and fabric cleaners.
CC These sequences have decreased adsorption to insoluble substrates,
CC thereby increasing mobility and increasing hydrolysis of the substrates
XX

XX Sequence 279 AA;

Query Match 68.0%; Score 34; DB 2; Length 279;

Best Local Similarity 80.0%; Pred. No. 1.7e+02;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ASIAARVLD 10

Db 96 ASILAVRVL 105

Search completed: March 31, 2005, 12:02:29
Job time : 86.25 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 31, 2005, 11:51:44 ; Search time 21.4844 Seconds
(without alignments)
38.220 Million cell updates/sec

Title: US-10-614-959-12
Perfect score: 50
Sequence: 1 ASIAARVLDY 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	46	92.0	11	4	US-09-383-667-19
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4	34	68.0	278	2	US-08-865-203-6
5	34	68.0	278	2	US-07-849-420-6
6	34	68.0	278	3	US-09-253-854-6
7	34	68.0	278	3	US-08-955-424-6
8	34	68.0	279	2	US-09-135-658-4
9	34	68.0	279	4	US-09-512-251A-6
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12	34	68.0	279	6	5472855-6
13	34	68.0	279	6	5472855-6
14	33	66.0	85	4	US-09-698-286A-10
15	33	66.0	194	4	US-09-710-279-622
16	33	66.0	223	3	US-09-134-001C-3417
17	33	66.0	331	4	US-09-248-786A-18164
18	33	66.0	364	4	US-09-488-039A-12051
19	33	66.0	402	4	US-09-602-787A-508
20	33	66.0	867	4	US-09-540-236-3193
21	33	66.0	914	4	US-09-902-540-16309
22	32	64.0	230	4	US-09-252-991A-17003
23	32	64.0	280	4	US-09-724-797-34
24	32	64.0	480	4	US-09-252-991A-31470
25	31	62.0	111	4	US-09-902-540-10906
26	31	62.0	177	3	US-08-975-762-38
27	31	62.0	177	3	US-08-975-762-55

28	31	62.0	177	3	US-08-821-324-38	Sequence 38, Appl
29	31	62.0	177	3	US-09-295-028-38	Sequence 38, Appl
30	31	62.0	177	3	US-09-295-028-55	Sequence 55, Appl
31	31	62.0	177	3	US-09-106-582-38	Sequence 38, Appl
32	31	62.0	177	3	US-09-106-582-55	Sequence 55, Appl
33	31	62.0	177	4	US-09-159-469-38	Sequence 38, Appl
34	31	62.0	177	4	US-09-159-469-38	Sequence 38, Appl
35	31	62.0	177	4	US-09-693-542-38	Sequence 38, Appl
36	31	62.0	243	4	US-09-693-542-55	Sequence 55, Appl
37	31	62.0	243	4	US-09-270-767-45191	Sequence 45191, A
38	31	62.0	264	3	US-09-066-046-321	Sequence 22, Appl
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45	31	62.0	555	4	US-09-489-039A-14332	Sequence 14332, A

ALIGNMENTS

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RESULT 1
US-09-383-667-12
; Sequence 12, Application US/09383667
; Patent No. 6624295
; GENERAL INFORMATION:
; APPLICANT: Adams, Camelia W.
; APPLICANT: Devaux, Brigitte
; APPLICANT: Eaton, Dan L.
; APPLICANT: Hase, Philip B.
; APPLICANT: Judice, J. Kevin
; APPLICANT: Kirchhofer, Daniel
; APPLICANT: Suggest, Shelley
; TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
; FILE REFERENCE: Pl661R2
; CURRENT APPLICATION NUMBER: US/09/383,667
; CURRENT FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098,233
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: US 60/122,767
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 12
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-383-667-12
; Query Match 100.0%; Score 50; DB 4; Length 11;
; Best Local Similarity 100.0%; Pred. No. 0.00018;
; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 ASIAARVLDY 11

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US-09-383-667-19
; Sequence 19, Application US/09383667
; Patent No. 6624295
; GENERAL INFORMATION:
; APPLICANT: Adams, Camelia W.
; APPLICANT: Devaux, Brigitte
; APPLICANT: Eaton, Dan L.
; APPLICANT: Hase, Philip B.
; APPLICANT: Judice, J. Kevin
; APPLICANT: Kirchhofer, Daniel
; APPLICANT: Suggest, Shelley
; TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
; FILE REFERENCE: Pl661R2

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CURRENT APPLICATION NUMBER: US/09/383,667
CURRENT FILING DATE: 1999-08-26
EARLIER APPLICATION NUMBER: US 60/098,233
EARLIER FILING DATE: 1998-08-28
EARLIER APPLICATION NUMBER: US 60/122,767
EARLIER FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 32
SEQ ID NO 19
LENGTH: 11
TYPE: PRT
ORGANISM: Homo sapiens
US-09-383-667-19

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Best Local Similarity 90.9%; Pred. No. 0.0013;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASIAARVLDY 11
Db 1 ASIAARVLDY 11

RESULT 3
US-09-342-648-2
Sequence 2, Application US/09342648
Patent No. 6248584
GENERAL INFORMATION:
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Odell, Joan
APPLICANT: Rafalski, Antoni
TITLE OF INVENTION: Transcription Coactivators
FILE REFERENCE: BB-1169-B
CURRENT APPLICATION NUMBER: US/09/342,648
CURRENT FILING DATE: 1999-06-29
EARLIER APPLICATION NUMBER: 60/092,659
EARLIER FILING DATE: July 13, 1998
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Microsoft Office 97
SEQ ID NO 2
LENGTH: 755
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
NAME/KEY: UNSURE
LOCATION: (179)
FEATURE:
NAME/KEY: UNSURE
LOCATION: (185)
FEATURE:
NAME/KEY: UNSURE
LOCATION: (241)
US-09-342-648-2

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Best Local Similarity 72.7%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ASIAARVLDY 11
Db 240 AXIADTRLVDY 250

RESULT 4
US-08-865-203-6
Sequence 6, Application US/08865203
Patent No. 5935815
GENERAL INFORMATION:
APPLICANT: van de Ven, Willem Jan Marie
APPLICANT: van den Ouweland, Anna Maria Wilhelmina
APPLICANT: van Duijnhoven, Johannes Lambertus Petrus
APPLICANT: Robroek, Antonius Johannes Maria
APPLICANT: Koning, Piet Nico Maria
TITLE OF INVENTION: Pharmaceutical Composition Having An

TITLE OF INVENTION: Endoproteolytic Activity; A Process for
TITLE OF INVENTION: Endoproteolytically Processing (Precursor)
TITLE OF INVENTION: Proteins And For The (Micro)Biological
TITLE OF INVENTION: Production Of Proteins
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOFMANN & BARON, LLP
STREET: 350 Jericho Turnpike
CITY: Jericho
STATE: New York
COUNTRY: U.S.A.
ZIP: 11753

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/865,203
FILING DATE: 29-MAY-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Tran, Jessica H.
REGISTRATION NUMBER: 40,846
REFERENCE/DOCKET NUMBER: 294-41 DIV II
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 822-3550
TELEFAX: (516) 822-3582
TELEX:

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 278 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-865-203-6

Query Match 68.0%; Score 34; DB 2; Length 278;
Best Local Similarity 80.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAARVLD 10
Db 96 ASIAARVLD 105

RESULT 5
US-07-849-420-6
Sequence 6, Application US/07849420
Patent No. 5989856
GENERAL INFORMATION:
APPLICANT: van de Ven, Willem Jan Marie
APPLICANT: van den Ouweland, Anna Maria Wilhelmina
APPLICANT: van Duijnhoven, Johannes Lambertus Petrus
APPLICANT: Robroek, Antonius Johannes Maria
APPLICANT: Koning, Piet Nico Maria
TITLE OF INVENTION: Pharmaceutical Composition Having An
TITLE OF INVENTION: Endoproteolytic Activity; A Process for
TITLE OF INVENTION: Endoproteolytically Processing (Precursor)
TITLE OF INVENTION: Proteins And For The (Micro)Biological
TITLE OF INVENTION: Production Of Proteins
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DUNHAM
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10112

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/849,420
FILING DATE: 19920624
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Moran, Thomas F.
REGISTRATION NUMBER: 16,579
REFERENCE/DOCKET NUMBER: 2805/41413
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 977-9550
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 278 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-849-420-6

Query Match 68.0%; Score 34; DB 2; Length 278;
Best Local Similarity 80.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASIAARVLD 10
||| |||
Db 96 ASILAVRVD 105

RESULT 6

US-09-253-854-6
Sequence 6, Application US/09253854
Patent No. 6132717
GENERAL INFORMATION:
APPLICANT: van de Ven, Willem Jan Marie;
APPLICANT: van den Ouweland, Anna Maria Wilhelmina;
APPLICANT: Van Duijnoven, Johannes Lambertus Petrus;
APPLICANT: Robroek, Antonius Johannes Maria; and
APPLICANT: Konig, Piet Nico Maria
TITLE OF INVENTION: Pharmaceutical Composition Having An
TITLE OF INVENTION: Endoproteolytic Activity; A Process for
TITLE OF INVENTION: Endoproteolytically Processing (Precursor)
TITLE OF INVENTION: Proteins And For The (Micro)Biological
TITLE OF INVENTION: Production Of Proteins
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:
ADDRESSEE: HOPFMANN & BARON, LLP
STREET: 350 Jericho Turnpike
CITY: Jericho
STATE: New York
COUNTRY: U.S.A.
ZIP: 11753
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/253,854
FILING DATE: Unassigned
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Tran, Jessica H.
REGISTRATION NUMBER: 40,846
REFERENCE/DOCKET NUMBER: 294-41 DIV II/CON
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 822-3550
TELEFAX: (516) 822-3582
TELEX:
INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 278 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-253-854-6

Query Match 68.0%; Score 34; DB 3; Length 278;
Best Local Similarity 80.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASIAARVLD 10
||| |||
Db 96 ASILAVRVD 105

RESULT 7

US-08-955-424-6
Sequence 6, Application US/08955424
Patent No. 6274365
GENERAL INFORMATION:
APPLICANT: Van de Ven, Willem Jan Marie
APPLICANT: Van den Ouweland, Anna Maria Wilhelmina
APPLICANT: Van Duijnoven, Johannes Lambertus Petrus
APPLICANT: Konig, Piet Nico Maria
APPLICANT: Robroek, Antonius Johannes Maria
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION HAVING AN ENDOPEPTOLYTIC
TITLE OF INVENTION: ACTIVITY; A PROCESS FOR ENDOPEPTOLYTICALLY PROCESSING
TITLE OF INVENTION: (PRECURSOR) PROTEINS AND FOR THE (MICRO) BIOLOGICAL
TITLE OF INVENTION: SEQUENCE LISTINGS 1-12 294-41 DIV/FWC
FILE REFERENCE: SEQUENCE LISTINGS 1-12 294-41 DIV/FWC
CURRENT APPLICATION NUMBER: US/08/955,424
CURRENT FILING DATE: 1997-10-22
EARLIER APPLICATION NUMBER: 08/568,152
EARLIER FILING DATE: 1995-06-12
EARLIER APPLICATION NUMBER: 07/849,420
EARLIER FILING DATE: 1992-06-24
EARLIER APPLICATION NUMBER: PCT/NL90/00151
EARLIER FILING DATE: 1990-10-21
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGTH: 278
TYPE: PRT
ORGANISM: Thermactinomyces vulgaris
US-08-955-424-6

Query Match 68.0%; Score 34; DB 3; Length 278;
Best Local Similarity 80.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASIAARVLD 10
||| |||
Db 96 ASILAVRVD 105

RESULT 8

US-09-135-658-4
Sequence 4, Application US/09135658
Patent No. 5972683
GENERAL INFORMATION:
APPLICANT: Tsai, Ying-Chieh
TITLE OF INVENTION: MUTANT TYPE SUBSTITUTED YAB AND ITS APPLICATION
FILE REFERENCE: 6653-011-999
CURRENT APPLICATION NUMBER: US/09/135,658
CURRENT FILING DATE: 1998-08-18
EARLIER APPLICATION NUMBER: 86112766
EARLIER FILING DATE: 1997-09-04
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0 - beta
SEQ ID NO 4
LENGTH: 279

TYPE: PRT
ORGANISM: Bacillus subtilis
US-09-135-658-4

Query Match 68.0%; Score 34; DB 2; Length 279;
Best Local Similarity 80.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIARAVID 10
Db 96 ASIARAVID 105

RESULT 9
US-09-512-251A-6
Sequence 6, Application US/09512251A
Patent No. 655315
GENERAL INFORMATION:
APPLICANT: Hansen, Peter
APPLICANT: Bauditz, Peter
APPLICANT: Mikkelsen, Frank
APPLICANT: Andersen, Kim
TITLE OF INVENTION: Protease Variants and Compositions
FILE REFERENCE: 5349, 204-US
CURRENT APPLICATION NUMBER: US/09/512,251A
CURRENT FILING DATE: 2000-02-24
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patent version 3.1
SEQ ID NO 6
LENGTH: 279
TYPE: PRT
ORGANISM: Bacillus
US-09-512-251A-6

Query Match 68.0%; Score 34; DB 4; Length 279;
Best Local Similarity 80.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIARAVID 10
Db 96 ASIARAVID 105

RESULT 10
US-09-515-150A-6
Sequence 6, Application US/09515150A
Patent No. 6558938
GENERAL INFORMATION:
APPLICANT: Hansen, Peter
APPLICANT: Bauditz, Peter
APPLICANT: Mikkelsen, Frank
APPLICANT: Andersen, Kim
TITLE OF INVENTION: Protease Variants and Compositions
FILE REFERENCE: 5348, 204-US
CURRENT APPLICATION NUMBER: US/09/515,150A
CURRENT FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patent version 3.1
SEQ ID NO 6
LENGTH: 279
TYPE: PRT
ORGANISM: Bacillus
US-09-515-150A-6

Query Match 68.0%; Score 34; DB 4; Length 279;
Best Local Similarity 80.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIARAVID 10
Db 96 ASIARAVID 105

RESULT 11
US-09-196-281-9
Sequence 9, Application US/09196281A
Patent No. 6605458
GENERAL INFORMATION:
APPLICANT: Hansen, Peter K.
APPLICANT: Bauditz, Peter
APPLICANT: Mikkelsen, Frank
TITLE OF INVENTION: Protease Variants And Compositions
FILE REFERENCE: 5435, 200-US
CURRENT APPLICATION NUMBER: US/09/196,281A
CURRENT FILING DATE: 1998-11-19
EARLIER APPLICATION NUMBER: 1332/97
EARLIER FILING DATE: 1997-11-21
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 9
LENGTH: 279
TYPE: PRT
ORGANISM: Bacillus
US-09-196-281-9

Query Match 68.0%; Score 34; DB 4; Length 279;
Best Local Similarity 80.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIARAVID 10
Db 96 ASIARAVID 105

RESULT 12
5472855-6
Patent No. 5472855
APPLICANT: CARTER, PAUL J.; WELLS, JAMES A.
TITLE OF INVENTION: SUBSTRATE ASSISTED CATALYSIS
NUMBER OF SEQUENCES: 31
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/287,964
FILING DATE: 22-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 90,902
FILING DATE: 12-JUL-1993
APPLICATION NUMBER: 823,039
FILING DATE: 14-JAN-1992
APPLICATION NUMBER: 35,652
FILING DATE: 06-APR-1987
APPLICATION NUMBER: 334,081
FILING DATE: 04-APR-1989
APPLICATION NUMBER: 127,134
FILING DATE: 01-DEC-1987
APPLICATION NUMBER: 846,627
FILING DATE: 01-APR-1986
APPLICATION NUMBER: 858,594
FILING DATE: 30-APR-1986
APPLICATION NUMBER: 614,612
FILING DATE: 29-MAY-1984
APPLICATION NUMBER: 614,615
FILING DATE: 29-MAY-1984
APPLICATION NUMBER: 614,617
FILING DATE: 29-MAY-1984
APPLICATION NUMBER: 614,491
FILING DATE: 29-MAY-1984
SEQ ID NO: 6
LENGTH: 279
5472855-6

Query Match 68.0%; Score 34; DB 6; Length 279;
Best Local Similarity 80.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIARAVID 10

Db 96 ASILARVLD 105

RESULT 13

5472855-6
; Patent No. 5472855
; APPLICANT: CARTER, PAUL J.; WELLS, JAMES A.
; TITLE OF INVENTION: SUBSTRATE ASSISTED CATALYSIS
; NUMBER OF SEQUENCES: 31
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/287,964
; FILING DATE: 22-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 90,902
; FILING DATE: 12-JUL-1993
; APPLICATION NUMBER: 823,039
; FILING DATE: 14-JAN-1992
; APPLICATION NUMBER: 35,652
; FILING DATE: 06-APR-1987
; APPLICATION NUMBER: 334,081
; FILING DATE: 04-APR-1989
; APPLICATION NUMBER: 127,134
; FILING DATE: 01-DEC-1987
; APPLICATION NUMBER: 846,627
; FILING DATE: 01-APR-1986
; APPLICATION NUMBER: 858,594
; FILING DATE: 30-APR-1986
; APPLICATION NUMBER: 614,612
; FILING DATE: 29-MAY-1984
; APPLICATION NUMBER: 614,615
; FILING DATE: 29-MAY-1984
; APPLICATION NUMBER: 614,617
; FILING DATE: 29-MAY-1984
; APPLICATION NUMBER: 614,491
; FILING DATE: 29-MAY-1984
; SEQ ID NO: 6:
; LENGTH: 279
5472855-6

Query Match 66.0%; Score 34; DB 6; Length 279;
Best Local Similarity 80.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ASILARVLD 10
Db 96 ASILARVLD 105

RESULT 14

US-09-698-286A-10
; Sequence 10, Application US/09698286A
; Patent No. 6677442
; GENERAL INFORMATION:
; APPLICANT: University of Kentucky Research Foundation
; TITLE OF INVENTION: Human REV1 Gene and Protein As Diagnostic, Preventive, and Therap
; FILE REFERENCE: 050229-0247
; CURRENT APPLICATION NUMBER: US/09/698,286A
; FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: 60/162,140
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 85
; TYPE: PRT
; ORGANISM: C. elegans, A. thaliana, S. cerevisiae, S. pombe and H. sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (17)-(22)
; OTHER INFORMATION: Gap in alignment
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (50)-(60)

; OTHER INFORMATION: Gap in alignment
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (30)-(33)
; OTHER INFORMATION: Gap in alignment
US-09-698-286A-10

Query Match 66.0%; Score 33; DB 4; Length 85;
Best Local Similarity 70.0%; Pred. No. 9.8;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 SIARVLDY 11
Db 71 SIARVLDY 80

RESULT 15

US-09-710-279-622
; Sequence 622, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMBERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P03480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 622
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-710-279-622

Query Match 66.0%; Score 33; DB 4; Length 194;
Best Local Similarity 60.0%; Pred. No. 26;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 SIARVLDY 11
Db 106 NVASASVDY 115

RESULT 16

US-09-134-001C-3417
; Sequence 3417, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3417
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3417

Query Match 66.0%; Score 33; DB 3; Length 223;
Best Local Similarity 60.0%; Pred. No. 31;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 SIIMAAVLDY 11
Db 135 NVASASVLDY 144

RESULT 17

US-09-248-796A-18164
; Sequence 18164, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248, 796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 18164
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-18164

Query Match 66.0%; Score 33; DB 4; Length 331;
Best Local Similarity 60.0%; Pred. No. 50;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIIMAAVLDY 10
Db 262 ASVAAMAKME 271

RESULT 18

US-09-489-039A-12051
; Sequence 12051, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489, 039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12051
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12051

Query Match 66.0%; Score 33; DB 4; Length 364;
Best Local Similarity 54.5%; Pred. No. 56;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 ASIIMAAVLDY 11
Db 220 ASVACPSILDY 230

RESULT 19

US-09-602-787A-508
; Sequence 508, Application US/09602787A
; Patent No. 6696561
; GENERAL INFORMATION:
; APPLICANT: Pompeius, Mark
; APPLICANT: Krüger, Burkhard

APPLICANT: Sch"der, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: Haberkauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
FILE REFERENCE: BGI-125CD
CURRENT APPLICATION NUMBER: US/09/602,787A
CURRENT FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: USN 60/141031
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: DE 19931454.3
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931478.0
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931563.9
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19932122.1
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932124.8
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932125.6
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932128.0
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932180.9
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932182.5
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932190.6
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932191.4
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932209.0
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932212.0
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932227.9
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932228.7
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932229.5
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932230.9
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932927.3
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19933005.0
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19933006.9
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19940764.9
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19940765.7
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19940766.5
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19940830.0
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19940831.9
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19940832.7
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19940833.5
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19941378.9
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: DE 19941379.7
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: DE 19941395.9
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: DE 19942077.7
PRIOR FILING DATE: 1999-09-03

;; PRIOR APPLICATION NUMBER: DE 19942078.5
;; PRIOR FILING DATE: 1999-09-03
;; PRIOR APPLICATION NUMBER: DE 19942079.3
;; PRIOR FILING DATE: 1999-09-03
;; PRIOR APPLICATION NUMBER: DE 19942088.2
;; PRIOR FILING DATE: 1999-09-03
;; NUMBER OF SEQ ID NOS: 678
;; SEQ ID NO 508
;; LENGTH: 402
;; TYPE: PRT
;; ORGANISM: Corynebacterium glutamicum
US-09-602-787A-508

Query Match 66.0%; Score 33; DB 4; Length 402;
Best Local Similarity 63.6%; Pred. No. 63;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 ASIAARVLDY 11
Db 260 ASIAPAAIADY 270

RESULT 20
US-09-540-236-3193
; Sequence 3193, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRHALIS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540.236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 3193
; LENGTH: 867
; TYPE: PRT
; ORGANISM: M.catarrrhalis
US-09-540-236-3193

Query Match 66.0%; Score 33; DB 4; Length 867;
Best Local Similarity 60.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 SIAARVLDY 11
Db 439 SVADARVWDF 448

RESULT 21
US-09-902-540-16309
; Sequence 16309, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(115849)B
; CURRENT APPLICATION NUMBER: US/09/902.540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 16309
; LENGTH: 910
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-16309

Query Match 66.0%; Score 33; DB 4; Length 910;
Best Local Similarity 60.0%; Pred. No. 1.7e+02;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
OY 2 SIAARVLDY 11
Db 844 NVAATRVYDY 853

RESULT 22
US-09-252-991A-17003
; Sequence 17003, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17003
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17003

Query Match 64.0%; Score 32; DB 4; Length 234;
Best Local Similarity 87.5%; Pred. No. 54;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 IAAARVLD 10
Db 9 ISAAARVLD 16

RESULT 23
US-09-724-797-34
; Sequence 34, Application US/09724797
; Patent No. 6733998
; GENERAL INFORMATION:
; APPLICANT: Jon S. THORSON
; TITLE OF INVENTION: MICROMONOPORA ECHINOSPORA GENES
; TITLE OF INVENTION: ENCODING FOR BIOSYNTHESIS OF
; FILE REFERENCE: 2653-40
; CURRENT APPLICATION NUMBER: US/09/724.797
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/111,325
; PRIOR FILING DATE: 1998-12-07
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Bacteria
US-09-724-797-34

Query Match 64.0%; Score 32; DB 4; Length 280;
Best Local Similarity 75.0%; Pred. No. 67;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 AAARVLDY 11
Db 8 AAARVLDY 15

RESULT 24
US-09-252-991A-31470
; Sequence 31470, Application US/09252991A
; Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 31142
SEQ ID NO 31470
LENGTH: 480
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31470

Query Match 64.0%; Score 32; DB 4; Length 480;
Best Local Similarity 63.6%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ASIAARVLDY 11
||:|||||
Db 236 ASVLDARELDY 246

RESULT 25
US-09-902-540-10906
Sequence 10906, Application US/09902540
Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(115849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 10906
LENGTH: 111
TYPE: PRT
ORGANISM: Myxococcus xanthus
US-09-902-540-10906

Query Match 62.0%; Score 31; DB 4; Length 111;
Best Local Similarity 85.7%; Pred. No. 36;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AARVLDY 11
||:|||||
Db 40 AARLDY 46

RESULT 26
US-08-975-762-38
Sequence 38, Application US/08975762
Patent No. 6207169
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
City: Seattle
STATE: Washington

TREATMEN

COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,762
FILING DATE: 21-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.439
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 177 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Entlichia
US-08-975-762-38

Query Match 62.0%; Score 31; DB 3; Length 177;
Best Local Similarity 54.5%; Pred. No. 64;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASIAARVLDY 11
||:|||||
Db 23 AGMLAKVLDY 33

RESULT 27
US-08-975-762-55
Sequence 55, Application US/08975762
Patent No. 6207169
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
City: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,762
FILING DATE: 21-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.439
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:

TREATMEN

LENGTH: 177 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-975-762-55

Query Match 62.0%; Score 31; DB 3; Length 177;
Best Local Similarity 54.5%; Pred. No. 64;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAARVLDY 11
| : ||| :
Db 23 AGMLAAKVLDF 33

RESULT 28
US-08-821-324-38
; Sequence 38, Application US/08821324
; Patent No. 6231869
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Houghton, Raymond
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/821,324
; FILING DATE: 21-MAR-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.439
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Ehrlichia
US-08-821-324-38

Query Match 62.0%; Score 31; DB 3; Length 177;
Best Local Similarity 54.5%; Pred. No. 64;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAARVLDY 11
| : ||| :
Db 23 AGMLAAKVLDF 33

RESULT 29
US-09-295-028-38
; Sequence 38, Application US/09295028
; Patent No. 6277381

; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
; FILE REFERENCE: 210121.439C4
; CURRENT APPLICATION NUMBER: US/09/295,028
; CURRENT FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PasteSeq for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Ehrlichia sp.
US-09-295-028-38

Query Match 62.0%; Score 31; DB 3; Length 177;
Best Local Similarity 54.5%; Pred. No. 64;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAARVLDY 11
| : ||| :
Db 23 AGMLAAKVLDF 33

RESULT 30
US-09-295-028-55
; Sequence 55, Application US/09295028
; Patent No. 6277381
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
; FILE REFERENCE: 210121.439C4
; CURRENT APPLICATION NUMBER: US/09/295,028
; CURRENT FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Ehrlichia sp.
US-09-295-028-55

Query Match 62.0%; Score 31; DB 3; Length 177;
Best Local Similarity 54.5%; Pred. No. 64;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAARVLDY 11
| : ||| :
Db 23 AGMLAAKVLDF 33

RESULT 31
US-09-106-582-38
; Sequence 38, Application US/09106582
; Patent No. 6306402
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Houghton, Raymond
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington

THERAPY

COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106,582
FILING DATE: 29-JUN-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Makl, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.439C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-682-4900
TELEFAX: 206-682-6031
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 177 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Ehrlichia
US-09-106-582-38

Query Match 62.0%; Score 31; DB 3; Length 177;
Best Local Similarity 54.5%; Pred. No. 64;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASIAARVLDY 11
| : ||| :
Db 23 AGMLAKVLDY 33

RESULT 32
US-09-106-582-55
Sequence 55, Application US/09106582
Patent No. 6306402
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106,582
FILING DATE: 29-JUN-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Makl, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.439C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-682-4900
TELEFAX: 206-682-6031
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:

LENGTH: 177 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-106-582-55

Query Match 62.0%; Score 31; DB 3; Length 177;
Best Local Similarity 54.5%; Pred. No. 64;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASIAARVLDY 11
| : ||| :
Db 23 AGMLAKVLDY 33

RESULT 33
US-09-159-469-38
Sequence 38, Application US/09159469
Patent No. 6607728
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/159,469
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/106,582
FILING DATE: 29-JUN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Makl, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.439C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-682-4900
TELEFAX: 206-682-6031
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 177 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Ehrlichia
US-09-159-469-38

Query Match 62.0%; Score 31; DB 4; Length 177;
Best Local Similarity 54.5%; Pred. No. 64;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASIAARVLDY 11
| : ||| :
Db 23 AGMLAKVLDY 33

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RESULT 34
US-09-159-469-55
; Sequence 55, Application US/09159469
; Patent No. 6607728
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: THERAPY OF EHRlichia INFECTION
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/159,469
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/106,582
; FILING DATE: 29-JUN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-159-469-55

Query Match      62.0%; Score 31; DB 4; Length 177;
Best Local Similarity 54.5%; Pred. No. 64;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Cy 1 ASIAARYLDY 11
Db 23 AGMLAKYLDY 33

RESULT 35
US-09-693-542-38
; Sequence 38, Application US/09693542
; Patent No. 6673356
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
; TITLE OF INVENTION: AND TREATMENT OF EHRlichia INFECTION
; FILE REFERENCE: 210121.439C6
; CURRENT APPLICATION NUMBER: US/09/693,542
; CURRENT FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 177
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; TYPE: PRT
; ORGANISM: Ehrlichia sp.
US-09-693-542-38

Query Match      62.0%; Score 31; DB 4; Length 177;
Best Local Similarity 54.5%; Pred. No. 64;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Cy 1 ASIAARYLDY 11
Db 23 AGMLAKYLDY 33

RESULT 36
US-09-693-542-55
; Sequence 55, Application US/09693542
; Patent No. 6673356
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
; TITLE OF INVENTION: AND TREATMENT OF EHRlichia INFECTION
; FILE REFERENCE: 210121.439C6
; CURRENT APPLICATION NUMBER: US/09/693,542
; CURRENT FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Ehrlichia sp.
US-09-693-542-55

Query Match      62.0%; Score 31; DB 4; Length 177;
Best Local Similarity 54.5%; Pred. No. 64;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Cy 1 ASIAARYLDY 11
Db 23 AGMLAKYLDY 33

RESULT 37
US-09-270-767-45191
; Sequence 45191, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45191
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-45191

Query Match      62.0%; Score 31; DB 4; Length 243;
Best Local Similarity 66.7%; Pred. No. 93;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Cy 3 IAAARYLDY 11
Db 204 LPAARYLDY 212

RESULT 38
US-09-066-046-22
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; Sequence 22, Application US/09066046A
; Patent No. 6204252
; GENERAL INFORMATION:
; APPLICANT: MURPHY, Cheryl
; STOREY, James
; BELTZ, Gerald A.
; COUGHLIN, Richard T.
; TITLE OF INVENTION: CHARACTERIZATION OF GRANULOCYTIC
; EHRlichIA AND METHODS OF USE
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HALE AND DORR LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: United States
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/066,046A
; FILING DATE: 24-Apr-1998
; CLASSIFICATION: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Superko, Colleen
; REGISTRATION NUMBER: 39,850
; REFERENCE/DOCKET NUMBER: 106,941.155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 526-6000
; TELEFAX: (617) 526-5000
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 264 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-066-046-22

Query Match 62.0%; Score 31; DB 3; Length 264;
Best Local Similarity 54.5%; Pred. No. 1e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAARVLDY 11
DB 20 AGMLAAKVLDF 30

RESULT 39
US-09-252-991A-32574
; Sequence 32574, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 32574
; LENGTH: 338
; TYPE: PRT
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32574

Query Match 62.0%; Score 31; DB 4; Length 338;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 AARVLDY 11
DB 137 AARVLDY 143

RESULT 40
US-09-252-991A-28830
; Sequence 28830, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 28830
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28830

Query Match 62.0%; Score 31; DB 4; Length 374;
Best Local Similarity 77.8%; Pred. No. 1.6e+02;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASIAAARVL 9
DB 235 AATAAARLL 243

Search completed: March 31, 2005, 12:13:26
Job time : 22.4844 secs
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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: March 31, 2005, 12:10:00 ; Search time 61.5312 Seconds
(without alignments)
59.279 Million cell updates/sec

Title: US-10-614-959-12
Perfect score: 50
Sequence: 1 ASIAAARVLDY 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1413372 seqs, 331592847 residues

Total number of hits satisfying chosen parameters: 1413372

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*

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- 2: /cgn2_6/ptodata/1/pubppaa/PCIT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep:*
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- 6: /cgn2_6/ptodata/1/pubppaa/PCITUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubppaa/US08_NEW_PUB.pep:*
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- 9: /cgn2_6/ptodata/1/pubppaa/US09A_PUBCOMB.pep:*
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- 11: /cgn2_6/ptodata/1/pubppaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubppaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubppaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubppaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubppaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubppaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/1/pubppaa/US10E_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubppaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	37	74.0	573	15	US-10-425-114-45544
3	37	74.0	1203	16	US-10-437-963-120758
4	36	72.0	652	15	US-10-369-493-14668
5	36	72.0	652	15	US-10-369-493-15165
6	36	72.0	655	15	US-10-369-493-14406
7	36	72.0	656	15	US-10-369-493-11635
8	36	72.0	1064	16	US-10-437-963-189048
9	35	70.0	45	16	US-10-437-963-201347
10	35	70.0	107	16	US-10-437-963-175236
11	34	68.0	198	16	US-10-767-701-38892
12	34	68.0	231	15	US-10-369-493-17091
13	34	68.0	279	14	US-10-336-324-6

14	34	68.0	279	14	US-10-403-105-9	Sequence 9, Appl1
15	34	68.0	642	16	US-10-767-701-45651	Sequence 45651, A
16	34	68.0	671	15	US-10-369-493-7093	Sequence 7093, Ap
17	34	68.0	674	15	US-10-369-493-4338	Sequence 4338, Ap
18	34	68.0	691	15	US-10-425-114-70274	Sequence 70274, A
19	34	68.0	827	16	US-10-437-963-146706	Sequence 146706,
20	34	68.0	1000	16	US-10-437-963-122779	Sequence 122779,
21	33	66.0	274	14	US-10-238-075-276	Sequence 276, App
22	33	66.0	299	15	US-10-032-585-7697	Sequence 7697, Ap
23	33	66.0	299	14	US-10-425-114-40808	Sequence 40808, A
24	33	66.0	331	14	US-10-156-761-8701	Sequence 8701, Ap
25	33	66.0	358	15	US-10-282-122A-62045	Sequence 62045, A
26	33	66.0	358	15	US-10-282-122A-63923	Sequence 63923, A
27	33	66.0	367	15	US-10-282-122A-62857	Sequence 62857, A
28	33	66.0	367	15	US-10-282-122A-64830	Sequence 64830, A
29	33	66.0	402	15	US-10-627-476-508	Sequence 508, App
30	33	66.0	449	9	US-09-738-626-6555	Sequence 6555, Ap
31	33	66.0	453	15	US-10-369-493-21054	Sequence 21054, A
32	33	66.0	466	16	US-10-437-963-136788	Sequence 136788,
33	33	66.0	469	15	US-10-417-700A-49	Sequence 49, Appl
34	33	66.0	509	15	US-10-282-122A-77407	Sequence 77407, A
35	33	66.0	670	15	US-10-369-493-11847	Sequence 11847, A
36	33	66.0	867	15	US-10-282-122A-63141	Sequence 63141, A
37	33	66.0	1958	14	US-10-152-886-53	Sequence 53, Appl
38	32	64.0	144	15	US-10-425-114-53118	Sequence 53118, A
39	32	64.0	146	15	US-10-425-114-53613	Sequence 53613, A
40	32	64.0	220	16	US-10-437-963-107871	Sequence 107871,
41	32	64.0	221	16	US-10-437-963-187946	Sequence 187946,
42	32	64.0	342	15	US-10-369-493-21401	Sequence 21401, A
43	32	64.0	343	15	US-10-424-592-172724	Sequence 172724,
44	32	64.0	365	15	US-10-369-493-17087	Sequence 17087, A
45	32	64.0	404	15	US-10-425-114-49539	Sequence 49539, A

ALIGNMENTS

RESULT 1
US-10-389-566-831
Sequence 831, Application US/10389566
Publication No. US20040025202A1
GENERAL INFORMATION:
APPLICANT: Monsanto Technology, LLC
INVENTOR: Laurie, Cathy C
TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
FILE REFERENCE: 38-77(52800)D
CURRENT FILING DATE: 2003-03-31
PRIOR APPLICATION NUMBER: US 60/365,301
PRIOR FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: US 60/391,786
PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/392,018
PRIOR FILING DATE: 2002-06-26
NUMBER OF SEQ ID NOS: 2459
SOFTWARE: PatentIn version 3.2
SEQ ID NO 831
LENGTH: 408
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
NAME/KEY: misc feature
LOCATION: (103) (106)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-389-566-831

Query Match 74.0%; Score 37; DB 15; Length 408;
Best Local Similarity 80.0%; Pred. No. 55;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
CY 1 ASIAAARVLD 10
DB 275 ASIAAARVLD 284

RESULT 2

US-10-425-114-45544
 ; Sequence 45544, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jindong
 ; APPLICANT: Zhou, Yinua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E
 ; APPLICANT: Tabaska, Jack E
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 ; FILE REFERENCE: 38-21(5313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; PRIORITY FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 45544
 ; LENGTH: 573
 ; TYPE: PRT
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: 700800359_F11.dep
 US-10-425-114-45544

Query Match

Best Local Similarity 74.0%; Score 37; DB 15; Length 573;
 Pred. No. 79;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAARVLDY 11
 |:|||||

DB 58 ANIADTRVLDY 68

RESULT 3

US-10-437-963-120758
 ; Sequence 120758, Application US/10437963
 ; Publication No. US20040123343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yinua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazuk, Brad
 ; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
 ; FILE REFERENCE: 38-21(53221)B
 ; CURRENT APPLICATION NUMBER: US/10/437,963
 ; PRIORITY FILING DATE: 2003-05-14
 ; NUMBER OF SEQ ID NOS: 204966
 ; SEQ ID NO 120758
 ; LENGTH: 1203
 ; TYPE: PRT
 ; ORGANISM: Oryza sativa
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_2384C.1.dep
 US-10-437-963-120758

Query Match

Best Local Similarity 74.0%; Score 37; DB 16; Length 1203;
 Pred. No. 1,7e+02;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASIAARVLD 10
 |:|||||

DB 330 ASVAATRIILD 339

RESULT 4

US-10-369-493-14688
 ; Sequence 14688, Application US/10369493
 ; Publication No. US20030233675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; FILE REFERENCE: 38-10(52052)B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; PRIORITY FILING DATE: 2003-02-28
 ; PRIORITY APPLICATION NUMBER: US 60/360,039
 ; PRIORITY FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 14688
 ; LENGTH: 652
 ; TYPE: PRT
 ; ORGANISM: Agrobacterium tumefaciens
 US-10-369-493-14688

Query Match

Best Local Similarity 72.0%; Score 36; DB 15; Length 652;
 Pred. No. 1,4e+02;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAARVLDY 11
 |:|||||

DB 255 AATTAARAIDY 265

RESULT 5

US-10-369-493-15165
 ; Sequence 15165, Application US/10369493
 ; Publication No. US20030233675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; FILE REFERENCE: 38-10(52052)B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; PRIORITY FILING DATE: 2003-02-28
 ; PRIORITY APPLICATION NUMBER: US 60/360,039
 ; PRIORITY FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 15165
 ; LENGTH: 652
 ; TYPE: PRT
 ; ORGANISM: Agrobacterium tumefaciens
 US-10-369-493-15165

Query Match

Best Local Similarity 72.0%; Score 36; DB 15; Length 652;
 Pred. No. 1,4e+02;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAARVLDY 11
 |:|||||

DB 255 AATTAARAIDY 265

RESULT 6

US-10-369-493-14406
 ; Sequence 14406, Application US/10369493
 ; Publication No. US20030233675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.


```

; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 14406
; LENGTH: 659
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
; US-10-369-493-14406

Query Match          72.0%; Score 36; DB 15; Length 655;
Best Local Similarity 63.6%; Pred. No. 1.4e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 ASIAARVLDY 11
       |||:|||||
Db      255 AATAAARAIDY 265

RESULT 7
; US-10-369-493-11635
; Sequence 11635, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 11635
; LENGTH: 656
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
; US-10-369-493-11635

Query Match          72.0%; Score 36; DB 15; Length 656;
Best Local Similarity 63.6%; Pred. No. 1.4e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 ASIAARVLDY 11
       |||:|||||
Db      255 AATAAARAIDY 265

RESULT 8
; US-10-437-963-189048
; Sequence 189048, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
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; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 189048
; LENGTH: 1064
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_85594C.1.pcp
; US-10-437-963-189048

Query Match          72.0%; Score 36; DB 16; Length 1064;
Best Local Similarity 80.0%; Pred. No. 2.4e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 ASIAARVLD 10
       |||:|||||
Db      116 ASIAARVLD 125

RESULT 9
; US-10-437-963-201347
; Sequence 201347, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 201347
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_96731C.1.pcp
; US-10-437-963-201347

Query Match          70.0%; Score 35; DB 16; Length 45;
Best Local Similarity 88.9%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 SIARARVLD 10
       |||:|||||
Db      16 SIARARVLD 24

RESULT 10
; US-10-437-963-175236
; Sequence 175236, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
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; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 175236
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(107)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_73100C.1.pep
US-10-437-963-175236

Query Match
Best Local Similarity 70.0%; Score 35; DB 16; Length 107;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASIAAARVLD 10
Db 34 ASIAAARVSD 43

RESULT 11
US-10-767-701-38892
; Sequence 38892, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 38892
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C77436_1.pep
US-10-767-701-38892

Query Match
Best Local Similarity 68.0%; Score 34; DB 16; Length 198;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AARVLDY 11
Db 114 AARVLDY 120

RESULT 12
US-10-369-493-17091
; Sequence 493-17091, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
```

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; SEQ ID NO 17091
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Caulobacter crescentus
US-10-369-493-17091

Query Match
Best Local Similarity 68.0%; Score 34; DB 15; Length 231;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASIAAARVLD 10
Db 100 ATIAARKLD 109

RESULT 13
US-10-336-324-6
; Sequence 6, Application US/10336324
; Publication No. US20030176304A1
; GENERAL INFORMATION:
; APPLICANT: Hansen, Peter
; APPLICANT: Bauditz, Peter
; APPLICANT: Mikkelsen, Frank
; APPLICANT: Andersen, Kim
; TITLE OF INVENTION: Protease Variants and Compositions
; FILE REFERENCE: 5349,204-US
; CURRENT APPLICATION NUMBER: US/10/336,324
; CURRENT FILING DATE: 2003-01-03
; PRIOR APPLICATION NUMBER: US/09/512,251A
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 279
; TYPE: PRT
; ORGANISM: Bacillus
US-10-336-324-6

Query Match
Best Local Similarity 68.0%; Score 34; DB 14; Length 279;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAAARVLD 10
Db 96 ASIAAARVLD 105

RESULT 14
US-10-403-105-9
; Sequence 9, Application US/10403105
; Publication No. US20030180933A1
; GENERAL INFORMATION:
; APPLICANT: Hansen, Peter K.
; APPLICANT: Bauditz, Peter
; APPLICANT: Mikkelsen, Frank
; TITLE OF INVENTION: Protease Variants And Compositions
; FILE REFERENCE: 5435,200-US
; CURRENT APPLICATION NUMBER: US/10/403,105
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US/09/196,281A
; PRIOR FILING DATE: 1998-11-19
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 1332/97
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 279
; TYPE: PRT
; ORGANISM: Bacillus
US-10-403-105-9

Query Match
Best Local Similarity 68.0%; Score 34; DB 14; Length 279;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAARVLD 10
||| |||
Db 96 ASIAARVLD 105

RESULT 15
US-10-767-701-45651
; Sequence 45651, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 45651
; LENGTH: 642
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C1583_1.pep
US-10-767-701-45651

Query Match 68.0%; Score 34; DB 16; Length 642;
Best Local Similarity 63.6%; Pred. No. 3.5e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAARVLD 11
||| |||
Db 127 ANMADTRVLDY 137

RESULT 16
US-10-369-493-7093
; Sequence 7093, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 7093
; LENGTH: 671
; TYPE: PRT
; ORGANISM: Burkholderia cepacia
US-10-369-493-7093

Query Match 68.0%; Score 34; DB 15; Length 671;
Best Local Similarity 54.5%; Pred. No. 3.7e+02;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASIAARVLDY 11
||| |||
Db 255 AAVALARVAVY 265

RESULT 17
US-10-369-493-4338

; Sequence 4338, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 4338
; LENGTH: 674
; TYPE: PRT
; ORGANISM: Burkholderia fungorum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(674)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-4338

Query Match 68.0%; Score 34; DB 15; Length 674;
Best Local Similarity 54.5%; Pred. No. 3.7e+02;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASIAARVLDY 11
||| |||
Db 255 AAVALARVAVY 265

RESULT 18
US-10-425-114-70274
; Sequence 70274, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53133)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 70274
; LENGTH: 691
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZKROB73050D03_F11.pep
US-10-425-114-70274

Query Match 68.0%; Score 34; DB 15; Length 691;
Best Local Similarity 63.6%; Pred. No. 3.8e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAARVLDY 11
||| |||
Db 176 ANMADTRVLDY 186

RESULT 19
US-10-437-963-146706
; Sequence 146706, Application US/10437963
; Publication No. US20040123343A1

```

; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 146706
; LENGTH: 827
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_47304C.1.pep
US-10-437-963-146706

Query Match          68.0%; Score 34; DB 16; Length 827;
Best Local Similarity 88.9%; Pred. No. 4.6e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 SIIMARVLD 10
Db 153 SIIMARVLD 161

RESULT 20
US-10-437-963-122779
; Sequence 122779, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 122779
; LENGTH: 1000
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_25676C.1.pep
US-10-437-963-122779

Query Match          68.0%; Score 34; DB 16; Length 1000;
Best Local Similarity 77.8%; Pred. No. 5.6e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 IIAARVLDY 11
Db 870 VAAADVLDY 878

RESULT 21
US-10-238-075-276
; Sequence 276, Application US/10238075
; Publication No. US20030146324A1
; GENERAL INFORMATION:
; APPLICANT: I.N.S.E.R.M.
; TITLE OF INVENTION: Polynucleotides which are of nature B2/D+ A- and which are isolate
; FILE REFERENCE: BLANDINE
; CURRENT APPLICATION NUMBER: US/10/238,075
; CURRENT FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 0003145
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 1576
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 276
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-238-075-276

Query Match          66.0%; Score 33; DB 14; Length 204;
Best Local Similarity 63.6%; Pred. No. 1.7e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIIMARVLDY 11
Db 151 AQIAAARMVEY 161

RESULT 22
US-10-032-585-7697
; Sequence 7697, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.
; APPLICANT: Bo, Jiang
; APPLICANT: Charles, Boone
; APPLICANT: Howard, Bussey
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
; FILE REFERENCE: 10182-005-999
; CURRENT APPLICATION NUMBER: US/10/032,585
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7697
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Candida albicans
US-10-032-585-7697

Query Match          66.0%; Score 33; DB 14; Length 274;
Best Local Similarity 60.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASIIMARVLD 10
Db 205 ASVAAAKVME 214

RESULT 23
US-10-425-114-40808
; Sequence 40808, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovacic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 40808
```

```

; APPLICANT: I.N.S.E.R.M.
; TITLE OF INVENTION: Polynucleotides which are of nature B2/D+ A- and which are isolate
; FILE REFERENCE: BLANDINE
; CURRENT APPLICATION NUMBER: US/10/238,075
; CURRENT FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 0003145
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 1576
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 276
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-238-075-276

Query Match          66.0%; Score 33; DB 14; Length 204;
Best Local Similarity 63.6%; Pred. No. 1.7e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIIMARVLDY 11
Db 151 AQIAAARMVEY 161

RESULT 22
US-10-032-585-7697
; Sequence 7697, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.
; APPLICANT: Bo, Jiang
; APPLICANT: Charles, Boone
; APPLICANT: Howard, Bussey
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
; FILE REFERENCE: 10182-005-999
; CURRENT APPLICATION NUMBER: US/10/032,585
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7697
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Candida albicans
US-10-032-585-7697

Query Match          66.0%; Score 33; DB 14; Length 274;
Best Local Similarity 60.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASIIMARVLD 10
Db 205 ASVAAAKVME 214

RESULT 23
US-10-425-114-40808
; Sequence 40808, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovacic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 40808
```

LENGTH: 299
TYPE: PRT
ORGANISM: Schizochytrium aggregatum
FEATURE:
OTHER INFORMATION: Clone ID: LIB3033-037-H2_FLI.pep
US-10-425-114-40808

Query Match 66.0%; Score 33; DB 15; Length 299;
Best Local Similarity 70.0%; Pred. No. 2.5e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 SIAARVLDY 11
DB 33 SIAVTRVLDH 42

RESULT 24
US-10-156-761-8701
Sequence 8701, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
PRIOR FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 8701
LENGTH: 331
TYPE: PRT
ORGANISM: Streptomyces avermitilis
US-10-156-761-8701

Query Match 66.0%; Score 33; DB 14; Length 311;
Best Local Similarity 60.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 SIAARVLDY 11
DB 306 SVAATRTLDF 315

RESULT 25
US-10-282-122A-62045
Sequence 62045, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyekind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 62045
LENGTH: 358
TYPE: PRT
ORGANISM: Mycobacterium avium
US-10-282-122A-62045

Query Match 66.0%; Score 33; DB 15; Length 358;
Best Local Similarity 60.0%; Pred. No. 3e+02;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASIAARVLD 10
DB 13 SVAARVLD 22

RESULT 26
US-10-282-122A-63923
Sequence 63923, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyekind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27

```

; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63923
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Mycobacterium leprae
US-10-282-122A-63923

Query Match      66.0%; Score 33; DB 15; Length 358;
Best Local Similarity 60.0%; Pred. No. 3e+02;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ASIAARVLD 10
Db      13 SSVAAARVMD 22

RESULT 27
US-10-282-122A-62857
; Sequence 62857, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62857
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Mycobacterium bovis
US-10-282-122A-62857
```

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Query Match      66.0%; Score 33; DB 15; Length 367;
Best Local Similarity 60.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ASIAARVLD 10
Db      13 SSVAAARVMD 22

RESULT 28
US-10-282-122A-64830
; Sequence 64830, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64830
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-282-122A-64830

Query Match      66.0%; Score 33; DB 15; Length 367;
Best Local Similarity 60.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ASIAARVLD 10
Db      13 SSVAAARVMD 22

RESULT 29
US-10-627-476-508
; Sequence 508, Application US/10627476
; Publication No. US20040030116A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Pompejus, Mark
; APPLICANT: Kroege, Burkhard
; APPLICANT: Schoder, Hartwig
; APPLICANT: Seider, Oekar
; APPLICANT: Haberhauser, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; FILE REFERENCE: BGI-125CPCN
; CURRENT APPLICATION NUMBER: US/10/627,476
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: 09/602,787
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: USSN 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931454.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931478.0
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931563.9
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932122.1
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932124.8
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932180.9
; PRIOR FILING DATE: 1999-07-09
; REMAINING PRIOR APPLICATION data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 678
; SEQ ID NO 508
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
; US-10-627-476-508

Query Match      66.0%; Score 33; DB 15; Length 402;
Best Local Similarity 63.6%; Pred. No. 3.4e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 ASIAARVLDY 11
DB      260 ASIAPAALDY 270

RESULT 30
US-09-738-626-6555
; Sequence 6555, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
```

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; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 6555
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
; US-09-738-626-6555

Query Match      66.0%; Score 33; DB 9; Length 449;
Best Local Similarity 63.6%; Pred. No. 3.8e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 ASIAARVLDY 11
DB      307 ASIAPAALDY 317

RESULT 31
US-10-369-493-21054
; Sequence 21054, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 21054
; LENGTH: 453
; TYPE: PRT
; ORGANISM: SYNECHOCOCUS SP. WH 8102
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(453)
; OTHER INFORMATION: unsure at all Xaa locations
; US-10-369-493-21054

Query Match      66.0%; Score 33; DB 15; Length 453;
Best Local Similarity 54.5%; Pred. No. 3.9e+02;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      1 ASIAARVLDY 11
DB      268 AAVALARSINY 278

RESULT 32
US-10-437-963-136788
; Sequence 136788, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
```

```

; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 136788
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_38332C.1.pep
US-10-437-963-136788

Query Match      66.0%; Score 33; DB 16; Length 466;
Best Local Similarity 80.0%; Pred. No. 4e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 SIAAARVLDY 11
Db      106 SIAAARGIDY 115

RESULT 33
US-10-417-700A-49
; Sequence 49, Application US/10417700A
; Publication No. US20040033581A1
; GENERAL INFORMATION:
; APPLICANT: ECOCPIA BIOSCIENCES INC.
; APPLICANT: ZAZOPOULOS, Emmanuel
; APPLICANT: STRAFA, Alfredo
; APPLICANT: FARNEY, Chris
; TITLE OF INVENTION: Specialized dual condensation/epimerization domain in non-ribosom
; FILE REFERENCE: 3002-14US
; CURRENT APPLICATION NUMBER: US/10/417,700A
; CURRENT FILING DATE: 2003-04-17
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 49
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Pseudomonas syringae pv. syringae strain B301D
US-10-417-700A-49

Query Match      66.0%; Score 33; DB 15; Length 469;
Best Local Similarity 63.6%; Pred. No. 4e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 ASIAARVLDY 11
Db      396 ASIGAQRUCDY 406

RESULT 34
US-10-282-122A-77407
; Sequence 77407, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zvekind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
```

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; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77407
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Vibrio cholerae
US-10-282-122A-77407

Query Match      66.0%; Score 33; DB 15; Length 509;
Best Local Similarity 70.0%; Pred. No. 4.4e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 SIAAARVLDY 11
Db      7 SIALTRVLEY 16

RESULT 35
US-10-369-493-11847
; Sequence 11847, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldner, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 11847
; LENGTH: 670
; TYPE: PRT
; ORGANISM: Mesorhizobium loti
US-10-369-493-11847

Query Match      66.0%; Score 33; DB 15; Length 670;
Best Local Similarity 60.0%; Pred. No. 5.8e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 SIAAARVLDY 11
Db      259 SVALARAVDY 268

RESULT 36
US-10-282-122A-63141
; Sequence 63141, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
```


APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyckind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remainder Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 63141
LENGTH: 867
TYPE: PRT
ORGANISM: Moraxella catarrhalis
US-10-282-122A-63141

Query Match 66.0%; Score 33; DB 15; Length 867;
Best Local Similarity 60.0%; Pred. No. 7.7e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 SIAARVLDY 11
DB 439 SVADRWDF 448

RESULT 37
US-10-152-886-53
Sequence 53, Application US/10152886
Publication No. US2003006491A1
GENERAL INFORMATION:
APPLICANT: ECOPRIA BIOSCIENCES INC.
APPLICANT: Farnet, Chris
APPLICANT: Staffa, Alfredo
APPLICANT: Zazopoulos, Emmanuel
TITLE OF INVENTION: GENES AND PROTEINS INVOLVED IN THE BIOSYNTHESIS OF ENEDIYNE RING
TITLE OF INVENTION: STRUCTURES
FILE REFERENCE: 3011-305
CURRENT APPLICATION NUMBER: US/10/152,886
CURRENT FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PatentIn version 3.0
SEQ ID NO 53
LENGTH: 1958
TYPE: PRT

ORGANISM: Kitasatosporia sp.
US-10-152-886-53

Query Match 66.0%; Score 33; DB 14; Length 1958;
Best Local Similarity 70.0%; Pred. No. 1.8e+03;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAARVLD 10
DB 649 ASVAGLRVLD 658

RESULT 38
US-10-425-114-53118
Sequence 53118, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53113)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 53118
LENGTH: 144
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: 700162177_FLI pep
US-10-425-114-53118

Query Match 64.0%; Score 32; DB 15; Length 144;
Best Local Similarity 63.6%; Pred. No. 1.8e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ASIAARVLDY 11
DB 89 SSTAAALDY 99

RESULT 39
US-10-425-114-53613
Sequence 53613, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53113)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 53613
LENGTH: 146
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: UC-ZMFLMO17209D08_FLI pep
US-10-425-114-53613

Query Match 64.0%; Score 32; DB 15; Length 146;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;

Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 SIAPARYLD 10
 Db 82 SVSSARYLD 90

RESULT 40

US-10-437-963-107871
 ; Sequence 107871, Application US/10437963
 ; Publication No. US2004012343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazuk, Brad
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53221)B
 ; CURRENT APPLICATION NUMBER: US/10/437,963
 ; CURRENT FILING DATE: 2003-05-14
 ; NUMBER OF SEQ. ID NOS: 204966
 ; SEQ ID NO 107871
 ; LENGTH: 220
 ; TYPE: PRT
 ; ORGANISM: Oryza sativa
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_12180C.1.pep
 ; US-10-437-963-107871

Query Match 64.0%; Score 32; DB 16; Length 220;
 Best Local Similarity 87.5%; Pred. No. 2.9e+02;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASIAPARY 8
 Db 53 ASVAPARY 60

Search completed: March 31, 2005, 12:46:08
 Job time : 62.5312 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: March 31, 2005, 11:51:19 ; Search time 15.6406 Seconds
(without alignments)
67.669 Million cell updates/sec

Title: US-10-614-959-12
Perfect score: 50
Sequence: 1 ASIAAARVLDY 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	72.0	663	2 AF2984	3-methylcrotonyl-C
2	36	72.0	709	2 A98299	3-methylcrotonyl-C
3	35	70.0	143	2 S43071	hypothetical prote
4	35	70.0	692	2 S56849	probable membrane
5	35	70.0	696	2 AB1210	teichoic acid bios
6	34	68.0	231	2 D87715	carboxymethylenab
7	34	68.0	279	1 SUMYTV	thermolase (BC 3.4
8	34	68.0	579	2 I40371	methyltransferase
9	34	68.0	649	2 T18883	hypothetical prote
10	34	68.0	956	2 B71468	probable insulinas
11	33	66.0	162	2 AF1059	probable transcript
12	33	66.0	202	2 AF2831	DNA polymerase III
13	33	66.0	202	2 B97609	probable DNA polym
14	33	66.0	220	2 B98878	conserved hypotet
15	33	66.0	264	2 G69213	hypothetical prote
16	33	66.0	358	2 T45400	hypothetical prote
17	33	66.0	367	2 C70858	hypothetical prote
18	33	66.0	397	2 C84904	hypothetical prote
19	33	66.0	441	2 A75619	cobyrinic acid a.c
20	33	66.0	482	2 H70463	glycine dehydrogen
21	33	66.0	509	2 G62104	glutamate-cRNA synt
22	33	66.0	614	2 S45053	membrane protein E
23	33	66.0	1027	2 T27970	hypothetical prote
24	33	66.0	1232	2 T01655	multidrug resistan
25	32	64.0	305	2 B85437	methionyl aminope
26	32	64.0	342	2 G69502	histidinol-phospha
27	32	64.0	363	2 D64640	hypothetical prote
28	32	64.0	365	2 C87712	carbohydrate kinas
29	32	64.0	409	2 AG2869	N-cardamoyl-beta-a

30	32	64.0	415	2 A97646	n-cardamoyl-beta-a
31	32	64.0	435	2 T20819	hypothetical prote
32	32	64.0	448	2 T16256	hypothetical prote
33	32	64.0	576	1 B70558	probable ABC trans
34	32	64.0	655	2 G96524	protein T1N15.9 [1
35	32	64.0	777	2 G95940	probable xanthine
36	32	64.0	817	2 T49642	hypothetical prote
37	31	62.0	119	2 T16347	hypothetical prote
38	31	62.0	131	2 AG2388	hypothetical prote
39	31	62.0	144	2 C75376	hypothetical prote
40	31	62.0	172	2 S75615	hypothetical prote
41	31	62.0	177	2 B83036	probable bacteriof
42	31	62.0	230	2 AF3541	glutathione transf
43	31	62.0	249	2 A81001	electron transfer
44	31	62.0	249	2 F82018	electron transfer
45	31	62.0	254	2 AC3018	conserved hypothet

ALIGNMENTS

```

RESULT 1
AF2984 3-methylcrotonyl-CoA carboxylase alpha subunit [imported] - Agrobacterium tumefaciens (s
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision.11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AF2984
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.B.; Chen, Y.; Woo, L
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kuttyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A>Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AF2984
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-663 <KUR>
A:Cross-references: UNIPROT:Q8U955; GB:AA008689; PTDN:AA44232.1; PTD:gl7741880; GSPDB:G
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: mcca
A:Map position: linear chromosome
C:Superfamily: propionyl-CoA carboxylase alpha chain; biotin carboxylase homology; lipoy
Query Match 72.0%; Score 36; DB 2; Length 663;
Best Local Similarity 63.6%; Pred. No. 27;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Cy 1 ASIAAARVLDY 11
Db 258 AATAAARVLDY 268

RESULT 2
A98299 3-methylcrotonyl-CoA carboxylase alpha chain (AF310338) [imported] - Agrobacterium tumef
C:Species: Agrobacterium tumefaciens
C:Date: 22-Oct-2001 #sequence_revision.22-Oct-2001 #text_change 09-Jul-2004
C:Accession: A98299
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A>Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: A98299
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-709 <KUR>
A:Cross-references: UNIPROT:Q8U955; GB:AA007870; PTDN:AAK9915.1; PTD:gl5159866; GSPDB:G
C:Genetics:
A:Gene: AGR_L_2704

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A;Map position: linear chromosome
 C;Superfamily: propionyl-CoA carboxylase alpha chain; biotin carboxylase homology; lipoy

Query Match 72.0%; Score 36; DB 2; Length 709;
 Best Local Similarity 63.6%; Pred. No. 29;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAARVLDY 11
 |||:|||||
 Db 304 AATMAARADY 314

RESULT 3
 S43071
 hypothetical protein 5 - human herpesvirus 6
 C;Species: human herpesvirus 6
 C;Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
 C;Accession: S43071
 R;Thompson, J.; Choudhury, S.; Kashanchi, F.; Doniger, J.; Berneman, Z.; Frenkel, N.; RC
 Oncogene 9, 1167-1175, 1994
 A;Title: A transforming fragment within the direct repeat region of human herpesvirus 6
 A;Reference number: S43067; MUID:94181269; PMID:8134119
 A;Accession: S43071
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-143 <THO>
 A;Cross-references: UNIPROT:Q69582; EMBL:X73675; NID:G469952; PIDN:CA52028.1; PID:G4695
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1993

Query Match 70.0%; Score 35; DB 2; Length 143;
 Best Local Similarity 88.9%; Pred. No. 8.7;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASIAARVLT 9
 |||:|||||
 Db 7 ASIAARVLT 15

RESULT 4
 S56849
 probable membrane protein YUL073w - yeast (*Saccharomyces cerevisiae*)
 N;Alternate names: hypothetical protein HRC558; hypothetical protein J083
 C;Species: *Saccharomyces cerevisiae*
 C;Date: 05-May-1995 #sequence_revision 08-Sep-1995 #text_change 09-Jul-2004
 C;Accession: S56849; S56847; S50798; S47117; S57736
 R;Rose, M.; Koeltter, P.; Entian, K.D.
 submitted to the Protein Sequence Database, September 1995
 A;Reference number: S56848
 A;Accession: S56849
 A;Molecule type: DNA
 A;Residues: 1-692 <ROS>
 A;Cross-references: UNIPROT:P40358; EMBL:Z49348; NID:G1008228; PID:G1008229; MIPS:YUL073
 R;Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F.
 submitted to the Protein Sequence Database, September 1995
 A;Reference number: S56835
 A;Accession: S56847
 A;Molecule type: DNA
 A;Residues: 135-692 <POH>
 A;Cross-references: EMBL:Z49348; MIPS:YUL073w
 R;Vandenbol, M.; Durand, P.; Dion, C.; Portetelle, D.; Hilger, F.
 Yeast 11, 57-60, 1995
 A;Title: Sequence of a 17.1 kb DNA fragment from chromosome X of *Saccharomyces cerevisiae*
 A;Reference number: S50798; MUID:95282514; PMID:7762302
 C;Accession: S50798
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 135-692 <VAN>
 A;Cross-references: EMBL:Z34288; NID:G498992; PIDN:CA84049.1; PID:G498993
 R;Vandenbol, M.; Durand, P.; Dion, C.; Portetelle, D.; Hilger, F.
 submitted to the EMBL Data Library, June 1994
 A;Description: Sequence analysis of a 17.1 kb DNA fragment from chromosome X of *Sacchar*
 A;Reference number: S47117

A;Accession: S47117
 A;Molecule type: DNA
 A;Residues: 135-692 <VAN>
 A;Cross-references: EMBL:Z34288; NID:G498992; PID:G498993
 R;Sor, F.J.
 submitted to the EMBL Data Library, June 1995
 A;Reference number: S57731
 A;Accession: S57736
 A;Molecule type: DNA
 A;Residues: 1-692 <SOR>
 A;Cross-references: EMBL:X88851; NID:G895892; PID:G895898
 C;Genetics:
 A;Gene: SCD:JEM1
 A;Cross-references: SGD:S0003609; MIPS:YUL073w
 A;Map position: 10L
 C;Keywords: transmembrane protein
 F;585-655/Domain: dnaJ amino-terminal homology <DNV>

Query Match 70.0%; Score 35; DB 2; Length 692;
 Best Local Similarity 70.0%; Pred. No. 45;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 SIAARVLDY 11
 |||:|||||
 Db 245 SIAARVLDY 254

RESULT 5
 AE1210
 teichoic acid biosynthesis protein B homolog lmo1085 [imported] - *Listeria monocytogenes*
 C;Species: *Listeria monocytogenes*
 C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
 C;Accession: AE1210
 R;Glaeser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker,
 .; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Duseurget, O.; Entian, K.D.; Feiht, H.,
 D.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A;Authors: Kretz, U.; Kunz, M.; Kunz, F.; Kurpkat, G.; Madueno, E.; Maicouram, A.; Mat
 ok, C.; Schlueter, T.; Simoes, N.; Tietz, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,
 A;Title: Comparative genomics of *Listeria* species.
 A;Reference number: AB1077; MUID:21537279; PMID:11679669
 A;Accession: AE1210
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-696 <GUA>
 A;Cross-references: UNIPROT:Q8Y833; GB:NC_003210; PIDN:CAC99163.1; PID:G16410487; GSPDB:C
 A;Experimental source: strain EGD-e
 C;Genetics:
 A;Gene: lmo1085

Query Match 70.0%; Score 35; DB 2; Length 696;
 Best Local Similarity 75.0%; Pred. No. 45;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 AAARVLDY 11
 |||:|||||
 Db 685 AAARVLDY 692

RESULT 6
 D87715
 carboxymethylglutaminolactamase [imported] - *Caulobacter crescentus*
 C;Species: *Caulobacter crescentus*
 C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
 C;Accession: D87715
 R;Nieman, W.C.; Feildby, T.V.; Paulsen, I.T.; Nelson, K.E.; Eissen, J.; Heidelberg, J.I.
 B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Hatt, D.H.; Kolon
 u, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A;Title: Complete Genome Sequence of *Caulobacter crescentus*.
 A;Reference number: A87249; MUID:21173698; PMID:11259647
 A;Accession: D87715
 A;Status: preliminary

A:Molecule type: DNA
 A:Residues: 1-231 <STO>
 A:Cross-references: UNIPROT:Q9A213; GB:AE005673; NID:g3142534; PIDN:AAK25720.1; GSPDB:C
 C:Species: Thermococcus
 C:Genetics: CC3758
 C:Superfamily: carboxymethylglutaminase

Query Match 68.0%; Score 34; DB 2; Length 231;
 Best Local Similarity 80.0%; Pred. No. 23;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASIAARVLD 10
 |||
 Db 100 ATIAARVLD 109

RESULT 7
 SUMTVV
 thermilase (EC 3.4.21.66) - Thermococcus vulgaris

C:Species: Thermococcus vulgaris
 C>Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 09-Jul-2004
 C:Accession: A00973
 R:Meloun, B.; Baudys, M.; Koscka, V.; Hausdorf, G.; Frommel, C.; Hohne, W.E.
 FEBS Lett. 183, 195-200, 1985
 A:Title: Complete primary structure of thermilase from Thermococcus vulgaris and its
 A:Reference number: A00973
 A:Accession: A00973
 A:Molecule type: protein
 A:Residues: 1-279 <MEU>
 A:Cross-references: UNIPROT:P04072

C:Comment: This protein is enzymatically similar to a proteinase from Streptomyces sp.
 C:Superfamily: subtilisin; subtilisin homology
 C:Keywords: hydrolase; serine proteinase
 F:29-233/Domain: subtilisin homology <SBT>
 F:38/71,225/Active site: Asp, His, Ser #status predicted

Query Match 68.0%; Score 34; DB 1; Length 279;
 Best Local Similarity 80.0%; Pred. No. 28;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAARVLD 10
 |||
 Db 96 ASIAARVLD 105

RESULT 8

140371
 methyltransferase - Bacillus stearothermophilus (fragment)
 C:Species: Bacillus stearothermophilus
 C>Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
 C:Accession: I40371
 R:Rina, M.; Markaki, M.; Bouricis, V.
 Gene 150, 71-73, 1994
 A:Title: Sequence of the cloned bseC gene: M.BseC reveals high homology to M.BanIII.
 A:Reference number: I40371; MUID:95047552; PMID:7959066
 A:Accession: I40371
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-579 <RES>
 A:Cross-references: UNIPROT:P43423; EMBL:X79509; NID:g619638; PIDN:CAA56041.1; PID:g6196

C:Genetics: bseC
 C:Superfamily: site-specific methyltransferase (adenine-specific) Paer71
 Query Match 68.0%; Score 34; DB 2; Length 579;
 Best Local Similarity 54.5%; Pred. No. 60;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 ASIAARVLD 11
 |||
 Db 26 AEVIAKRLDY 36

RESULT 9
 T38883
 hypothetical protein SPAC4H3.03c - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C:Accession: T38883
 R:Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
 submitted to the EMBL Data Library, February 1996
 A:Reference number: Z21807
 A:Accession: T38883
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
 A:Residues: 1-649 <MDR>
 A:Cross-references: UNIPROT:Q10211; EMBL:Z69380; PIDN:CAA93342.1; GSPDB:GN00066; SPDB:SP
 A:Experimental source: strain 972h-; cosmid c4H3
 C:Genetics: SPDB:SPAC4H3.03c
 A:Map position: 1
 C:Superfamily: Schizosaccharomyces pombe hypothetical protein SPAC4H3.03c

Query Match 68.0%; Score 34; DB 2; Length 649;
 Best Local Similarity 70.0%; Pred. No. 68;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASIAARVLD 10
 |||
 Db 631 AIAARVLD 640

RESULT 10

B71468
 probable insulinase family/proteinase III - Chlamydia trachomatis (serotype D, strain UW
 C:Species: Chlamydia trachomatis
 C>Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
 C:Accession: B71468
 R:Stephens, R.S.; Kaiman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,
 Science 282, 754-759, 1998
 A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trac
 A:Reference number: A71570; MUID:9900809; PMID:9784136
 A:Accession: B71468
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-956 <ARN>
 A:Cross-references: UNIPROT:O84812; GB:AE001353; GB:AE001273; NID:g3329271; PIDN:AA66840
 A:Experimental source: serotype D, strain UW-3/Cx
 C:Genetics: ptx

C:Superfamily: insulin-degrading enzyme (IDE)

Query Match 68.0%; Score 34; DB 2; Length 956;
 Best Local Similarity 77.8%; Pred. No. 1e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 IAAARVLD 11
 |||
 Db 916 IAAARVLD 924

RESULT 11

AF1059
 probable transcription regulator SRY4801 [imported] - Salmonella enterica subsp. enteric

C:Species: Salmonella enterica subsp. enterica serovar Typh
 A>Note: this species has also been called Salmonella typh
 C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 C:Accession: AF1059
 R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
 th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
 S.; Moule, S.; O'Gaora, P.
 Nature 413, 848-852, 2001
 A:Authors: Park, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
 A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
 A:Reference number: AB0502; MUID:21534947; PMID:11677608
 A:Accession: AF1059

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-162 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD06923.1; PID:G16505571; GSPDB:GN00176
C;Genetics:
A;Gene: STY4801

Query Match 66.0%; Score 33; DB 2; Length 162;
Best Local Similarity 75.0%; Pred. No. 26;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 AARVLDY 11
Db 112 AVARILDY 119

RESULT 12
AF2831
DNA polymerase III, epsilon subunit [imported] - *Agrobacterium tumefaciens* (strain C58,
C;Species: *Agrobacterium tumefaciens*
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AF2831
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monke, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, H.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743313
A;Accession: AF2831
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-202 <KUR>
A;Cross-references: UNIPROT:Q8UDP4; GB:AE008688; PIDN:AAL43068.1; PID:G17740536; GSPDB:G
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atuz077
A;Map position: circular chromosome

Query Match 66.0%; Score 33; DB 2; Length 202;
Best Local Similarity 88.9%; Pred. No. 32;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASIAARVL 9
Db 156 ASIAARAL 164

RESULT 13
B97609
probable DNA polymerase III, epsilon chain [imported] - *Agrobacterium tumefaciens* (strai
C;Species: *Agrobacterium tumefaciens*
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: B97609
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quicilo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tun*
A;Reference number: A97359; MUID:21608551; PMID:117433194
A;Accession: B97609
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-202 <KUR>
A;Cross-references: UNIPROT:Q8UDP4; GB:AE007869; PIDN:AAK87827.1; PID:G15157207; GSPDB:G
C;Genetics:
A;Gene: AGR_C_3764
A;Map position: circular chromosome

Query Match 66.0%; Score 33; DB 2; Length 202;
Best Local Similarity 88.9%; Pred. No. 32;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASIAARVL 9
Db 156 ASIAARAL 164

RESULT 14
F89878
conserved hypothetical protein SA0939 [imported] - *Staphylococcus aureus* (strain N315)
C;Species: *Staphylococcus aureus*
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: F89878
R;Kuroda, M.; Ohra, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaico, C.; Sekimizu, K.; i
C.; Shiba, T.; Hattori, W.; Ogasawara, N.; Hayashi, H.; Hirataku, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: F89878
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-220 <KUR>
A;Cross-references: UNIPROT:Q99V10; GB:BA000018; PID:G13700889; PIDN:BA842185.1; GSPDB:G
A;Experimental source: strain N315
C;Genetics:
A;Gene: SA0939
C;Superfamily: conserved hypothetical protein MG323

Query Match 66.0%; Score 33; DB 2; Length 220;
Best Local Similarity 60.0%; Pred. No. 35;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 SIAARVLDY 11
Db 131 NVASASVLDY 140

RESULT 15
G69213
hypothetical protein MTH852 - *Methanobacterium thermoautotrophicum* (strain Delta H)
C;Species: *Methanobacterium thermoautotrophicum*
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: G69213
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; E
; Qu, D.; Spadofora, R.; Vicatore, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Javan, N.,
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of *Methanobacterium thermoautotrophicum* Delta H: funct
A;Reference number: A69000; MUID:98037514; PMID:93711463
A;Accession: G69213
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-264 <MTH>
A;Cross-references: UNIPROT:Q26940; GB:AB000862; GB:AE000666; NID:G2621943; PIDN:AB85356
A;Experimental source: strain Delta H
C;Genetics:
A;Gene: MTH852

Query Match 66.0%; Score 33; DB 2; Length 264;
Best Local Similarity 54.5%; Pred. No. 43;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASIAARVLDY 11
Db 94 ASIAAVLINV 104

RESULT 16
T45400
hypothetical protein MCB637.07 [imported] - *Mycobacterium leprae*
C;Species: *Mycobacterium leprae*
C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 09-Jul-2004
C;Accession: T45400
R;Parkhill, J.; Barrett, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, September 1997
A:Reference number: Z16918
A:Accession: T45400
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-358 <PAR>
A:Cross-references: UNIPROT:O33099; EMBL:Z99263; PIDN:CAB16422.1
A:Experimental source: cosmid B637
C:Genetics:
A:Note: MLCB637.07
C:Superfamily: probable membrane protein YDL033c

Query Match 66.0%; Score 33; DB 2; Length 358;
Best Local Similarity 60.0%; Pred. No. 59;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 ASIAAARVLD 10
|||
Db 13 SSVAAARVMD 22

RESULT 17
C70858
hypothetical protein Rv3024c - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: C70858
R:Coile, S.T.; Broesch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Felwell, T.; Gentile, S.; Hamlin, N.; Holtroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, J.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: C70858
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-367 <COL>
A:Cross-references: UNIPROT:O53271; GB:AL021287; GB:AL123456; NID:g3261508; PIDN:CA1610
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: Rv3024c
C:Superfamily: probable membrane protein YDL033c

Query Match 66.0%; Score 33; DB 2; Length 367;
Best Local Similarity 60.0%; Pred. No. 60;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 ASIAAARVLD 10
|||
Db 13 SSVAAARVMD 22

RESULT 18
C84904
hypothetical protein At2g46550 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: C84904
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffatt, K.S.; Cronin, L.A.; Shen, M.; VanKen, S.E.; Umayam, L.; Tallon, L.; euse, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: C84904
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-397 <STO>
A:Cross-references: UNIPROT:O9ZPY4; GB:AE002093; NID:g4415936; PIDN:AAD20166.1; GSPDB:GN
C:Genetics:
A:Gene: At2g46550
A:Map position: 2

Query Match 66.0%; Score 33; DB 2; Length 397;
Best Local Similarity 63.6%; Pred. No. 65;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 ASIAAARVLDY 11
|||
Db 192 ASLVAORSLDY 202

RESULT 19
A75619
cobyrinic acid a,c-diamide synthase - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: A75619
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M.; Shen, M.; Vamathavan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Mai, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: A75619
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-441 <WHI>
A:Cross-references: UNIPROT:O9RZV2; GB:AE001826; NID:g6460827; PIDN:AAF12571.1; PID:g646
A:Experimental source: strain R1
C:Genetics:
A:Gene: DRB0009
A:Map position: megaplaamid
A:Genome: plasmid
A:Note: plasmid MP1
C:Superfamily: cobyrinic acid a,c-diamide synthase

Query Match 66.0%; Score 33; DB 2; Length 441;
Best Local Similarity 70.0%; Pred. No. 73;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 ASIAAARVLD 10
|||
Db 205 AALAAARVLD 214

RESULT 20
H70463
glycine dehydrogenase (decarboxylating) - Aquifex aeolicus
C:Species: Aquifex aeolicus
C>Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C:Accession: H70463
R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov, V.
Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98196666; PMID:9537320
A:Accession: H70463
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-482 <AF>
A:Cross-references: UNIPROT:O67740; GB:AE000762; NID:g2984163; PIDN:AA07701.1; PID:g298
A:Experimental source: strain VFS
C:Genetics:
A:Gene: gceP1
C:Superfamily: glycine dehydrogenase (decarboxylating)

Query Match 66.0%; Score 33; DB 2; Length 482;
Best Local Similarity 63.6%; Pred. No. 80;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 ASIAAARVLDY 11
|||
Db 391 ASDVAKRILDY 401

RESULT 21
G82104
glutamy1-tRNA synthetase VC2214 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C/Species: Vibrio cholerae
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C/Accession: G82104
R/Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;
Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, R.
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A/Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A/Reference number: A82035; MUID:20406833; PMID:10952301
A/Accession: G82104
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-509 <HE>
A/Cross-references: UNIPROT:O31153; GB:AE004293; GB:AE003852; NID:93656766; PIDN:AA9535
A/Experimental source: serogroup O1; strain N16961; biotype El Tor
C/Genetics:
A/Map position: 1
A/Suprafamily: glutamate-tRNA ligase; glutamine-tRNA ligase homology

Query Match 66.0%; Score 33; DB 2; Length 509;
Best Local Similarity 70.0%; Pred. No. 85;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 SIAARVLDY 11
Db 7 SIALTRVLEY 16

RESULT 22
S45053
membrane protein END2 - Yeast (Saccharomyces cerevisiae)
N/Alternate names: protein I2515; protein YLR088w
C/Species: Saccharomyces cerevisiae
C/Date: 03-May-1994 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004
C/Accession: S45053; S64922
R/Hamburger, D.; Egerton, M.; Riezman, H.
Submitted to the EMBL Data Library, May 1994
A/Description: End2p: a membrane protein with a functional ER retention sequence affects
A/Reference number: S45053
A/Accession: S45053
A/Molecule type: DNA
A/Residues: 1-614 <HM>
A/Cross-references: UNIPROT:P39012; EMBL:X79409; NID:6495141; PID:6495142
R/Benes, V.; Rechmann, S.; Nentwich, U.; Schwager, C.; Amorge, W.; Voss, H.
Submitted to the Protein Sequence Database, May 1996
A/Reference number: S64920
A/Accession: S64922
A/Molecule type: DNA
A/Residues: 1-614 <BM>
A/Cross-references: EMBL:Z73260; NID:91360458; PID:e245542; PID:91360459; MIPS:YLR088w
A/Experimental source: strain S288C
C/Genetics:
A/Map position: 12R
A/Suprafamily: MIPs:YLR088w; SGD:S0004078
A/Key words: transmembrane protein
F/26-42/Domain: transmembrane #status predicted <TM1>
F/361-377/Domain: transmembrane #status predicted <TM2>
F/392-408/Domain: transmembrane #status predicted <TM3>
F/419-435/Domain: transmembrane #status predicted <TM4>
F/464-480/Domain: transmembrane #status predicted <TM5>
F/538-554/Domain: transmembrane #status predicted <TM6>
F/582-598/Domain: transmembrane #status predicted <TM7>

Query Match 66.0%; Score 33; DB 2; Length 614;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 SIAARVLDY 11
Db 202 SIAARVLDY 211

RESULT 23
T27970
hypothetical protein ZK675.2 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 12-Jul-2004
C/Accession: T27970
R/Sims, M.
Submitted to the EMBL Data Library, November 1994
A/Reference number: Z20448
A/Accession: T27970
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1027 <ML>
A/Cross-references: UNIPROT:Q09615; EMBL:Z46812; PIDN:CAA86844.1; GSPDB:GN00020; CESP:ZK
A/Experimental source: clone ZK675
C/Genetics:
A/Map position: 2
A/Insertions: 39/3; 176/3; 226/3; 268/1; 325/2; 471/3; 639/1; 702/3; 835/1; 919/1
C/Suprafamily: DNA polymerase, REV1 type

Query Match 66.0%; Score 33; DB 2; Length 1027;
Best Local Similarity 70.0%; Pred. No. 1.8e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 SIAARVLDY 11
Db 325 SIAAGKPLDY 334

RESULT 24
T06165
multidrug resistance protein 1 homolog - barley
C/Species: Hordeum vulgare (barley)
C/Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C/Accession: T06165
R/Davies, T.G.B.; Theodoulou, F.L.; Hallahan, D.L.; Forde, B.G.
Gene 199, 195-202, 1997
A/Title: Cloning and characterization of a novel P-glycoprotein homologue from barley.
A/Reference number: Z15500; MUID:98019088; PMID:9358056
A/Accession: T06165
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-1232 <DAV>
A/Cross-references: UNIPROT:Q23998; EMBL:Y10099; NID:92292906; PIDN:CAA71179.1; PID:92292
A/Experimental source: cv. Maris Mink
C/Suprafamily: multidrug resistance protein; ATP-binding cassette homology
F/381-575/Domain: ATP-binding cassette homology <ABC>

Query Match 66.0%; Score 33; DB 2; Length 1232;
Best Local Similarity 60.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 ASIAARVLD 10
Db 329 ASVAATRILE 338

RESULT 25
E85437
methionyl aminopeptidase-like protein [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C/Accession: E85437
R/anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A/Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A/Reference number: A85001; MUID:20083488; PMID:10617198

A:Accession: E85437
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-305 <STO>
A:Cross-references: UNIPROT:Q9SM64; GB:NC_001268; NID:97270653; PIDN:CAB80370.1; GSPDB:C
C:Genetics:
A:Gene: AT937040
A:Map position: 4
C:Superfamily: Escherichia coli methionyl aminopeptidase

Query Match 64.0%; Score 32; DB 2; Length 305;
Best Local Similarity 63.6%; Pred. No. 80;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ASIAARVLDY 11
: |||||
Db 74 SGIAARVDRY 84

RESULT 26
G69502
histidinol-phosphate aminotransferase (hisc-2) homolog - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: G69502
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirschner, E.F.
; Glodek, A.; Zhou, L.; Overbeek, R.; Cockayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artlich, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A:Reference number: A69250; MUID:98049343; PMID:9389475
A:Accession: G69502
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-342 <KLE>
A:Cross-references: UNIPROT:O28255; GB:AE000963; GB:AE000782; NID:g2689286; PIDN:AA88922
C:Superfamily: probable histidinol-phosphate transaminase

Query Match 64.0%; Score 32; DB 2; Length 342;
Best Local Similarity 70.0%; Pred. No. 90;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 SIAARVLDY 11
: |||||
Db 245 AIAARSLDY 254

RESULT 27
D64640
hypothetical protein HP0964 - Helicobacter pylori (strain 26695)
C:Species: Helicobacter pylori
C>Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C:Accession: D64640
R:Tomb, J.F.; White, O.; Kexlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khaliak, H.G.; Glodek, A.; McKen
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; MUID:97394467; PMID:9252185
A:Accession: D64640
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-363 <TOM>
A:Cross-references: UNIPROT:O25617; GB:AE000605; GB:AE000511; NID:g2314103; PIDN:AA0801
C:Genetics:
A:Start codon: GTG

Query Match 64.0%; Score 32; DB 2; Length 363;
Best Local Similarity 63.6%; Pred. No. 96;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ASIAARVLDY 11
: |||||
Db 188 AIIKAGVLDY 198

RESULT 28
C87712
carbohydrate kinase, pfkF family [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: C87712
R:Merham, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: C87712
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-365 <STO>
A:Cross-references: UNIPROT:Q9A233; GB:AE005673; NID:g13425505; PIDN:AAK25695.1; GSPDB:G
C:Genetics:
A:Gene: CC3733

Query Match 64.0%; Score 32; DB 2; Length 365;
Best Local Similarity 60.0%; Pred. No. 97;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SIAARVLDY 11
: |||||
Db 338 SIAARVIDH 347

RESULT 29
AG2869
N-carbamoyl-beta-alanine amidohydrolase [imported] - Agrobacterium tumefaciens (strain C
C:Species: Agrobacterium tumefaciens
C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AG2869
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayvin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krepan, W.; Perry, M.; Gordon-Kamm, F
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AG2869
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-409 <KUR>
A:Cross-references: UNIPROT:Q8UCU8; GB:AE008688; PIDN:AA43373.1; PID:g17740869; GSPDB:G
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: amAB
A:Map position: N-carbamyl-L-amino acid amidohydrolase
C:Superfamily: N-carbamyl-L-amino acid amidohydrolase

Query Match 64.0%; Score 32; DB 2; Length 409;
Best Local Similarity 60.0%; Pred. No. 11e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ASIAARVLD 10
: |||||
Db 235 AGIAARILR 244

RESULT 30
A97646
n-cabamoyl-beta-alanine amidohydrolase (PA0444) [imported] - Agrobacterium tumefaciens
C:Species: Agrobacterium tumefaciens

C/Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
 C/Accession: A97646
 R/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quirollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
 A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tumefaciens* strain A97646
 A/Reference number: A97646; MUID:21608551; PMID:117433194
 A/Accession: A97646
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-415 <KOR>
 A/Cross-references: UNIPROT:Q8UCU8; GB:AE007869; PIDN:AAK88122.1; PID:G15157556; GSPDB:G15157556
 A/Map position: circular chromosome
 C/Superfamily: N-cardamyl-L-amino acid amidohydrolase

Query Match 64.0%; Score 32; DB 2; Length 415;
 Best Local Similarity 60.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 ASIAAARVLD 10
 |||:|||||:
 Db 241 AGIAAARILE 250

RESULT 31
 T20819
 hypothetical protein F13B12.4 - *Caenorhabditis elegans*
 C/Species: *Caenorhabditis elegans*
 C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C/Accession: T20819
 R/Wild, A.
 submitted to the EMBL Data Library, April 1996
 A/Reference number: Z19329
 A/Accession: T20819
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-435 <WIL>
 A/Cross-references: UNIPROT:Q19374; EMBL:Z70683; PIDN:CAA94589.1; GSPDB:GNO0022; CESP:FA19374
 A/Experimental source: clone F13B12
 C/Genetics:
 A/Gene: CESP:F13B12.4
 A/Map position: 4
 A/Insertions: 38/1; 104/1; 161/3; 358/2

Query Match 64.0%; Score 32; DB 2; Length 435;
 Best Local Similarity 60.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 ASIAAARVLD 10
 |||:|||||:
 Db 324 ASVATMRILD 333

RESULT 32
 T16256
 hypothetical protein F35C8.3 - *Caenorhabditis elegans*
 C/Species: *Caenorhabditis elegans*
 C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C/Accession: T16256
 R/Wu, X.
 submitted to the EMBL Data Library, November 1995
 A/Description: The sequence of C. elegans cosmid F35C8.
 A/Reference number: Z18486
 A/Accession: T16256
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-448 <WUX>
 A/Cross-references: UNIPROT:Q9UAH1; EMBL:U40941; NID:G1072184; PID:G1072189; PIDN:AAA817
 C/Genetics:
 A/Gene: CESP:F35C8.3
 A/Map position: 3
 A/Insertions: 70/1; 97/1; 134/1; 162/3; 201/3; 253/3; 308/3; 362/3; 393/3; 413/3

C/Superfamily: kinase-related transforming protein, protein kinase homology

Query Match 64.0%; Score 32; DB 2; Length 448;
 Best Local Similarity 63.6%; Pred. No. 1.2e+02;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 ASIAAARVLDY 11
 |||:|||||:
 Db 45 AAFAAARNTLY 55

RESULT 33
 B70558
 Probable ABC transporter cydC - *Mycobacterium tuberculosis* (strain H37RV)
 C/Species: *Mycobacterium tuberculosis*
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C/Accession: B70558
 R/Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998
 A/Authors: Squares, R.; Suleston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A/Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome
 A/Reference number: A70500; MUID:98295987; PMID:9634230
 A/Accession: B70558
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-576 <COL>
 A/Cross-references: UNIPROT:O06137; GB:Z95554; GB:AL123456; NID:G3361771; PIDN:CAB08897.1
 A/Experimental source: strain H37RV
 C/Genetics:
 A/Gene: cydC
 C/Superfamily: *Mycobacterium tuberculosis* probable ABC transporter cydC; ATP-binding cassette; Key words: ATP
 F/358-556/Domain: ATP-binding cassette homology <ABC>

Query Match 64.0%; Score 32; DB 1; Length 576;
 Best Local Similarity 87.5%; Pred. No. 1.6e+02;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 IAARVLD 10
 |||:|||||:
 Db 313 IAARVLD 320

RESULT 34
 G96524
 protein T1N15.9 (imported) - *Arabidopsis thaliana*
 C/Species: *Arabidopsis thaliana* (mouse-ear cress)
 C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C/Accession: G96524
 R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Jensen, N.F.; Hughes, B.; Hultzer, L.
 Nature 408, 816-820, 2000
 A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luross, J.S.; Maitl, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I. Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A/Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
 A/Reference number: A86141; MUID:21016719; PMID:11130712
 A/Accession: G96524
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-655 <STO>
 A/Cross-references: UNIPROT:Q9LPT7; GB:AE005173; NID:98778668; PIDN:AAF9696.1; GSPDB:GNK
 C/Genetics:
 A/Gene: T1N15.9
 A/Map position: 1

Query Match 64.0%; Score 32; DB 2; Length 655;
 Best Local Similarity 70.0%; Pred. No. 1.8e+02;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 SIARAVLDY 11
: ||| |||
Db 475 AIGAAAGLDY 484

RESULT 35

G95940

probable xanthine dehydrogenase (EC 1.1.1.204) [imported] - *Sinorhizobium meliloti* (strainC:Species: *Sinorhizobium meliloti*

C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004

C:Accession: G95940

R:Finan, T.M.; Weidner, S.; Wong, K.; Buhtmeister, J.; Chain, P.; Vorholter, F.J.; Hernan

Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001

A:Title: The complete sequence of the 1,683-kb pSymb megaplasmid from the N2-fixing endo

A:Reference number: A95842; MUID:21396508; PMID:1141431

A:Accession: G95940

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-777 <KUR>

A:Cross-references: UNIPROT:Q92VB7; GB:AUS91985; PIDN:CAC49191.1; PID:g15140676; GSPDB:C

A:Experimental source: strain 1021, megaplasmid pSymb

R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,

Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;

L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,

hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yen, K.

A:Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.

A:Reference number: A96039; MUID:21368234; PMID:11474104

A:Contents: annotation

C:Genetics:

A:Gene: xdbB1; SMD21287

A:Genome: plasmid

C:Superfamily: carbon monoxide dehydrogenase molybdoprotein

C:Keywords: oxidoreductase

Query Match 64.0%; Score 32; DB 2; Length 777;

Best Local Similarity 70.0%; Pred. No. 2.1e+02;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 SIARAVLDY 11
: ||| |||
Db 740 SMAAASVADY 749

RESULT 36

T49642

hypothetical protein B5022.240 [imported] - *Neurospora crassa*C:Species: *Neurospora crassa*

C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004

C:Accession: T49642

R:Schule, U.; Aign, V.; Hohelsel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,

submitted to the Protein Sequence Database, May 2000

A:Reference number: Z25022

A:Accession: T49642

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-817 <SCH>

A:Cross-references: UNIPROT:Q9P5S8; EMBL:AL355932; GSPDB:GN00116; NCSP:B5022.240

C:Genetics:

A:Gene: NCSP:B5022.240

A:Map position: 6

A:introns: 37/1

Query Match 64.0%; Score 32; DB 2; Length 817;

Best Local Similarity 63.6%; Pred. No. 2.2e+02;

Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ASIAARVLDY 11
: : ||| |||

Db 146 AGLDARVADY 156

RESULT 37

T16347

hypothetical protein F42G9.4 - *Caenorhabditis elegans*C:Species: *Caenorhabditis elegans*

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C:Accession: T16347

R:Ratch, A.

submitted to the EMBL Data Library, March 1996

A:Description: The sequence of C. elegans cosmid F42G9.

A:Reference number: Z18498

A:Accession: T16347

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-119 <TAI>

A:Cross-references: UNIPROT:Q20348; EMBL:U00051; NID:g1216305; PID:g485118; PIDN:AAA9135

A:Experimental source: strain Bristol N2

C:Genetics:

A:Gene: CESP:F42G9.4

A:introns: 56/2; 91/3

C:Superfamily: *Caenorhabditis elegans* hypothetical protein F42G9.4

Query Match 62.0%; Score 31; DB 2; Length 119;

Best Local Similarity 60.0%; Pred. No. 48;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 SIARAVLDY 11
: : ||| |||
Db 77 SITSAYLDY 86

RESULT 38

AC2388

hypothetical protein all4663 [imported] - *Nostoc* sp. (strain PCC 7120)C:Species: *Nostoc* sp. PCC 7120A:Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120

C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C:Accession: AC2388

R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Itiguchi

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S

DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Ana*

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AC2388

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-131 <KUR>

A:Cross-references: UNIPROT:Q8VNA4; GB:BA000019; PIDN:BA876362.1; PID:g17133800; GSPDB:C

C:Genetics:

A:Gene: all4663

C:Superfamily: *Neisseria meningitidis* hypothetical protein NME0979

Query Match 62.0%; Score 31; DB 2; Length 131;

Best Local Similarity 80.0%; Pred. No. 54;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 SIARAVLDY 11
: ||| ||| |||
Db 7 SIARAVLDY 16

RESULT 39

C75376

hypothetical protein - *Deinococcus radiodurans* (strain R1)C:Species: *Deinococcus radiodurans*

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C:Accession: C75376

R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;

M.; Shen, M.; Vamathevan, J.D.; Lam, P.; McDonald, L.; Ulterback, T.; Zalewski, C.; Ma

S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A/Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.

A/Reference number: A75250; MUID:20036896; PMID:10567266

A/Accession: C75376

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-144 <WHI>

A/Cross-references: UNIPROT:Q9RTZ1; GB:AE002004; GB:AE000513; NID:96459366; PIDN:AAF1117

A/Experimental source: strain R1

C/Genetics:

A/Gene: DR1607

A/Map position: 1

C/Superfamily: *Deinococcus radiodurans* hypothetical protein DR1607

Query Match

62.0%; Score 31; DB 2; Length 144;

Best Local Similarity 77.8%; Pred. No. 59;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 SIARVYLD 10

Db 32 AIAARVLD 40

RESULT 40

S75615

hypothetical protein sir1956 - *Synechocystis* sp. (strain PCC 6803)

C/Species: *Synechocystis* sp.

A/Variety: PCC 6803

C/Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C/Accession: S75615

R/Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;

O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda

DNA Res. 3, 109-136, 1996

A/Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*

S.

A/Reference number: S74322; MUID:97061201; PMID:8905231

A/Accession: S75615

A/Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-172 <KAN>

A/Cross-references: UNIPROT:P74092; EMBL:D90912; GB:AB001339; NID:91653228; PIDN:BAA1817

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match

62.0%; Score 31; DB 2; Length 172;

Best Local Similarity 66.7%; Pred. No. 71;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 IAAARVLDY 11

Db 93 IAAARVLDY 101

Search completed: March 31, 2005, 12:11:15
Job time : 17.6406 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 31, 2005, 11:42:54 ; Search time 73.0469 Seconds
(without alignments)
77.113 Million cell updates/sec

Title: US-10-614-959-12
Perfect score: 50
Sequence: 1 ASIAAARVLDY 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	74.0	421	2	Q6H820 oryza sativ
2	37	74.0	694	2	Q8EF52 shewanella
3	37	74.0	1203	2	Q8S2E4 oryza sativ
4	37	74.0	1234	2	Q8GU81 oryza sativ
5	36	72.0	402	2	Q62CX8 burkholderi
6	36	72.0	402	2	Q63M18 burkholderi
7	36	72.0	663	2	Q8UA95 agrobacteri
8	36	72.0	709	2	Q7CSK5 agrobacteri
9	36	72.0	723	2	Q8H034 oryza sativ
10	36	72.0	778	2	Q7MA36 wolinnella s
11	36	72.0	1072	2	Q69X93 oryza sativ
12	35	70.0	143	2	Q69582 human hepe
13	35	70.0	184	2	Q6A091 desulfotale
14	35	70.0	329	2	Q9RJR7 streptomyce
15	35	70.0	692	1	VJH3 YEAST
16	35	70.0	696	2	Q8Y833 listeria mo
17	35	70.0	1228	2	Q6MK31 bdelioidri
18	35	70.0	6977	2	Q7R034 giardia lam
19	35	68.0	153	2	Q6NA42 rhodospseudo
20	34	68.0	231	2	Q9A213 calubacter
21	34	68.0	279	1	THET THEVU
22	34	68.0	322	2	Q6AH23 thelsonia x
23	34	68.0	342	2	Q8ZSL1 pyrobaculum
24	34	68.0	342	2	Q8ZXL8 pyrobaculum
25	34	68.0	342	2	Q9LV51 arabidopsis
26	34	68.0	344	2	Q9FV51 arabidopsis
27	34	68.0	568	2	Q8P714 xanthomonas
28	34	68.0	568	2	Q8P714 xanthomonas
29	34	68.0	579	1	MTCL_BACST
30	34	68.0	579	2	Q9R0K2 bacillus st
31	34	68.0	589	2	Q7F1D1 oryza sativ

32	34	68.0	596	2	Q7QH89 anopheles g
33	34	68.0	649	1	VAY3_SCHPO
34	34	68.0	827	2	Q6ZG00 oryza sativ
35	34	68.0	866	2	Q6FY30 candida gla
36	34	68.0	874	2	Q67R60 symbiobacte
37	34	68.0	912	2	Q8ZM19 pyrobaculum
38	34	68.0	920	2	Q8A1R0 bacteroides
39	34	68.0	945	2	Q7E2J3 oryza sativ
40	34	68.0	956	2	Q84812 chlamydia t
41	34	68.0	1206	2	Q8ZXP1 pyrobaculum
42	34	68.0	2785	2	Q8ZV89 pyrobaculum
43	34	66.0	162	2	Q8Z129 salmoneilla
44	33	66.0	162	2	Q8ZK37 salmoneilla
45	33	66.0	162	2	Q83SS1 salmoneilla

ALIGNMENTS

RESULT 1					
ID	Q6H820	PRELIMINARY;	PRT;	421 AA.	
AC	Q6H820;				
DT	05-JUL-2004 (TREMBlrel. 27, Created)				
DT	05-JUL-2004 (TREMBlrel. 27, Last sequence update)				
DT	05-JUL-2004 (TREMBlrel. 27, Last annotation update)				
DE	GCN5-related N-acetyltransferase-like.				
CN	Name=O1297_C09.4;				
OS	Oryza sativa (japonica cultivar-group).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;				
OC	Euphorbiaceae; Oryzae; Oryza.				
OX	NCHI_TaxID=33947;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Sasaki T., Matsumoto T., Yamamoto K.;				
RL	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AP004087; BAD25129.1; -				
DR	GO; GO:0008080; F:N-acetyltransferase activity; IEA.				
DR	GO; GO:0016740; F:transferase activity; IEA.				
DR	InterPro; IPR000182; GCN5acetyl_trans.				
DR	InterPro; IPR000504; RNA_rec_mot.				
DR	Pfam; PF00583; Acetyltransf_1; 1.				
DR	PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.				
KW	Transferase.				
SEQ	SEQUENCE 421 AA; 44979 MW; 7A966BFFC673920 CRC64;				
Query Match					
Best Local		Similarity	74.0%;	Score 37;	DB 2; Length 421;
Matches		8;	Conservative	1;	Mismatches 1; Indels 0; Gaps 0.
Qy	1 ASIAAARVLD 10				
Db	288 ASIAAARVLD 297				
RESULT 2					
ID	Q8EF52	PRELIMINARY;	PRT;	694 AA.	
AC	Q8EF52;				
DT	01-MAR-2003 (TREMBlrel. 23, Created)				
DT	01-MAR-2003 (TREMBlrel. 23, Last sequence update)				
DT	01-MAR-2004 (TREMBlrel. 26, Last annotation update)				
DE	Acetyl-CoA carboxylase, biotin carboxylase, putative.				
GN	OrderedLocusNames=SO1894;				
OS	Shewanella oneidensis.				
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;				
OC	Shewanellaceae; Shewanella.				
OX	NCHI_TaxID=70863;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=MR-1;				
RX	MEBLINE=22297686; PubMed=12368813; DOI=10.1038/nbt749;				

RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
 RA Read T.D., Eisen J.A., Seshadri R., Ward N.L., Meche B.A.,
 RA Clayton R.A., Meyer T., Tsaplin A., Scott J., Beaman M.J.,
 RA Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S.,
 RA Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Nayam L.A.,
 RA White O., Wolf A.M., Vamathevan J.J., Weidman J.F., Impriali M.,
 RA Lee K., Berry K.J., Lee C., Mueller J., Khouri H.M., Gill J.,
 RA Uterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O.,
 RA Venter J.C., Neilson K.H., Fraser C.M.,
 RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
 RT *Shewanella oneidensis*,"
 RT Nat. Biotechnol. 20:1118-1123(2002).
 DR EMBL: AE015632; AAN54946.1; -.
 DR HSSP: P24182; 1DVL.
 DR TIGR: SO1894; -.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0009374; F:ATP binding; IEA.
 DR GO: GO:0016874; F:ligase activity; IEA.
 DR GO: GO:0008152; P:metabolism; IEA.
 DR InterPro: IPR01882; Biotin_BS.
 DR InterPro: IPR005482; Biotin_carb_C.
 DR InterPro: IPR000089; Biotin_lipoyl.
 DR InterPro: IPR005481; Cbase_L_N.
 DR InterPro: IPR005479; Cbp synth_L_D2.
 DR InterPro: IPR011053; Hybrid_motif.
 DR InterPro: IPR011054; Rudmtc_hyd_motif.
 DR Pfam: PF02785; Biotin_carb_C; 1.
 DR Pfam: PF00364; Biotin_lipoyl; 1.
 DR Pfam: PF00289; Cbase_L_chain; 1.
 DR Pfam: PF02786; Cbase_L_D2; 1.
 DR PROSITE: PS00188; BIOTIN; 1.
 DR PROSITE: PS00866; CBASE_1; UNKNOWN_1.
 DR PROSITE: PS00867; CBASE_2; UNKNOWN_1.
 DR Biotin; Complete proteome.
 SQ SEQUENCE 694 AA; 75656 MW; 05C4ECD8F03C998F CRC64;

Query Match 74.0%; Score 37; DB 2; Length 694;
 Best Local Similarity 54.5%; Pred. No. 1.1e+02;
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ASIAAARVLDY 11
 Db 268 AAVAAAKAIDY 278

RESULT 3
 Q8S2E4 PRELIMINARY; PRT; 1203 AA.
 AC Q8S2E4;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Putative P-glycoprotein.
 GN Name=P0022F10.15;
 OS Oryza sativa (japonica cultivar-group).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 CC Eriactoidae; Oryzaceae; Oryza.
 OC NCB1_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA PubMed=12447438; DOI=10.1038/nature01184;
 RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
 RA Wu J., Nilmura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanemori H.,
 RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
 RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
 RA Hijiwata S., Honda M., Ichikawa Y., Ikonuma A., Iijima M., Ikeda M.,
 RA Ikono M., Itoh S., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,
 RA Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
 RA Machida K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
 RA Natsuki N., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
 RA Namiki H., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,
 RA Shimokawa T., Shimura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,

RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
 RA Zhong H., Yama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
 RA Yano M., Jiang J., Gojobori T.,
 RT "The genome sequence and structure of rice chromosome 1,"
 RT Nature 420:312-316(2002).
 CC -1- SIMILARITY: Belongs to the ABC transporter family.
 DR EMBL: AP003229; BAB89499.1; -.
 DR HSSP: P08716; 1MT0.
 DR Gramene; Q8S2E4; -.
 DR GO: GO:0016021; C:Integral to membrane; IEA.
 DR GO: GO:0005524; F:ATPase activity; IEA.
 DR GO: GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
 DR GO: GO:0000166; F:nucleotide binding; IEA.
 DR GO: GO:0006810; P:transport; IEA.
 DR InterPro: IPR003593; AAA_ATPase.
 DR InterPro: IPR011527; ABC_membrane_1.
 DR InterPro: IPR011140; ABC_TM_transp.
 DR InterPro: IPR003439; ABC_transporter.
 DR Pfam: PF00664; ABC_membrane; 2.
 DR Pfam: PF00005; ABC_tran; 2.
 DR ProDom: PD000006; ABC_transporter; 2.
 DR SMART: SM00382; AAA; 2.
 DR PROSITE: PS50929; ABC_TMFP; 2.
 DR PROSITE: PS00211; ABC_TRANSPORTER_1; 2.
 DR PROSITE: PS50893; ABC_TRANSPORTER_2; 2.
 DR ATP-binding.
 SQ SEQUENCE 1203 AA; 131506 MW; B7838BDC1B5F19AA CRC64;

Query Match 74.0%; Score 37; DB 2; Length 1203;
 Best Local Similarity 70.0%; Pred. No. 1.9e+02;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ASIAAARVLD 10
 Db 330 ASVAATRIID 339

RESULT 4
 Q8G0B1 PRELIMINARY; PRT; 1234 AA.
 AC Q8G0B1;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE MDR-like ABC transporter.
 GN Name=mdr17;
 OS Oryza sativa (japonica cultivar-group).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 CC Eriactoidae; Oryzaceae; Oryza.
 OC NCB1_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Jaisneki M., Ducos E., Martinola E., Boutry M.,
 RT "The ATP-binding cassette transporters: structure, function and gene
 RT family comparison between rice and Arabidopsis,"
 RL Plant Physiol. 0:0-0(0).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Ducos E.,
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the ABC transporter family.
 DR EMBL: AJ535055; CAD59577.1; -.
 DR HSSP: P08716; 1MT0.
 DR Gramene; Q8G0B1; -.
 DR GO: GO:0016021; C:Integral to membrane; IEA.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
 DR GO: GO:0000166; F:nucleotide binding; IEA.
 DR GO: GO:0006810; P:transport; IEA.
 DR InterPro: IPR003593; AAA_ATPase.
 DR InterPro: IPR011527; ABC_membrane_1.
 DR InterPro: IPR001140; ABC_TRANSPORTER_2; 2.
 DR ATP-binding.

DR InterPro; IPR003439; ABC transporter.
 DR Pfam; PF00664; ABC membrane; 2.
 DR Pfam; PF00005; ABC trans; 2.
 DR ProDom; PD00006; ABC transporter; 2.
 DR SMART; SM00382; AAA_2.
 DR PROSITE; PS50929; ABC_TM1F_2.
 DR PROSITE; PS00211; ABC_TRANSPORTER_1; 2.
 DR PROSITE; PS50893; ABC_TRANSPORTER_2; 2.
 KM ATP-binding.
 SQ SEQUENCE 1234 AA; 134571 MW; C5F9E9D75D28AC93 CRC64;

Query Match 74.0%; Score 37; DB 2; Length 1234;
 Best Local Similarity 70.0%; Pred. No. 2e+02;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ASIAARVLD 10
 Db 330 ASVAARILD 339

RESULT 5

062CX8 PRELIMINARY; PRT; 402 AA.
 AC 062CX8;
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Major facilitator superfamily protein.
 GN ORFNames=BMA0712;
 OS Burkholderia mallei ATCC 23344.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Burkholderia.
 OX NCBI_TaxID=243160;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 23344;
 RA Niernan W.C., Deshazer D., Kim H.S., Tetteijn H., Nelson K.E.,
 RA Feldblyum T., Ulrich R.L., Ronning G.M., Brinkac L.M., Daugherty S.C.,
 RA Davidson T.D., Deboy R.T., Dimitrov G., Dodson R.J., Durkin A.S.,
 RA Gwinn M.L., Haft D.H., Khouri H., Kolonay J.F., Madupu R.,
 RA Mohammad Y., Nelson W.C., Radune D., Romero C.M., Sarrin S.,
 RA Selengut U., Shamblin C., Sullivan S.A., White O., Yu Y., Zafar N.,
 RA Zhou L., Fraser C.M.;
 RT "Structural flexibility in the Burkholderia mallei genome."
 RL Proc. Natl. Acad. Sci. U.S.A. 101:14247-14251(2004).
 DR EMBL; CP000011; AA046877.1;-.
 SQ SEQUENCE 402 AA; 41596 MW; 6FCAL6B80F4B18EA CRC64;

Query Match 72.0%; Score 36; DB 2; Length 402;
 Best Local Similarity 70.0%; Pred. No. 1.1e+02;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASIAARVLD 10
 Db 106 ATVAARILD 115

RESULT 6

063M18 PRELIMINARY; PRT; 402 AA.
 AC 063M18;
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Putative transporter protein.
 GN ORFNames=BPS0842;
 OS Burkholderia pseudomallei K96243.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Burkholderia.
 OX NCBI_TaxID=272560;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K96243;

RX PubMed=15377794;
 RA Holden M.T.G., Tildall R.W., Peacock S.J., Cerdano-Tarraga A.M.,
 RA Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.,
 RA Bentley S.D., Sebahia M., Thomson N.R., Bason N., Beacham I.R.,
 RA Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
 RA Chillingworth T., Cronin A., Crosser B., Davis P., Deshazer D.,
 RA Fellwell T., Fraser A., Hance Z., Hauser H., Holtroyd S., Jagels K.,
 RA Keith K.E., Maddison M., Moul S., Price C., Quail M.A.,
 RA Rabinowitsch E., Rutherford K., Sanders M., Simmonds M.,
 RA Songvilai S., Stevens K., Tumapa S., Vesaratchavee M.,
 RA Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.,
 RT "Genomic plasticity of the causative agent of melioidosis,
 RT Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
 DR EMBL; BX571966; CAH38304.1;-.
 SQ SEQUENCE 402 AA; 41596 MW; 6FCAL6B80F4B18EA CRC64;

Query Match 72.0%; Score 36; DB 2; Length 402;
 Best Local Similarity 70.0%; Pred. No. 1.1e+02;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASIAARVLD 10
 Db 106 ATVAARILD 115

RESULT 7

08UA95 PRELIMINARY; PRT; 663 AA.
 AC 08UA95;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE 3-methylcrotonyl-CoA carboxylase alpha subunit.
 GN Name=mcca; OrderedLocNames=Atu3479;
 OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
 OX NCBI_TaxID=176299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Dupont;
 RX MEDLINE=21608550; PubMed=11741193; DOI=10.1126/science.1066804;
 RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
 RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F., Woo L.,
 RA Chen Y., Paulsen I.T., Eichen J.A., Karp P.D., Boyce D. St.,
 RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
 RA Kutayavlin T., Levy R., Li M.-Y., McClelland E., Palmieri A.,
 RA Raymond C., Rouse G., Saenphimachak C., Wu Z., Romero P., Perry M.,
 RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Zafar N.,
 RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
 RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
 RA Neeter E.W.;
 RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
 RT C58."
 RL Science 294:2317-2323(2001).
 DR EMBL; AE009278; AAL44292.1;-.
 DR PIR; A98299; A98299.
 DR PIR; AF2984; AF2984.
 DR HSSP; P24182; 1BNC.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0009374; F:biotin binding; IEA.
 DR GO; GO:0016874; F:ligase activity; IEA.
 DR GO; GO:0008152; P:metabolism; IEA.
 DR Pfam; PF02785; Biotin_carp_C; 1.
 DR Pfam; PF00364; Biotin_lipoYL; 1.
 DR Pfam; PF00289; CPSase_L_chain; 1.
 DR PROSITE; PS00188; BIOTIN; 1.
 DR PROSITE; PS00866; CPSASE_1; UNKNOWN_1.
 DR PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
 KM Biotin; Complete proteome.
 SQ SEQUENCE 663 AA; 71187 MW; 2366201C5F36D292 CRC64;

Query Match 72.0%; Score 36; DB 2; Length 663;
 Best Local Similarity 63.6%; Pred. No. 1.7e+02;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAPARVDY 11
 |||||
 Db 258 AATMAARAIDY 268

RESULT 8
 Q7CSK5 PRELIMINARY; PRT; 709 AA.
 AC Q7CSK5;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE AGR L. 2704P.
 GN OrderedLocustNames=AGR L. 2704;
 OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
 NCBI_TaxID=176299;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Cereon;
 RA MEDLINE=21608551; PubMed=11743194; DOI=10.1126/science.1066803;
 RA Goodner B., Hinkle G., Galtung S., Miller N., Blanchard M.,
 RA Quirillo B., Goldman B.S., Cao Y., Akenazi M., Halling L.,
 RA Houmlel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
 RA Wolan C., Allinger M., Doughly D., Scott C., Lappas C., Markelz B.,
 RA Planagan C., Crowell C., Gerson J., Lomo C., Sear C., Strub G.,
 RA Clelo C., Slater S.,
 RT "Genome sequence of the plant pathogen and biotechnology agent
 RT Agrobacterium tumefaciens C58.";
 RL Science 294:2323-2328(2001).
 DR EMBL: AB008334; AAK89915.1; -.
 DR HSP: P02905; IBD0.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0009374; F:biotin binding; IEA.
 DR GO: GO:0016874; F:ligase activity; IEA.
 DR GO: GO:0008152; P:metabolism; IEA.
 DR InterPro: IPR001882; Biotin_BS.
 DR InterPro: IPR005482; Biotin_carb_C.
 DR InterPro: IPR000089; Biotin_lipoyl.
 DR InterPro: IPR005481; CPase_L_N.
 DR InterPro: IPR005479; Cphp synth_L_D2.
 DR InterPro: IPR011053; Hybrid motif.
 DR InterPro: IPR011054; Rudmt_hyb motif.
 DR Pfam: PF02785; Biotin_carb_C; 1.
 DR Pfam: PF00364; Biotin_lipoyl; 1.
 DR Pfam: PF00289; CPase_L_chain; 1.
 DR PROSITE: PS00188; BIOTIN; 1.
 DR PROSITE: PS00866; CPASE_1; UNKNOWN_1.
 DR PROSITE: PS00867; CPASE_2; UNKNOWN_1.
 KW Biotin.
 SQ SEQUENCE 709 AA; 76278 MW; 1F43A1F11919EFD0 CRC64;
 Query Match 72.0%; Score 36; DB 2; Length 709;
 Best Local Similarity 63.6%; Pred. No. 1.8e+02;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAPARVDY 11
 |||||
 Db 304 AATMAARAIDY 314

RESULT 9
 Q8H034 PRELIMINARY; PRT; 723 AA.
 AC Q8H034;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE Hypothetical protein OJ1172F09.9.
 GN Name=OJ1172F09.9;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 NCBI_TaxID=39947;
 RX [1]
 RP SEQUENCE FROM N.A.
 RA Wing R.A., Yu Y., Soderlund C., Kim H.-R., Rambo T., Currie J.,
 RA Collura K., McCombie D.W.R., de la Bastide M., Spiegel L., Preston R.,
 RA Kirchoff K., Kuit K., Nascimento L., Zutterern T., Balla V., Bell M.,
 RA Baker J., Santos L., Miller B., Kaczenderger F., Muller S., King L.,
 RA Yang C., O'Shaughnessy A., Palmer L., Dedhia N.,
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC119796; AAO17354.1; -.
 DR Gramene; Q8H034; -.
 DR InterPro: IPR008938; ARM.
 KW Hypothetical protein.
 SQ SEQUENCE 723 AA; 78613 MW; 3FD842215E6ED1FD CRC64;

Query Match 72.0%; Score 36; DB 2; Length 723;
 Best Local Similarity 80.0%; Pred. No. 1.9e+02;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASIAPARVDY 10
 |||||
 Db 616 ASIAPARVDY 625

RESULT 10
 Q7MA36 PRELIMINARY; PRT; 778 AA.
 AC Q7MA36;
 DT 01-MAR-2004 (TREMBlrel. 26, Created)
 DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE FLAGELLAR FUNCTIONAL PROTEIN.
 GN Name=PF1A; OrderedLocustNames=MS0490;
 OS Wolinella succinogenes.
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
 OC Helicobacteraceae; Wolinella.
 NCBI_TaxID=844;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DMZ 1740;
 RX MEDLINE=22882897; PubMed=14500908; DOI=10.1073/pnas.1932838100;
 RA Baar C., Eppinger M., Raddatz G., Simon U., Lanz C., Kimmek O.,
 RA Nandakumar R., Gross R., Rosinus A., Keller H., Jagtap P., Linke B.,
 RA Meyer F., Lederer H., Schuster S.C.;
 RT "Complete genome sequence and analysis of Wolinella succinogenes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:11690-11695(2003).
 DR EMBL: BX571658; CAB06628.1; -.
 DR GO: GO:0019861; C:Flagellum; IEA.
 DR InterPro: IPR008940; Prey1_trans.
 DR InterPro: IPR001440; TPR.
 DR InterPro: IPR008941; TPR-like.
 DR Pfam: PF00515; TPR_1; 1.
 DR PROSITE: PSS0293; TPR_REGION; 1.
 KW Complete proteome; Flagellum.
 SQ SEQUENCE 778 AA; 89775 MW; 3E2F992CE949C27E CRC64;

Query Match 72.0%; Score 36; DB 2; Length 778;
 Best Local Similarity 63.6%; Pred. No. 2e+02;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAPARVDY 11
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 Db 322 ASIAPARVDY 332

RESULT 11
 Q6X93


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ID Q69X93 PRELIMINARY; PRT; 1072 AA.
AC Q69X93;
DT 25-OCT-2004 (TREMblrel. 28, Created)
DT 25-OCT-2004 (TREMblrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMblrel. 28, Last annotation update)
DE Putative receptor-like protein Kinase 2.
GN Name=P0633E08.13;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OC NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nhyponbare(GA3) genomic DNA, chromosome 6, PAC
RT clone:P0633E08."
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AP003622; BAD32908.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR007090; LRR_plant.
DR InterPro; IPR003591; LRR_1yp.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00560; LRR_1; 22.
DR Pfam; PF00069; Kinase; 1.
DR PRINTS; PR00019; LEURICHRPT.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00369; LRR_Typ; 11.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN_1.
DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
DR ATP-binding; Kinase; Receptor; Serine/threonine-protein kinase;
KW Transferrase
SQ SEQUENCE 1072 AA; 114368 MW; E15B809971B15F78 CRC64;

Query Match 72.0%; Score 36; DB 2; Length 1072;
Best Local Similarity 80.0%; Pred. No. 2.7e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASIAARVLD 10
DB 116 ASIAARVLD 125

RESULT 12
Q69582 PRELIMINARY; PRT; 143 AA.
AC Q69582;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)
DE Herpesvirus type 6 DNA.
OS Human herpesvirus 6.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Roseolovirus.
OC NCBI_TaxID=10368;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINB=94181269; PubMed=8134119;
RA Thompson J., Choudhury S., Kashanchi F., Doniger J., Berneman Z.,
RA Frenkel N., Rosenthal L.J.;

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RT "A transforming fragment within the direct repeat region of human
RT herpesvirus type 6 that transactivates HIV-1."
RL Oncogene 9:1167-1175 (1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Thompson J.T.;
RL Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; X73675; CA52028.1; -.
DR PIR; S43071; S43071.
SQ SEQUENCE 143 AA; 13317 MW; EDF78898C3D11734 CRC64;

Query Match 70.0%; Score 35; DB 2; Length 143;
Best Local Similarity 88.9%; Pred. No. 63;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASIAARVLD 9
DB 7 ASIAARVLD 15

RESULT 13
Q6A091 PRELIMINARY; PRT; 184 AA.
AC Q6A091;
DT 25-OCT-2004 (TREMblrel. 28, Created)
DT 25-OCT-2004 (TREMblrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMblrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=DP0753;
OS Desulfotalea psychrophila.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacterales;
OC Desulfobulbaceae; Desulfotalea.
OC NCBI_TaxID=84980;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=LSV54 / DSM 12343;
RX PubMed=15305914;
RA Rabus R., Ruepp A., Frickey T., Ratei T., Fartmann B., Stark M.,
RA Bauer M., Zibet A., Lombardot T., Becker I., Amani J., Gellner K.,
RA Teeling H., Leuchner W.D., Gloeckner F.-O., Lupas A.N., Amani R.,
RA Klein H.-P.;
RT "The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium
RT from permanently cold Arctic sediments."
RL Environ. Microbiol. 6:887-902 (2004).
DR EMBL; CR522870; CAG35482.1; -.
KW Complete proteome.
SQ SEQUENCE 184 AA; 20792 MW; 8D9DCB5EDFAA60AF CRC64;

Query Match 70.0%; Score 35; DB 2; Length 184;
Best Local Similarity 80.0%; Pred. No. 81;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASIAARVLD 10
DB 99 ASIAARVLD 108

RESULT 14
Q9RJR7 PRELIMINARY; PRT; 329 AA.
AC Q9RJR7;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE Putative zinc-binding oxidoreductase.
GN ORFNames=SCF51.18;
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomyces.
OC NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=A3 (2) / M145;

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RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kleser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
RA Rabinowitsch E., Rajadream M.A., Rutherford K.M., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Metzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL; AL39105; CAB59716.1; -.
DR HSCP; O8J3C8; 11Y2.
DR GO; GO:0004024; F:alcohol dehydrogenase activity, zinc-dependent; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR InterPro; IPR02085; Adh zn family.
DR InterPro; IPR011032; GroES like.
DR Pfam; PF00107; ADH_zinc_N; 1.
KM Complete proteome.
SQ SEQUENCE 329 AA; 34155 MW; SDCAD4FB174FD042 CRC64;

QY Query Match 70.0%; Score 35; DB 2; Length 329;
Best Local Similarity 70.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 S1AAARYLDY 11
Db 189 SLAAAHVLDY 198
|:|||||
|:|||||

RESULT 15
YCH3_YEAST STANDARD; PRT; 692 AA.
ID YCH3_YEAST
AC P40358;
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-NOV-1995 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DE Hypothetical 80.4 kDa protein in SMC3-MAP18 intergenic region.
GN OrderedLocustNames=YJL073W; ORFNames=11083, HRC558;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes;
OC NCBI_TaxID=4932;
RX
RN [1]
RP SEQUENCE FROM N.A.
RA Rose M., Koetter P., Batian K.D.;
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Sor F.J.;
RC STRAIN=S288c;
RA
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 135-692 FROM N.A.
RC STRAIN=S288c;
RX MEDLINE=95282514; PubMed=7762302;
RA Vandenbol M., Durand P., Dion C., Portetelle D., Hilger F.;
RT "Sequence of a 17.1 kb DNA fragment from chromosome X of Saccharomyces
RT cerevisiae includes the mitochondrial ribosomal protein L8.";
RL Yeast 11:57-60(1995).
CC -1- SIMILARITY: Contains 1 J domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@ebi.ac.uk).
CC
CC EMBL; Z49348; CAA89365.1; -.

DR EMBL; X88851; CAA61312.1; -.
DR EMBL; Z34288; CAA84049.1; -.
DR PIR; S56849; S56849.
DR HSSP; P08622; 1BQZ.
DR GERMOLINE; 141687; -.
DR SGD; S00003609; JEM1.
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR GO; GO:0000300; C:periplasmic membrane; IDA.
DR GO; GO:0003767; F:co-chaperone activity; IGI.
DR GO; GO:0000742; P:karyogamy during conjugation with cellular . . . IGI.
DR GO; GO:0006457; P:protein folding; IGI.
DR InterPro; IPR001623; DnaJ_N.
DR Pfam; PF00226; DnaJ_1.
DR SMART; SM00271; DnaJ_1.
DR PROSITE; PS00636; DnaJ_1; FALSE_NEG.
DR PROSITE; PS50076; DnaJ_2; 1.
KM Hypothetical protein.
FT DOMAIN 560 569 Poly-Gln.
FT DOMAIN 585 655 J-domain.
SQ SEQUENCE 692 AA; 80381 MW; 9F612DD16866981B CRC64;

QY Query Match 70.0%; Score 35; DB 1; Length 692;
Best Local Similarity 70.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 S1AAARYLDY 11
Db 245 SLAAAHVLDY 254
|:|||||
|:|||||

RESULT 16
Q8Y833 PRELIMINARY; PRT; 696 AA.
ID Q8Y833
AC Q8Y833;
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE Lmo1085 protein.
GN OrderedLocustNames=lmo1085;
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OC NCBI_TaxID=1639;
RX
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EGD-e / Serovar 1/2a;
RX MEDLINE=21537279; PubMed=11679669; DOI=10.1126/science.1063447;
RA Glaeser P., Frangeul L., Buchrieser C., Ruanick C., Amend A.,
RA Baquero F., Berche P., Blocher H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani P., Couve E., de Daruval A., Denoux F.,
RA Dorian E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Eutman K.-D., Faïh H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkut G.,
RA Medueno E., Maitouman A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordsiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schluter T., Simoes N., Tietze A.,
RA Vazquez-Boland J.-A., Voss H., Weiland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
DR EMBL; AL591977; CAC99163.1; -.
DR PIR; A61210; A61210.
DR L1stList; LMO1085; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0047355; F:CDP-glycerol 1-glycerophosphotransferase acti. . . IEA.
DR GO; GO:0019350; F:ethanol acid biosynthesis; IEA.
DR Pfam; PF04464; Glypoe_transf; 1.
KM Complete proteome.
SQ SEQUENCE 696 AA; 81368 MW; 1668A867FB3408D CRC64;

QY Query Match 70.0%; Score 35; DB 2; Length 696;
Best Local Similarity 75.0%; Pred. No. 2.9e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 4 AAARVLDY 11
 DB 685 AAARLDY 692

RESULT 17

Q6MK31 PRELIMINARY; PRT; 1228 AA.
 ID 06MK31
 AC 06MK31;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE ABC-type multidrug transporter with fused ATPase and permease domain.
 GN OrderedLocustNames=Bq2583;
 OS Bdellovibrio bacteriovorus.
 OC Bdellovibriaceae; Bdellovibrio.
 CC NCBI_TaxID=959;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
 RX PubMed=14752164; DOI=10.1126/science.1093027;
 RA Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C., Kellner H., Lambert C., Evans K.J., Goessmann A., Meyer F., Sackett R.E., Schuster S.C.;
 RA "A predator unmasked: life cycle of Bdellovibrio bacteriovorus from a genomic perspective";
 RT Science 303:689-692(2004).
 CC -1- SIMILARITY: Belongs to the ABC transporter family.
 DR GO: GO:0016021; C:integral to membrane; IEA.
 DR GO: GO:0005524; F:ATPase activity; coupled to transmembrane m. . .; IEA.
 DR GO: GO:0004262; F:ATPase activity; coupled to transmembrane m. . .; IEA.
 DR GO: GO:0006810; P:transport; IEA.
 DR InterPro: IPR003593; AAA_ATPase.
 DR InterPro: IPR011527; ABC_membrane_1.
 DR InterPro: IPR001140; ABC_TM_transp.
 DR InterPro: IPR003439; ABC_transporter.
 DR InterPro: IPR008949; Terpenoid_synth.
 DR Pfam: PF00005; ABC_tran; 2.
 DR ProDom: PD000006; ABC_transporter; 1.
 DR SMART: SM00382; AAA; 2.
 DR PROSITE: PS00929; ABC_TMIF; 2.
 DR PROSITE: PS00211; ABC_TRANSPORTER_1; 2.
 DR PROSITE: PS00893; ABC_TRANSPORTER_2; 2.
 KW ATP-binding; Complete proteome.
 SQ SEQUENCE 1228 AA; 136602 MW; CFPD9468FE20A1800 CRC64;

Query Match 70.0%; Score 35; DB 2; Length 1228;
 Best Local Similarity 54.5%; Pred. No. 5e+02;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 ASIAARVLDY 11
 DB 352 AKVGARRLDY 362

RESULT 18

Q7R034 PRELIMINARY; PRT; 6977 AA.
 ID 07R034
 AC 07R034;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE GLP 456 20463 41396.
 OS Giardia lamblia ATCC 50803.
 CC Eukaryota; Diplomonadida; Hexamitidae; Giardinae; Giardia.
 CC NCBI_TaxID=164922;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=WB C6;
 RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D., Olsen G.J., Sogin M.L.;
 RT "Draft sequence of the Giardia lamblia genome";
 RL Submitted (MAR-2003) to the EMBL/Genbank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is preliminary data.
 CC CC
 DR EMBL; AACB0100038; EAA40653.1; .
 DR InterPro: IPR000408; Reg_chromatins.
 DR PROSITE: PS00626; RCCL2; UNKNOWN 1.
 SQ SEQUENCE 6977 AA; 782914 MW; C5C1DEB7211452A3 CRC64;

Query Match 70.0%; Score 35; DB 2; Length 6977;
 Best Local Similarity 72.7%; Pred. No. 2.7e+03;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 ASIAARVLDY 11
 DB 4408 ASIAARILAY 4418

RESULT 19

Q6NA42 PRELIMINARY; PRT; 153 AA.
 ID 06NA42
 AC 06NA42;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein precursor.
 OS OrderedLocustNames=RPAL1344;
 OC Rhodospseudomonas palustris.
 CC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 CC Bradyrhizobiaceae; Rhodopseudomonas.
 CC NCBI_TaxID=1076;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CGA009 / ATCC BAA-98;
 RX PubMed=14704707; DOI=10.1038/nbt923;
 RA Latimer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L., Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R., Gibson J.L., Hanson T.E., Bobst C., Torres y Torres J.L., Peters C., Harrison F.H., Gibson J., Harwood C.S.;
 RA "Complete genome sequence of the metabolically versatile photosynthetic bacterium Rhodospseudomonas palustris";
 RT Nat. Biotechnol. 22:55-61(2004).
 RL Nat. Biotechnol. 22:55-61(2004).
 DR EMBL; BX572597; CAB26787.1; .
 KW Complete proteome; Hypothetical protein; Signal.
 FT SIGNAL
 SQ SEQUENCE 153 AA; 16944 MW; DA305CD98D7B7B47 CRC64;

Query Match 68.0%; Score 34; DB 2; Length 153;
 Best Local Similarity 87.5%; Pred. No. 1.1e+02;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 AAARVLDY 11
 DB 33 AAARVLDY 40

RESULT 20

Q9A213 PRELIMINARY; PRT; 231 AA.
 ID 09A213
 AC 09A213;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Carboxymethylenebutenolidase.
 GN OrderedLocustNames=CC3758;
 OS Caulobacter crescentus.
 CC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;
 CC Caulobacteraceae; Caulobacter.
 CC NCBI_TaxID=155892;

```

RN [1]
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=2117369; PubMed=11259647; DOI=10.1073/pnas.061029298;
RA Nielsen W.C., Feldblum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eissen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Keleny J.F., Slat J., Craven M.B., Knorr H.M., Shetty J.,
RA Petry K.J., Utechtback T.R., Tran K., Wolf A.M., Yamachyan J.J.,
RA Ermolaeva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,
RA Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
DR EMBL; AE006033; AKK25720.1; -.
DR PIR; D87715; D87715.
DR HSSP; P11453; 1GCV.
DR TIGR; CC3758; -.
DR GO; GO:0016787; P:hydrolase activity; IEA.
DR InterPro; IPR002925; Dlenelactn_Hydro.
DR Pfam; PF01738; DLH; 1.
KM Complete proteome.
SQ SEQUENCE 231 AA; 24787 MW; 23E078162327869C CRC64;

Query March 68.0%; Score 34; DB 2; Length 231;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Cy 1 ASINARVLD 10
Db 100 ATINARKLD 109

RESULT 21
ID THEV THEVU STANDARD; PRT; 279 AA.
AC P04072;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Thermitase (EC 3.4.21.66).
OS Thermactinomycetes vulgaris.
OC Bacteria; Firmicutes; Bacillales; Thermactinomycetaceae;
OC Thermactinomycetes.
OX NCBI_TaxID=2026;
RN [1]
RP SEQUENCE.
RA Meloun B., Baudys M., Koscka V., Hausdorf G., Frommel C., Hohne W.E.;
RT "Complete primary structure of thermitase from Thermactinomycetes
RT vulgaris and its structural features related to the subtilisin-type
RT proteases.";
RL FEBS Lett. 183:195-200(1985).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=89171261; PubMed=2647518; DOI=10.1016/0014-5793(89)81194-9;
RA Teplyakov A.V., Kuranova I.P., Harutyunyan E.H., Frommel C.,
RA Hohne W.E.;
RT "Crystal structure of thermitase from Thermactinomycetes vulgaris at
RT 2.2-A resolution.";
RL FEBS Lett. 244:208-212(1989).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.98 ANGSTROMS).
RX MEDLINE=90096158; PubMed=2689655;
RA Gros P., Betzel C., Dauter Z., Wilson K.S., Hoi W.G.J.;
RT "Molecular dynamics refinement of a thermitase-egg-1 complex at
RT 1.98-A resolution and comparison of two crystal forms that differ in
RT calcium content.";
RL J. Mol. Biol. 210:347-367(1989).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (1.4 ANGSTROMS).
RX MEDLINE=90317828; PubMed=2196375;
RA Teplyakov A.V., Kuranova I.P., Harutyunyan E.H., Vainshtein B.K.,
RA Frommel C., Hohne W.E., Wilson K.S.;
RT "Crystal structure of thermitase at 1.4-A resolution.";
RL J. Mol. Biol. 214:261-279(1990).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=9113592; PubMed=1993669;
RA Gros P., Kalk K.H., Hoi W.G.J.;
RT "Calcium binding to thermitase. Crystallographic studies of thermitase
RT at 0, 5, and 100 mM calcium.";
RL J. Biol. Chem. 266:12953-12961(1991).
CC -1- CATALYTIC ACTIVITY: Hydrolysis of proteins, including collagen.
CC -1- COFACTOR: Binds 3 calcium ions or 2 calcium ions and 1 sodium ion
CC per subunit. The sodium ion is bound at calcium concentrations up
CC to 5 mM. At 100 mM calcium 3 calcium ions are bound.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the peptidase S8 family.
DR PIR; A00973; SUBTYV.
DR PDB; 1TEC; X-ray; E=1-279.
DR PDB; 1THM; X-ray; @=1-279.
DR PDB; 2TEC; X-ray; E=1-279.
DR PDB; 3TEC; X-ray; E=1-279.
DR MEROPS; S08.007; -.
DR InterPro; IPR000209; Pept_S8_S53.
DR Pfam; PF00082; Peptidase_S8; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR PROSITE; PS00136; SUBTILASE_ASP; 1.
DR PROSITE; PS00137; SUBTILASE_HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KM 3D-structure; Calcium-binding; Direct protein sequencing; Hydrolase;
KM Metal-binding; Serine protease.
FT ACT_SITE 38 71
FT ACT_SITE 71 38
FT ACT_SITE 225 225
FT METAL 5 5
FT METAL 47 47
FT METAL 57 57
FT METAL 60 60
FT METAL 62 62
FT METAL 64 64
FT METAL 66 66
FT METAL 82 82
FT METAL 85 85
FT METAL 87 87
FT METAL 89 89
FT TURN 6 7
FT HELIX 8 11
FT HELIX 14 17
FT TURN 18 19
FT HELIX 20 24
FT TURN 25 26
FT TURN 30 31
FT STRAND 33 38
FT TURN 43 44
FT TURN 46 51
FT TURN 52 57
FT STRAND 58 61
FT TURN 62 62
FT STRAND 71 80
FT HELIX 94 95
FT STRAND 97 102
FT STRAND 106 107
FT HELIX 112 124
FT TURN 125 126
FT STRAND 129 132
FT STRAND 136 136
FT HELIX 141 152
FT TURN 153 154
FT STRAND 156 160
FT STRAND 171 171
FT TURN 172 174
FT TURN 176 177
FT STRAND 186 187
FT TURN 190 190

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FT TURN 192 193
FT TURN 198 199
FT STRAND 202 205
FT STRAND 209 213
FT TURN 214 216
FT STRAND 217 221
FT HELIX 224 239
FT TURN 240 242
FT HELIX 245 254
FT TURN 255 255
FT STRAND 257 257
FT TURN 260 261
FT STRAND 262 262
FT TURN 263 265
FT STRAND 266 266
FT STRAND 269 270
FT HELIX 273 279
SQ SEQUENCE 279 AA; 28366 MW; 8065049BC927AC0 CRC64;

Query Match 68.0%; Score 34; DB 1; Length 279;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ASIAARVLD 10
Db 96 ASILAVRLD 105

RESULT 22

Q6AH23 PRELIMINARY; PRT; 322 AA.
AC Q6AH23;
DT 25-OCT-2004 (TRENBLREL. 28, Created)
DT 25-OCT-2004 (TRENBLREL. 28, Last sequence update)
DT 25-OCT-2004 (TRENBLREL. 28, Last annotation update)
DE Zinc-binding oxidoreductase.
GN OrderedLocustNames=Lxx02950;
OS Leifsonia xyli (subsp. xyli).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococcineae; Microbacteriaceae; Leifsonia.
OX NCBI_TaxID=59736;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CTCB07;
RX PubMed=15305603;
RA Monteiro-Vitorello C.B., Camargo L.E.A., Van Sluys M.A.,
RA Kitajima J.P., Trufi D., do Amaral A.M., Harakava R.,
RA de Oliveira J.C.F., Wood D., de Oliveira M.C., Miyaki C.Y.,
RA Takita M.A., da Silva A.C.R., Furlan L.R., Carraro D.M., Camarotte G.,
RA Almeida N.F., Jr., Carrier H., Coutinho L.L., El-Dorri H.A.,
RA Ferro M.T., Gagliardi P.R., Giglioli E., Goldman M.H.S.,
RA Goldman G.H., Kimura E.T., Ferro E.S., Kuramae E.R., Lemos E.G.M.,
RA Lemos M.V.F., Mauro S.M.Z., Machado M.A., Marino C.L., Menck C.F.,
RA Nunes L.R., Oliveira R.C., Pereira G.G., Siqueira W., de Souza A.A.,
RA Teal S.M., Zanca A.S., Simpson A.J.G., Brumley S.M., Sebubal J.C.;
RT "The genome sequence of the Gram-positive sugarcane pathogen Leifsonia
RT xyli subsp. xyli."
RL Mol. Plant Microbe Interact. 17:827-836(2004).
DR EMBL; AB016822; AAT8832.1;
DR GO; GO:0004024; F:alcohol dehydrogenase activity, zinc-dependent; IEA.
DR InterPro; IPR002085; Aah_zn_family.
DR InterPro; IPR002110; ANK_
DR InterPro; IPR011032; GroES_like.
DR Pfam; PF00107; ADH_zinc_N; 1.
DR PRINTS; PRO1415; ANKTRIN.
KW Complete proteome.
SQ SEQUENCE 322 AA; 33244 MW; 9DB928BF3B688BD CRC64;

Query Match 68.0%; Score 34; DB 2; Length 322;
Best Local Similarity 60.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 SIARVLDY 11
Db 191 SIAGAVIDY 200

RESULT 23

ID Q8ZSL1 PRELIMINARY; PRT; 342 AA.
AC Q8ZSL1;
DT 01-MAR-2002 (TRENBLREL. 20, Created)
DT 01-MAR-2002 (TRENBLREL. 20, Last sequence update)
DT 25-OCT-2004 (TRENBLREL. 28, Last annotation update)
DE PAREP2b.
GN OrderedLocustNames=PAE1657, PAE2128;
OS Pyrobaculum aerophilum.
OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
OC Thermoproteaceae; Pyrobaculum.
OX NCBI_TaxID=13773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IM2;
RX MEDLINE=21664397; PubMed=11792869; DOI=10.1073/pnas.241636498;
RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
RA Miller J.H.;
RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
RT aerophilum."
RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
DR EMBL; AE009858; AAL63965.1;
DR EMBL; AE009833; AAL63635.1;
KW Complete proteome.
SQ SEQUENCE 342 AA; 37164 MW; E85758D06FEA4343 CRC64;

Query Match 68.0%; Score 34; DB 2; Length 342;
Best Local Similarity 87.5%; Pred. No. 2.4e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 AARVLDY 11
Db 95 AAVRLDY 102

RESULT 24

ID Q8ZXL8 PRELIMINARY; PRT; 342 AA.
AC Q8ZXL8;
DT 01-MAR-2002 (TRENBLREL. 20, Created)
DT 01-MAR-2002 (TRENBLREL. 20, Last sequence update)
DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
DE PAREP2b.
GN OrderedLocustNames=PAE1214;
OS Pyrobaculum aerophilum.
OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
OC Thermoproteaceae; Pyrobaculum.
OX NCBI_TaxID=13773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IM2;
RX MEDLINE=21664397; PubMed=11792869; DOI=10.1073/pnas.241636498;
RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
RA Miller J.H.;
RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
RT aerophilum."
RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
DR EMBL; AE009809; AAL63329.1;
KW Complete proteome.
SQ SEQUENCE 342 AA; 37134 MW; F42758D0739A4A33 CRC64;

Query Match 68.0%; Score 34; DB 2; Length 342;
Best Local Similarity 87.5%; Pred. No. 2.4e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 AARVLDY 11
| | | | |

Db 95 AAVRLDY 102

RESULT 25

Q9LS05 PRELIMINARY; PRT; 342 AA.

AC Q9LS05

DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE Methionine aminopeptidase-like protein.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eudots II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20277480; PubMed=10819329;

RA Nakamura Y.;

RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence features of the regions of 4,504,864 bp covered by sixty P1 and TAC clones."

RT clones."

RL DNA Res. 7:131-135(2000).

RN [2]

RP SEQUENCE FROM N.A.

RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;

RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: Removes the amino-terminal methionine from nascent proteins (By similarity).

CC -1- CATALYTIC ACTIVITY: Release of N-terminal amino acids, preferentially methionine, from peptides and arylamides.

CC -1- COFACTOR: Cobalt; binds 2 ions per subunit (By similarity).

CC -1- SIMILARITY: Belongs to peptidase family M24A.

DR EMBL; AB028607; BAA95761.1; -.

DR HSSP; P07906; IC24.

DR GO; GO:0004239; F:methionyl aminopeptidase activity; IEA.

DR GO; GO:0008223; F:peptidase activity; IEA.

DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

DR InterPro; IPR000994; Peptidase_M24.

DR InterPro; IPR002467; Pept_M24A_MAP1.

DR Pfam; PF00557; Peptidase_M24_1.

DR PRINTS; PR00599; MAPPEPTIDASE.

DR TIGRFAMs; TIGR00500; met_pdae_1; 1.

KW Aminopeptidase; Cobalt; Hydrolase; Protease.

QX NCBI_TaxID=342; 37429 MW; 6850AF0B7F9A73B CRC64;

SEQUENCE 342 AA; 37429 MW; 6850AF0B7F9A73B CRC64;

Query Match 68.0%; Score 34; DB 2; Length 342;

Best Local Similarity 100.0%; Pred. No. 2.4e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AAVRLDY 11

Db 115 AAVRLDY 121

RESULT 26

Q9FV51 PRELIMINARY; PRT; 344 AA.

AC Q9FV51

DT 01-MAR-2001 (TREMBlrel. 16, Created)

DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)

DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE Methionine aminopeptidase-like protein.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eudots II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20514156; PubMed=11060042; DOI=10.1093/emboj/19.21.5916;

RA Giglione C., Serero A., Pierre M., Boisson B., Meinel T.;

RT "Identification of eukaryotic peptide deformylases reveals universality of N-terminal protein processing mechanisms."

RL EMO J. 19:5916-5929(2000).

CC -1- FUNCTION: Removes the amino-terminal methionine from nascent proteins (By similarity).

CC -1- CATALYTIC ACTIVITY: Release of N-terminal amino acids, preferentially methionine, from peptides and arylamides.

CC -1- COFACTOR: Cobalt; binds 2 ions per subunit (By similarity).

CC -1- SIMILARITY: Belongs to peptidase family M24A.

DR EMBL; AF250962; AAC33976.1; -.

DR HSSP; P07906; IC24.

DR GO; GO:0004239; F:methionyl aminopeptidase activity; IEA.

DR GO; GO:0008223; F:peptidase activity; IEA.

DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

DR InterPro; IPR000994; Peptidase_M24.

DR InterPro; IPR002467; Pept_M24A_MAP1.

DR Pfam; PF00557; Peptidase_M24_1.

DR PRINTS; PR00599; MAPPEPTIDASE.

DR TIGRFAMs; TIGR00500; met_pdae_1; 1.

KW Aminopeptidase; Cobalt; Hydrolase; Protease.

QX NCBI_TaxID=344; 37693 MW; BB12F00F3CF710BA CRC64;

SEQUENCE 344 AA; 37693 MW; BB12F00F3CF710BA CRC64;

Query Match 68.0%; Score 34; DB 2; Length 344;

Best Local Similarity 100.0%; Pred. No. 2.4e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AAVRLDY 11

Db 115 AAVRLDY 121

RESULT 27

Q8P7L4 PRELIMINARY; PRT; 568 AA.

AC Q8P7L4

DT 01-OCT-2002 (TREMBlrel. 22, Created)

DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)

DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)

DE Alkaline phosphatase.

GN Name=phoA; OrderedlocusNames=XCC2597;

OS Xanthomonas campestris (pv. campestris).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;

OC Xanthomonadaceae; Xanthomonas.

OX NCBI_TaxID=340;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 33913 / NCPPB 528;

RX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;

RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

RA Quagga R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Canargo L.E.A.,

RA Camarotte G., Camavan F., Cardozo J., Chambeiro F., Clapina L.P.,

RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,

RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,

RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

RA Spínola L.A.F., Takita M.A., Tamura R.B., Teixeira B.C., Tezza R.I.D.,

RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

RA Senubal J.C., Kitajima J.P.;

RT "Comparison of the genomes of two Xanthomonas pathogens with differing host specificities."

RT Nature 417:459-463(2002).

CC -1- SIMILARITY: Belongs to the alkaline phosphatase family.

DR EMBL; AEO12371; AAM41869.1; -.

DR HSSP; P05187; 1EW2.

DR GO; GO:0008152; P:metabolism; IEA.

DR InterPro; IPR001952; Alk_phosphatase.

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DR Pfam; PF00245; Alk_phosphatase; 1.
DR PRINTS; PR00113; ALKPHPTASE.
DR SMART; SM00098; alkPpc; 1.
DR Complete proteome.
SQ SEQUENCE 568 AA; 5996 MW; 94CA413CB2942DEC CRC64;

Query Match
Best Local Similarity 66.0%; Score 34; DB 2; Length 568;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 SIAARVLD 10
   :|||:|
Db 86 TVAAARILD 94

RESULT 28
Q08PY6 PRELIMINARY; PRT; 568 AA.
AC Q08PY6;
DT 01-OCT-2002 (TRENBLREL. 22, Created)
DT 01-OCT-2002 (TRENBLREL. 22, Last sequence update)
DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
DE Alkaline phosphatase.
GN Name=PhoA; OrderedLocNames=XAC2759;
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=92829;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=306 / ATCC 13902 / XV 101;
RX MEDLINE=2022145; PubMed=12024217; DOI=10.1038/417459a;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farh C.S., Parlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Canavara F., Cardozo J., Chamberg F., Ciapina L.P.,
RA Ciccarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spindola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities";
RL Nature 417:459-463(2002).
CC -I- SIMILARITY: Belongs to the alkaline phosphatase family.
DR EMBL; AE011916; AAM57604.1; -.
DR HSSP; P05187; 1EW2.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR001952; Alk_phosphatase.
DR Pfam; PF00245; Alk_phosphatase; 1.
DR PRINTS; PR00113; ALKPHPTASE.
DR SMART; SM00098; alkPpc; 1.
DR Complete proteome.
SQ SEQUENCE 568 AA; 60087 MW; E7514C0AF2BEF199 CRC64;

Query Match
Best Local Similarity 66.0%; Score 34; DB 2; Length 568;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 SIAARVLD 10
   :|||:|
Db 86 TVAAARILD 94

RESULT 29
MTCL_BACST STANDARD; PRT; 579 AA.
ID MTCL_BACST

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AC P43423;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Modification methylase BseCI (EC 2.1.1.72) (Adenine-specific
DE methyltransferase BseCI) (M.BseCI).
GN Name=BseCI;
OS Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
OX NCBI_TaxID=1422;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9504752; PubMed=7959066; DOI=10.1016/0378-1119(94)90860-5;
RA Rina M., Markaki M., Bouriotis V.;
RT "Sequence of the cloned bseCI gene: M. BseCI reveals high homology to
RT M. Bantii";
RL Gene 150:71-73(1994).
CC -I- FUNCTION: This methylase recognizes the double-stranded sequence
CC ATCGAT, causes specific methylation on A-5 on both strands, and
CC protects the DNA from cleavage by the BantII endonuclease.
CC -I- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + DNA adenine = S-
CC adenosyl-L-homocysteine + DNA 6-methylaminopurine.
CC -I- SIMILARITY: Belongs to the M4/M6-methyltransferase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@1db-sib.ch).
CC -----
DR EMBL; X79509; CA56041.1; -.
DR PIR; I40371; I40371.
DR HSSP; P14385; 2ADM.
DR REBASE; 3536; M.BseCI.
DR InterPro; IPR011038; Calycin.
DR InterPro; IPR002296; N12N6_mtfase.
DR InterPro; IPR000051; SAM_bind.
DR InterPro; IPR000052; SAM_bind.
DR PRINTS; PR00507; N12N6MTFRASE.
DR PROSITE; PS00092; N6_MTFASE; 1.
KW Methyltransferase; Restriction system; Transferase.
SQ SEQUENCE 579 AA; 66774 MW; A4805FBEBA01835C CRC64;

Query Match
Best Local Similarity 54.5%; Score 34; DB 1; Length 579;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 ASIAARVLD 11
   :|||:|
Db 26 AEVIAKRILD 36

RESULT 30
Q09OK2 PRELIMINARY; PRT; 579 AA.
ID Q09OK2
AC Q09OK2;
DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
DE DNA methyltransferase.
OS Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
OX NCBI_TaxID=1422;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IV.
RX MEDLINE=20062459; PubMed=10594225;
RA Vasquez C.C., Saavedra C.P., Pichante S.E.;
RT "Nucleotide sequence of the gene encoding the BseI VI DNA
RT methyltransferase; comparison with other amino-DNA
RT methyltransferases.";

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RL Curr. Microbiol. 40:114-118(2000).
RN [2]
RC SEQUENCE FROM N.A.
RA STRAIN=LV.
RA Vaquez C.C., Pichuanes S.E., Saavedra C.P.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF098974; AAF04626.1; -.
DR HSP; P14385; ZADM.
DR REBASE; 3547; M.BetLVI.
DR REBASE; 4520; C.BetLVI.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0008170; F:N-methyltransferase activity; IEA.
DR GO; GO:0008757; F:S-adenosylmethionine-dependent methyltransferase; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006306; P:DNA methylation; IEA.
DR InterPro; IPR011038; Calycin.
DR InterPro; IPR02296; N12N6_mifrase.
DR InterPro; IPR02052; N6_Mcase.
DR InterPro; IPR000051; SAM_bind.
DR PRINTS; PR00507; N12N6MTRASE.
DR PROSITE; PS00092; N6_Mcase; UNKNOWN_1.
KW Methyltransferase; Transferase.
SQ SEQUENCE 579 AA; 66820 MW; 4226B9CD43DD0E42 CRC64;

Query Match 68.0%; Score 34; DB 2; Length 579;
Best Local Similarity 54.5%; Pred. No. 3.9e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 ASIAARVLDY 11
DB 26 AEVIARVLDY 36

RESULT 31
Q7FID1 PRELIMINARY; PRT; 589 AA.
ID Q7FID1
AC Q7FID1
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative nucleolar protein.
GN Name=OJ1484.G09.128;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP003913; BAD03090.1; -.
DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR001678; Fmu_NOL1NOP2p.
DR InterPro; IPR002478; PUA.
DR Pfam; PF01189; NOL1NOP2_Fmu; 3.
DR Pfam; PF01472; PUA; 1.
DR PROSITE; PS01153; NOL1NOP2_SUN; 1.
DR PROSITE; PS50890; PUA; 1.
SQ SEQUENCE 589 AA; 64129 MW; E55B6B5A8EB1D95A CRC64;

Query Match 68.0%; Score 34; DB 2; Length 589;
Best Local Similarity 77.8%; Pred. No. 4e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 SIAARVLD 10
DB 272 SVVAAVLD 280

RESULT 32
Q7OH89 PRELIMINARY; PRT; 596 AA.
ID Q7OH89

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AC Q7OH89;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Eblp3954 (Fragment).
GN Name=eblp3954; ORFNames=ENSANG00000003144;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=PEST;
RC Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1 CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB0100816; EAA05237.1; -.
DR HSP; P06983; IAH5.
DR GO; GO:0004418; F:hydroxymethylbilane synthase activity; IEA.
DR GO; GO:0006779; P:porphyrin biosynthesis; IEA.
DR InterPro; IPR000860; Porphobil_deam.
DR Pfam; PR01379; Porphobil_deam; 1.
DR Pfam; PR03900; Porphobil_deamC; 1.
DR PRINTS; PR00151; PORPHBDMMASE.
DR PRODOM; PD002745; Porphobil_deam; 1.
DR TIGRFAMs; TIGR00212; hemC; 1.
DR PROSITE; PS00533; PORPHOBILINOGEN_DEAM; 1.
FT NON_TER 1
FT NON_TER 596
SQ SEQUENCE 596 AA; 65217 MW; 9F575CED931FPA1AE CRC64;

Query Match 68.0%; Score 34; DB 2; Length 596;
Best Local Similarity 66.7%; Pred. No. 4e+02;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 IAAARVLDY 11
DB 518 IASAKVLDY 526

RESULT 33
YAY3_SCHPO STANDARD; PRT; 649 AA.
ID YAY3_SCHPO
AC Q10211;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Hypothetical protein C4H3.03c in chromosome I.
GN ORFNames=SPAC4H3.03c;
OS Schizosaccharomyces pombe (Fission Yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21984801; PubMed=11859360; DOI=10.1038/nature724;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouris J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brookes K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Felwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hildalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymopiez B.,

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RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
 RA Borzyski K., Langer I., Beck A., Lebrach H., Reinhardt R., Pohl T.M.,
 RA Beer P., Zimmermann W., Medler S., Wambolt R., Punelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Rhode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shipkovski G.V., Useery D., Barrett B.G., Nurse P.,
 RA "The genome sequence of Schizosaccharomyces pombe.";
 RL Nature 415:871-880(2002).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
 DR EMBL; Z69380; CA93342.1; -.
 DR PIR; T38883; T38883.
 DR GenDB Spombe; SPAC4H3.03c; -.
 DR InterPro; IPR000165; Glyco_hydro_15.
 DR InterPro; IPR008928; Glyco_trans_6hp.
 DR Pfam; PF00723; Glyco_hydro_15; 1.
 DR Hypothetical protein; Transmembrane.
 FT TRANSMEM 265 285 Potential.
 FT TRANSMEM 564 584 Potential.
 FT TRANSMEM 626 646 Potential.
 SQ SEQUENCE 649 AA; 74488 MW; 0C97C10E603EB33D CRC64;

Query Match 68.0%; Score 34; DB 1; Length 649;
 Best Local Similarity 70.0%; Pred. No. 4.4e+02;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Gy 1 ASINARVLD 10
 Db 631 ASINARVLD 640

RESULT 34
 Q6ZG00 PRELIMINARY; PRT; 827 AA.
 AC Q6ZG00;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DE Putative brassinosteroid insensitive 1.
 GN Name=OJ11B_F05.16;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OC NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP004158; BAC9489.1; -.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR011009; Kinase_like.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR007090; LRR_plant.
 DR InterPro; IPR003591; LRR_Typ.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.

DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF00560; LRR_1; 7.
 DR PRINTS; PR00019; LEURICRPT.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00369; LRR_TYF; 6.
 DR SMART; SM00220; S_TIC; 1.
 DR SMART; SM00219; TYKIC; 1.
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
 SQ SEQUENCE 827 AA; 88805 MW; 10959C22DBA95A9F CRC64;

Query Match 68.0%; Score 34; DB 2; Length 827;
 Best Local Similarity 88.9%; Pred. No. 5.5e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Gy 2 SINARVLD 10
 Db 153 SINARVLD 161

RESULT 35
 Q6FY30 PRELIMINARY; PRT; 866 AA.
 AC Q6FY30;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DE Similarities with sp|P41223| Saccharomyces cerevisiae YDR351w SBE2 bud
 DE growth protein.
 GN ORFNames=CAGJ0A02486g;
 OS Candida glabrata CBS138.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
 OX NCBI_TaxID=284593;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CBS138;
 RG Genolavures;
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
 RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
 RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Batte V.,
 RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
 RA Boissarie A., Boyer J., Cattoi L., Confiantollet F., de Daruvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
 RA Hantreuve F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Niclaud J.M., Nikolaki M., Ozcas S., Ozier-Kalogeropoulos O.,
 RA Pellenz S., Potier S., Richard G.F., Straud M.L., Suleau A.,
 RA Swenne D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zenlou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J.,
 RA Wincker P., Souciet J.L.;
 RT "Genome evolution in yeasts."
 RL Nature 430:35-44(2004).
 DR EMBL; CR380947; CAG57765.1; -.
 SQ SEQUENCE 866 AA; 97660 MW; 42E49D2196D1874F CRC64;

Query Match 68.0%; Score 34; DB 2; Length 866;
 Best Local Similarity 63.6%; Pred. No. 5.8e+02;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Gy 1 ASINARVLD 11
 Db 810 ASINARVLD 820

RESULT 36
 Q67R60 PRELIMINARY; PRT; 874 AA.
 AC Q67R60;
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DE DNA polymerase I.

GN ORFNames=STH848;
 OS Symbiobacterium thermophilum.
 OC Bacteria; Actinobacteria; Symbiobacterium.
 OX NCBI_TaxID=2734;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IAM14863;
 RA Ueda K., Yamashita A., Ishikawa J., Shinada M., Matsui T.,
 RT "Complete genome sequence of an uncultured bacterium Symbiobacterium thermophilum."
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP006840; BAD39833.1; -
 DR InterPro; IPR002562; 3_5_exonuclease.
 DR InterPro; IPR002421; 5_3_exonuclease.
 DR InterPro; IPR008918; 5_3_exo_C.
 DR InterPro; IPR001098; DNA_pol.
 DR InterPro; IPR002298; DNA_pol.
 DR InterPro; IPR000513; Exo_N1.
 DR Pfam; PF01612; 3_5_exonuc; 1.
 DR Pfam; PF01367; 5_3_exonuc; 1.
 DR Pfam; PF02739; 5_3_exonuc; 1.
 DR Pfam; PF00476; DNA_pol_A; 1.
 DR PRINTS; PR00868; DNAPOLI.
 DR SMART; SM00475; 53EXOC; 1.
 DR SMART; SM00279; HhH2; 1.
 DR SMART; SM00482; POLAC; 1.
 DR TIGRFAMs; TIGR00593; pola; 1.
 SQ SEQUENCE 874 AA; 96743 MW; B5D7DFCCD2255EAC CRC64;

Query Match 68.0%; Score 34; DB 2; Length 874;
 Best Local Similarity 100.0%; Pred. No. 5.8e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AARVLDY 11
 |||||
 Db 563 AARVLDY 569

RESULT 37
 Q82W19 PRELIMINARY; PRT; 912 AA.
 AC Q82W19;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE ParEP2b.
 GN OrderedLocustNames=PAE1770;
 OS Pyrobaculum aerophilum.
 OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
 OC Thermoproteaceae; Pyrobaculum.
 OX NCBI_TaxID=13773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IM2 / ATCC 51768 / DSM 7523;
 RX MEDLINE=21664397; PubMed=11792863; DOI=10.1073/pnas.241636498;
 RA Fitz-Gibbon S.T., Ladner H., Kim U.-C., Stetter K.O., Simon M.T.,
 RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum aerophilum."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
 DR EMBL; AB009838; AAL63713.1; -
 KW Complete proteome.
 SQ SEQUENCE 912 AA; 102319 MW; 8C988BEF7DA3300E CRC64;

Query Match 68.0%; Score 34; DB 2; Length 912;
 Best Local Similarity 87.5%; Pred. No. 6.1e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 AARVLDY 11
 |||||
 Db 95 AARVLDY 102

RESULT 38
 Q8A1R0 PRELIMINARY; PRT; 920 AA.
 AC Q8A1R0;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Beta-nannosidase.
 GN OrderedLocustNames=BT3599;
 OS Bacteroides thetaiotaomicron.
 OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
 OC Bacteroidaceae; Bacteroides.
 OX NCBI_TaxID=818;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VP1-5482 / ATCC 29148;
 RX MEDLINE=2250858; PubMed=12663928; DOI=10.1126/science.1080029;
 RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
 RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis."
 RL Science 299:2074-2076(2003).
 DR EMBL; AB016941; AAC78704.1; -
 DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR008979; Gal_bind_like.
 DR InterPro; IPR006102; Glyco_hydro_21g.
 DR InterPro; IPR006104; Glyco_hydro_25b.
 DR Pfam; PF00703; Glyco_hydro_2; 1.
 DR Pfam; PF02837; Glyco_hydro_2_N; 1.
 KW Complete proteome.
 SQ SEQUENCE 920 AA; 106822 MW; 4DF439A6D7648666 CRC64;

Query Match 68.0%; Score 34; DB 2; Length 920;
 Best Local Similarity 66.7%; Pred. No. 6.1e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 IAARVLDY 11
 |||||
 Db 756 IAARVLDY 764

RESULT 39
 Q7EZJ3 PRELIMINARY; PRT; 945 AA.
 AC Q7EZJ3;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Putative valyl-tRNA synthetase.
 GN Name=P0428D12.115;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Eukaryota; Viridiplantae; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa niphonbare(GAS) genomic DNA, chromosome 7, PAC clone:P0428D12.";
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP004664; BAC83606.1; -
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004632; F:valine-tRNA ligase activity; IEA.
 DR GO; GO:0006438; P:valyl-tRNA aminoacylation; IEA.
 DR InterPro; IPR002300; tRNA-synt_1a.
 DR InterPro; IPR001412; tRNA-synt_1.
 DR InterPro; IPR002303; tRNA-synt_val.
 DR InterPro; IPR009080; tRNA-synt_val.
 DR InterPro; IPR010978; tRNA binding arm.
 DR InterPro; IPR009008; valRS_tiers_edit.
 DR Pfam; PF00133; tRNA-synt_1; 1.

DR PRINTS; PR00986; TRNASYNTHVAL.
 DR TIGRFAMs; TIGR00422; va1s; 1.
 DR PROSITE; PS00178; AA TRNA_LIGASE_I; 1.
 KW Aminoacyl-tRNA synthetase.
 SQ SEQUENCE 945 AA; 107631 MW; 418F8306AFB4FDAC CRC64;

Query Match 68.0%; Score 34; DB 2; Length 945;
 Best Local Similarity 77.8%; Pred. No. 6.3e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 IAAARVLDY 11
 :|||:
 Db 815 VAAADVLDY 823

RESULT 40

ID 084812 PRELIMINARY; PRT; 956 AA.
 AC 084812;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, last annotation update)
 DE Insulinase family/Protease III.
 GN Name=Pir; OrderedLocustNames=CT806;
 OS Chlamydia trachomatis.
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_TaxID=813;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=D / UW-3 / Cx;
 RX MEDLINE=99000809; PubMed=9784136; DOI=10.1126/science.282.5389.754;
 RA Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
 RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
 RA Davis R.W.;
 RT "Genome sequence of an obligate intracellular pathogen of humans:
 RT Chlamydia trachomatis.";
 RL Science 282:754-759(1998).
 DR EMBL; AE001353; AAC68402.1; -.
 DR PTR; B71468; B71468.
 DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001431; Insulinase like.
 DR InterPro; IPR007863; Peptidase M16_C.
 DR Pfam; PF00675; Peptidase_M16_I.
 DR Pfam; PF05193; Peptidase_M16_C; 2.
 DR Complete proteome; Protease.
 KW SEQUENCE 956 AA; 108366 MW; B0930E59D4FA486E CRC64;

Query Match 68.0%; Score 34; DB 2; Length 956;
 Best Local Similarity 77.8%; Pred. No. 6.3e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 IAAARVLDY 11
 :|||:
 Db 916 IAAARSMYD 924

Search completed: March 31, 2005, 12:09:41
 Job time : 76.2135 secs

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OM protein - protein search, using sw model

Run on: March 31, 2005, 11:42:18 ; Search time 100.75 Seconds
(without alignments)
49.905 Million cell updates/sec

Title: US-10-614-959-13
Perfect score: 66
Sequence: 1 SGSTSNIGNNYS 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	66	100.0	13	AAV79071	Anti-fact
2	66	100.0	109	AAU02544	AAU02544 Anti-adip
3	66	100.0	110	AAU02558	AAU02558 Anti-adip
4	66	100.0	110	AAU02612	AAU02612 Anti-adip
5	66	100.0	110	AAU02627	AAU02627 Anti-adip
6	66	100.0	110	AAU02629	AAU02629 Anti-adip
7	66	100.0	111	AAU02542	AAU02542 Anti-adip
8	66	100.0	111	AAU02551	AAU02551 Anti-adip
9	66	100.0	240	ABP45887	ABP45887 Human Bly
10	66	100.0	240	ADG96714	ADG96714 Single ch
11	66	100.0	242	ADG34301	ADG34301 Neurokini
12	66	100.0	242	ADG34317	ADG34317 Neurokini
13	66	100.0	243	ABP45916	ABP45916 Human Bly
14	66	100.0	243	AAO31147	AAO31147 Human CM
15	66	100.0	243	ADG96743	ADG96743 Single ch
16	66	100.0	243	ADG34310	ADG34310 Neurokini
17	66	100.0	243	ADG34306	ADG34306 Neurokini
18	66	100.0	244	ADG34303	ADG34303 Neurokini
19	66	100.0	245	ABP45915	ABP45915 Human Bly
20	66	100.0	245	ADG96742	ADG96742 Single ch
21	66	100.0	245	ADG98057	ADG98057 TNF proli
22	66	100.0	245	ADG83862	ADG83862 Chemokine
23	66	100.0	245	ADG34308	ADG34308 Neurokini
24	66	100.0	245	ADG34313	ADG34313 Neurokini
25	66	100.0	246	ABP45902	ABP45902 Human Bly

26	66	100.0	246	5	ABP45906	ABP45906 Human Bly
27	66	100.0	246	7	ADG96733	ADG96733 Single ch
28	66	100.0	246	7	ADG96729	ADG96729 Single ch
29	66	100.0	246	8	ADG83872	ADG83872 Chemokine
30	66	100.0	247	5	ABP45671	ABP45671 Human Bly
31	66	100.0	247	5	ABP45432	ABP45432 Human Bly
32	66	100.0	247	5	ABP45923	ABP45923 Human Bly
33	66	100.0	247	5	ABP45917	ABP45917 Human Bly
34	66	100.0	247	5	ABP45696	ABP45696 Human Bly
35	66	100.0	247	5	ABP45888	ABP45888 Human Bly
36	66	100.0	247	7	ADG30413	ADG30413 Human GMB
37	66	100.0	247	7	ADG30455	ADG30455 Human GMB
38	66	100.0	247	7	ADG96715	ADG96715 Single ch
39	66	100.0	247	7	ADG96498	ADG96498 Single ch
40	66	100.0	247	7	ADG96744	ADG96744 Single ch
41	66	100.0	247	7	ADG96259	ADG96259 Single ch
42	66	100.0	247	7	ADG96750	ADG96750 Single ch
43	66	100.0	247	7	ADG96523	ADG96523 Single ch
44	66	100.0	247	8	ADG83874	ADG83874 Chemokine
45	66	100.0	247	8	ADG34304	ADG34304 Neurokini

ALIGNMENTS

RESULT 1
AAV79071 standard; peptide: 13 AA.
XX
AC AAV79071;
DT 12-JUN-2000 (first entry)
XX
DE Anti-factor IX/IXa antibody L chain V domain CDRI amino acid sequence.
XX
XX Complementarity determining region 1; CDRI; antibody; Gla domain;
XX Factor IX/IXa; blood coagulation; deep venous thrombosis; light chain;
XX arterial thrombosis; unstable angina; post myocardial infarction;
XX coronary artery bypass graft; CABG; stroke; tumour growth; metastasis;
XX percutaneous transluminal coronary angioplasty; PTCA; inflammation;
XX septic shock; hypotension; adult respiratory distress syndrome; ARDS;
XX arterial fibrillation; disseminated intravascular coagulopathy; DIC.
XX
OS Homo sapiens.
XX
XX WO200012562-A1.
XX
PD 09-MAR-2000.
XX
XX 26-AUG-1999; 99WO-US019453.
XX
XX 28-AUG-1998; 98US-0098233P.
XX
XX 03-MAR-1999; 99US-0122767P.
XX
XX (GETH) GENENTECH INC.
XX
XX Adams CW, Devaux B, Baton DL, Haas PB, Judice JK, Kirchhofer D;
XX Suggest S;
XX
XX WPI; 2000-256595/22.
XX
XX Novel human anti-Factor IX/IXa antibodies against IX/IXa gamma-
XX carboxyglutamic acid domains useful as anti-coagulant in thrombosis,
XX stroke, and post myocardial infarction.
XX
XX Claim 8; Fig 2; 84pp; English.
XX
XX This sequence represents a complementarity determining region 1 (CDRI) of
XX the light chain variable domain of a human anti-factor IX/IXa Gla domain
XX antibody. Factor IXa is a vitamin K dependent plasma serine protease that
XX participates in the blood coagulation pathways. The Gla domain of factor
XX IXa and its zymogen factor IX contains important structural determinants
XX for interaction with high affinity binding sites on vascular endothelial

CC cells and platelets. Compositions comprising the antibodies are used for
CC the treatment or prophylaxis of thrombotic or coagulopathic diseases or
CC disorders in a mammal for which inhibiting a FIX/IXa mediated event is
CC indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable
CC angina, post myocardial infarction, post surgical thrombosis, coronary
CC artery bypass graft (CABG), percutaneous transluminal coronary
CC angioplasty (PTCA), stroke, tumour growth, invasion or metastasis,
CC inflammation, septic shock, hypotension, adult respiratory distress
CC syndrome (ARDS), arterial fibrillation and disseminated intravascular
CC coagulopathy (DIC)

XX
XX Sequence 13 AA;

Query Match 100.0%; Score 66; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SGSTSNIGNNYVS 13
DB 1 SGSTSNIGNNYVS 13

RESULT 2
AAU02544
ID AAU02544 standard; protein; 109 AA.
XX
AC AAU02544;
XX
DT 29-AUG-2001 (first entry)
XX
DE Anti-adipocyte monoclonal antibody light chain, FAT 31.
XX
KM Antibody; adipocyte; heavy chain; light chain; obesity; fat;
XX heart disease; complementarity determining region; CDR.
XX
OS Homo sapiens.
XX
PN WO200127279-A1.
XX
PD 19-APR-2001.
XX
PF 11-OCT-2000; 2000WO-GB003900.
XX
PR 12-OCT-1999; 99US-0158812P.
XX
PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Edwards BM, Main SH, Vaughan TJ;
XX
PS WPI; 2001-282031/29.
XX
DR N-PSDB; AAS03444.
XX
PT Panel of specific binding members of antibody molecules which bind to
XX whole adipocytes is used in the treatment of obesity and obesity related
XX diseases.
XX
PS Claim 1; Page 120; 182pp; English.

CC AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
CC and heavy chain complementarity determining regions (CDR) of the
CC invention. The antibodies can be used in the treatment of obesity and
CC obesity related diseases. The antibodies can be used to deliver drugs or
CC pro-drugs directly to the fat mass of an obese patient or the antibody
CC can be used as a therapeutic itself. Antibodies binding specifically to
CC adipocytes can be used to activate the immune system to destroy the cells
CC by complement mediated lysis. The antibodies may be labeled with a
CC detectable label such as radiolabel, fluorescent or chemical group and
CC used in methods of diagnosis in human subjects e.g. to determine the
CC presence of adipocyte antigen on the surface of an adipocyte to detect or
CC determine the presence or level of adipocytes in a cell or tissue sample.
CC The antibodies can be used as an alternative means of treatment for obese
CC patients other than undergoing surgery to remove excess fat. Antibodies

CC for different types of fat deposits can also be produced e.g. intra-
CC abdominal fat associated with heart disease

XX
XX Sequence 109 AA;

Query Match 100.0%; Score 66; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SGSTSNIGNNYVS 13
DB 23 SGSTSNIGNNYVS 35

RESULT 3
AAU02558
ID AAU02558 standard; protein; 110 AA.
XX
AC AAU02558;
XX
DT 29-AUG-2001 (first entry)
XX
DE Anti-adipocyte monoclonal antibody light chain, FAT 44.
XX
KM Antibody; adipocyte; heavy chain; light chain; obesity; fat;
XX heart disease; complementarity determining region; CDR.
XX
OS Homo sapiens.
XX
PN WO200127279-A1.
XX
PD 19-APR-2001.
XX
PF 11-OCT-2000; 2000WO-GB003900.
XX
PR 12-OCT-1999; 99US-0158812P.
XX
PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Edwards BM, Main SH, Vaughan TJ;
XX
PS WPI; 2001-282031/29.
XX
DR N-PSDB; AAS03458.
XX
PT Panel of specific binding members of antibody molecules which bind to
XX whole adipocytes is used in the treatment of obesity and obesity related
XX diseases.
XX
PS Claim 1; Page 128-129; 182pp; English.

CC AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
CC and heavy chain complementarity determining regions (CDR) of the
CC invention. The antibodies can be used in the treatment of obesity and
CC obesity related diseases. The antibodies can be used to deliver drugs or
CC pro-drugs directly to the fat mass of an obese patient or the antibody
CC can be used as a therapeutic itself. Antibodies binding specifically to
CC adipocytes can be used to activate the immune system to destroy the cells
CC by complement mediated lysis. The antibodies may be labeled with a
CC detectable label such as radiolabel, fluorescent or chemical group and
CC used in methods of diagnosis in human subjects e.g. to determine the
CC presence of adipocyte antigen on the surface of an adipocyte to detect or
CC determine the presence or level of adipocytes in a cell or tissue sample.
CC The antibodies can be used as an alternative means of treatment for obese
CC patients other than undergoing surgery to remove excess fat. Antibodies
CC for different types of fat deposits can also be produced e.g. intra-
CC abdominal fat associated with heart disease

XX
XX Sequence 110 AA;

Query Match 100.0%; Score 66; DB 4; Length 110;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
| | | | | | | | | |
Db 23 SGSTSNIGNNYVS 35

RESULT 4
AAU02612 standard; protein; 110 AA.

AAU02612;

29-AUG-2001 (first entry)

Anti-adipocyte monoclonal antibody light chain, FAT 99.

Antibody; adipocyte; heavy chain; light chain; obesity; fat;
heart disease; complementarity determining region; CDR.

Homo sapiens.

MO200127279-A1.

19-APR-2001.

11-OCT-2000; 2000WO-GB003900.

12-OCT-1999; 99US-0158812P.

(CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

Edwards BM, Main SH, Vaughan TJ;

WPI; 2001-282031/29.

N-PSDB; AAS03512.

Panel of specific binding members of antibody molecules which bind to
whole adipocytes is used in the treatment of obesity and obesity related
diseases.

Claim 1; Page 163; 182pp; English.

AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
and heavy chain complementarity determining regions (CDR) of the
invention. The antibodies can be used in the treatment of obesity and
obesity related diseases. The antibodies can be used to deliver drugs or
pro-drugs directly to the fat mass of an obese patient or the antibody
can be used as a therapeutic itself. Antibodies binding specifically to
adipocytes can be used to activate the immune system to destroy the cells
by complement mediated lysis. The antibodies may be labeled with a
detectable label such as radiolabel, fluorescent or chemical group and
used in methods of diagnosis in human subjects e.g. to determine the
presence of adipocyte antigen on the surface of an adipocyte to detect or
determine the presence or level of adipocytes in a cell or tissue sample.
The antibodies can be used as an alternative means of treatment for obese
patients other than undergoing surgery to remove excess fat. Antibodies
for different types of fat deposits can also be produced e.g. intra-
abdominal fat associated with heart disease

Sequence 110 AA;

Query Match 100.0%; Score 66; DB 4; Length 110;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
| | | | | | | | | |
Db 23 SGSTSNIGNNYVS 35

RESULT 5
AAU02627

ID AAU02627 standard; protein; 110 AA.

AAU02627;

29-AUG-2001 (first entry)

Anti-adipocyte monoclonal antibody light chain, FAT 112.

Antibody; adipocyte; heavy chain; light chain; obesity; fat;
heart disease; complementarity determining region; CDR.

Homo sapiens.

MO200127279-A1.

19-APR-2001.

11-OCT-2000; 2000WO-GB003900.

12-OCT-1999; 99US-0158812P.

(CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

Edwards BM, Main SH, Vaughan TJ;

WPI; 2001-282031/29.

N-PSDB; AAS03527.

Panel of specific binding members of antibody molecules which bind to
whole adipocytes is used in the treatment of obesity and obesity related
diseases.

Claim 1; Page 172; 182pp; English.

AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
and heavy chain complementarity determining regions (CDR) of the
invention. The antibodies can be used in the treatment of obesity and
obesity related diseases. The antibodies can be used to deliver drugs or
pro-drugs directly to the fat mass of an obese patient or the antibody
can be used as a therapeutic itself. Antibodies binding specifically to
adipocytes can be used to activate the immune system to destroy the cells
by complement mediated lysis. The antibodies may be labeled with a
detectable label such as radiolabel, fluorescent or chemical group and
used in methods of diagnosis in human subjects e.g. to determine the
presence of adipocyte antigen on the surface of an adipocyte to detect or
determine the presence or level of adipocytes in a cell or tissue sample.
The antibodies can be used as an alternative means of treatment for obese
patients other than undergoing surgery to remove excess fat. Antibodies
for different types of fat deposits can also be produced e.g. intra-
abdominal fat associated with heart disease

Sequence 110 AA;

Query Match 100.0%; Score 66; DB 4; Length 110;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
| | | | | | | | | |
Db 23 SGSTSNIGNNYVS 35

RESULT 6
AAU02629

AAU02629 standard; protein; 110 AA.

AAU02629;

29-AUG-2001 (first entry)

Anti-adipocyte monoclonal antibody light chain, FAT 113.

KM Antibody; adipocyte; heavy chain; light chain; obesity; fat;
KW heart disease; complementarity determining region; CDR.
XX
XX Homo sapiens.
XX
XX WO200127279-A1.
XX
XX PD 19-APR-2001.
XX
XX PF 11-OCT-2000; 2000WO-GB003900.
XX
XX PR 12-OCT-1999; 99US-0158812P.
XX
XX PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX PI Edwards BM, Main SH, Vaughan TJ;
XX
XX WPI; 2001-282031/29.
XX
XX DR N-PSDB; AAS03529.
XX
XX PT Panel of specific binding members of antibody molecules which bind to
XX whole adipocytes is used in the treatment of obesity and obesity related
XX diseases.
XX
XX PS Claim 1; Page 173; 182pp; English.
XX
CC AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
CC and heavy chain complementarity determining regions (CDR) of the
CC invention. The antibodies can be used in the treatment of obesity and
CC obesity related diseases. The antibodies can be used to deliver drugs or
CC pro-drugs directly to the fat mass of an obese patient or the antibody
CC can be used as a therapeutic itself. Antibodies binding specifically to
CC adipocytes can be used to activate the immune system to destroy the cells
CC by complement mediated lysis. The antibodies may be labeled with a
CC detectable label such as radiolabel, fluorescent or chemical group and
CC used in methods of diagnosis in human subjects e.g. to determine the
CC presence of adipocyte antigen on the surface of an adipocyte to detect or
CC determine the presence or level of adipocytes in a cell or tissue sample.
CC The antibodies can be used as an alternative means of treatment for obese
CC patients other than undergoing surgery to remove excess fat. Antibodies
CC for different types of fat deposits can also be produced e.g. intra-
CC abdominal fat associated with heart disease
CC
XX
XX Sequence 110 AA;
SQ
Query Match 100.0%; Score 66; DB 4; Length 110;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGGSTSNIGNNYVS 13
DB 23 SGGSTSNIGNNYVS 35
RESULT 7
AAU02542
ID AAU02542 standard; protein; 111 AA.
XX
XX AC AAU02542;
XX
XX DT 29-AUG-2001 (first entry)
XX
XX DE Anti-adipocyte monoclonal antibody light chain, FAT 30.
XX
XX KW Antibody; adipocyte; heavy chain; light chain; obesity; fat;
KW heart disease; complementarity determining region; CDR.
XX
XX OS Homo sapiens.
XX
XX PN WO200127279-A1.
XX
XX PD 19-APR-2001.

XX
XX PF 11-OCT-2000; 2000WO-GB003900.
XX
XX PR 12-OCT-1999; 99US-0158812P.
XX
XX PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX PI Edwards BM, Main SH, Vaughan TJ;
XX
XX WPI; 2001-282031/29.
XX
XX DR N-PSDB; AAS03442.
XX
XX PT Panel of specific binding members of antibody molecules which bind to
XX whole adipocytes is used in the treatment of obesity and obesity related
XX diseases.
XX
XX PS Claim 1; Page 118-119; 182pp; English.
XX
CC AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
CC and heavy chain complementarity determining regions (CDR) of the
CC invention. The antibodies can be used in the treatment of obesity and
CC obesity related diseases. The antibodies can be used to deliver drugs or
CC pro-drugs directly to the fat mass of an obese patient or the antibody
CC can be used as a therapeutic itself. Antibodies binding specifically to
CC adipocytes can be used to activate the immune system to destroy the cells
CC by complement mediated lysis. The antibodies may be labeled with a
CC detectable label such as radiolabel, fluorescent or chemical group and
CC used in methods of diagnosis in human subjects e.g. to determine the
CC presence of adipocyte antigen on the surface of an adipocyte to detect or
CC determine the presence or level of adipocytes in a cell or tissue sample.
CC The antibodies can be used as an alternative means of treatment for obese
CC patients other than undergoing surgery to remove excess fat. Antibodies
CC for different types of fat deposits can also be produced e.g. intra-
CC abdominal fat associated with heart disease
CC
XX
XX Sequence 111 AA;
SQ
Query Match 100.0%; Score 66; DB 4; Length 111;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGGSTSNIGNNYVS 13
DB 23 SGGSTSNIGNNYVS 35
RESULT 8
AAU02551
ID AAU02551 standard; protein; 111 AA.
XX
XX AC AAU02551;
XX
XX DT 29-AUG-2001 (first entry)
XX
XX DE Anti-adipocyte monoclonal antibody light chain, FAT 37.
XX
XX KW Antibody; adipocyte; heavy chain; light chain; obesity; fat;
KW heart disease; complementarity determining region; CDR.
XX
XX OS Homo sapiens.
XX
XX PN WO200127279-A1.
XX
XX PD 19-APR-2001.
XX
XX PF 11-OCT-2000; 2000WO-GB003900.
XX
XX PR 12-OCT-1999; 99US-0158812P.
XX
XX PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX PI Edwards BM, Main SH, Vaughan TJ;

XX WPI; 2001-282031/29.
 DR N-PSDB; AAS03451.
 XX Panel of specific binding members of antibody molecules which bind to
 PT whole adipocytes is used in the treatment of obesity and obesity related
 PT diseases.
 XX
 PS Claim 1; Page 124; 182pp; English.
 CC AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
 CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
 CC and heavy chain complementarity determining regions (CDR) of the
 CC invention. The antibodies can be used in the treatment of obesity and
 CC obesity related diseases. The antibodies can be used to deliver drugs or
 CC pro-drugs directly to the fat mass of an obese patient or the antibody
 CC can be used as a therapeutic itself. Antibodies binding specifically to
 CC adipocytes can be used to activate the immune system to destroy the cells
 CC by complement mediated lysis. The antibodies may be labeled with a
 CC detectable label such as radiolabel, fluorescent or chemical group and
 CC used in methods of diagnosis in human subjects e.g. to determine the
 CC presence of adipocyte antigen on the surface of an adipocyte to detect or
 CC determine the presence or level of adipocytes in a cell or tissue sample.
 CC The antibodies can be used as an alternative means of treatment for obese
 CC patients other than undergoing surgery to remove excess fat. Antibodies
 CC for different types of fat deposits can also be produced e.g. intra-
 CC abdominal fat associated with heart disease
 CC
 XX Sequence 111 AA;
 SQ
 Query Match 100.0%; Score 66; DB 4; Length 111;
 Best Local Similarity 100.0%; Pred. No. 0.0027; Mismatches 0; Indels 0; Gaps 0;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SGSTSNIGNNVYS 13
 |||||
 Db 24 SGSTSNIGNNVYS 36
 |||||
 RESULT 9
 ABP45887 ID ABP45887 standard; protein; 240 AA.
 XX AC ABP45887;
 XX DT 19-AUG-2002 (first entry)
 XX DE Human Blys binding scfv SEQ ID 1898.
 XX KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.
 XX OS Homo sapiens.
 XX PN WO200202641-A1.
 XX PD 10-JAN-2002.
 XX PF 15-JUN-2001; 2001WO-US019110.
 XX PR 16-JUN-2000; 2000US-0212210P.
 PR 17-OCT-2000; 2000US-0240816P.
 PR 16-MAR-2001; 2001US-0276248P.
 PR 21-MAR-2001; 2001US-0277379P.
 PR 25-MAY-2001; 2001US-0293499P.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 XX WPI; 2002-114799/15.
 DR Antibodies against B lymphocyte Stimulating polypeptides, useful for the
 XX diagnosis and treatment of cancers and immune disorders.
 PT
 PS Claim 1; Page 2666-2667; 3148pp; English.
 CC This invention describes novel antibodies that immunospecifically bind to
 CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antirheumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys
 CC and so may be used to detect and quaternize the presence of Blys in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of Blys. They may also be
 CC administered to treat diseases associated with aberrant Blys expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method of
 CC the invention
 CC
 XX Sequence 240 AA;
 SQ
 Query Match 100.0%; Score 66; DB 5; Length 240;
 Best Local Similarity 100.0%; Pred. No. 0.0059; Mismatches 0; Indels 0; Gaps 0;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SGSTSNIGNNVYS 13
 |||||
 Db 153 SGSTSNIGNNVYS 165
 |||||
 RESULT 10
 ADG96714 ID ADG96714 standard; protein; 240 AA.
 XX AC ADG96714;
 XX DT 11-MAR-2004 (first entry)
 XX DE Single chain antibody that immunospecifically binds Blys Segid 1898.
 XX KW antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
 KW B cell proliferation; differentiation; scfv; myasthenia gravis;
 KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
 KW carcinoma; lymphoma; antirheumatic; antirheumatic; neuroprotective;
 KW antiinflammatory; antiallergic; antiallergic; cytostatic.
 XX OS Unidentified.
 XX PN WO2003055979-A2.
 XX PD 10-JUL-2003.
 XX PF 14-NOV-2002; 2002WO-US036496.
 XX PR 16-NOV-2001; 2001US-0331469P.
 PR 19-DEC-2001; 2001US-0340817P.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 XX WPI; 2003-505530/47.
 DR Novel antibody that immunospecifically binds to a B lymphocyte stimulator
 PT (Blys), useful for detecting and treating diseases or disorders e.g.

PT rheumatoid arthritis, asthma and leukemia.
XX
XX Example 1; SEQ ID NO 1698; 394pp; English.
PS
CC This invention relates to novel antibodies that immunospecifically bind
CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
CC chromosome 13q34 and encodes a protein that is a member of the tumour
CC necrosis factor superfamily and induces both in vivo and in vitro B cell
CC proliferation and differentiation. Specifically, it refers to single
CC chain antibody molecules (scFvs) derived, preferably, from the variable
CC heavy CDR3 region that immunospecifically bind to a polypeptide, or
CC fragment thereof, of either human, murine, rat or monkey Blys. The
CC present invention refers to the use of such antibodies in various methods
CC for the detection, diagnosis and prognosis of diseases related to the
CC aberrant expression or inappropriate function of Blys or its receptor. As
CC such, these compositions are useful for identifying immune disorders
CC including myasthenia gravis and multiple sclerosis, inflammatory
CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
CC as AIDS and proliferative disorders including leukaemia, carcinoma and
CC lymphoma. Accordingly, they can be described as exhibiting various
CC activities such as antirheumatic, antiarthritic, neuroprotective,
CC antiinflammatory, antiallergic, antitoxic and cytostatic. This
CC polypeptide sequence is a single chain antibody that binds Blys of the
CC invention. NOTE: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 240 AA;
Query Match 100.0%; Score 66; DB 7; Length 240;
Best Local Similarity 100.0%; Pred. No. 0.0059;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGGSTSNIGNNYVS 13
Db 153 SGGSTSNIGNNYVS 165
RESULT 11
ADG34301 standard; protein; 242 AA.
XX
XX ADG34301;
XX
XX 26-FEB-2004 (first entry)
XX
XX Neurokinin B antibody SEQ ID NO:24.
XX
XX antibody; neurokinin B; hypotensive; gynaecological; gene therapy;
XX hyperextension; pre-eclampsia; NKB.
XX
XX Synthetic.
XX
XX WO2003102136-A2.
XX
XX 11-DEC-2003.
XX
XX 29-MAY-2003; 2003WO-US016802.
XX
XX 30-MAY-2002; 2002US-0383802P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM;
XX
XX WPI; 2004-053456/05.
XX
XX N-PSDB; ADG34282.
XX
XX New antibody that specifically binds neurokinin B, useful for preparing a
XX composition for treating or preventing hypertension or preeclampsia.
XX
XX Claim 2; SEQ ID NO 24; 127pp; English.

CC The invention relates to a novel antibody specifically binding neurokinin
CC B. An antibody of the invention has hypotensive, and gynaecological
CC activity, and may have a use in gene therapy. The antibody is useful for
CC preparing a composition for treating or preventing hypertension or pre-
CC eclampsia. The present sequence is used in the exemplification of the
CC invention.
XX
SQ Sequence 242 AA;
Query Match 100.0%; Score 66; DB 8; Length 242;
Best Local Similarity 100.0%; Pred. No. 0.006;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGGSTSNIGNNYVS 13
Db 154 SGGSTSNIGNNYVS 166
RESULT 12
ADG34317 standard; protein; 242 AA.
XX
XX ADG34317;
XX
XX 26-FEB-2004 (first entry)
XX
XX Neurokinin B antibody SEQ ID NO:40.
XX
XX antibody; neurokinin B; hypotensive; gynaecological; gene therapy;
XX hyperextension; pre-eclampsia; NKB.
XX
XX Synthetic.
XX
XX WO2003102136-A2.
XX
XX 11-DEC-2003.
XX
XX 29-MAY-2003; 2003WO-US016802.
XX
XX 30-MAY-2002; 2002US-0383802P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM;
XX
XX WPI; 2004-053456/05.
XX
XX N-PSDB; ADG34298.
XX
XX New antibody that specifically binds neurokinin B, useful for preparing a
XX composition for treating or preventing hypertension or preeclampsia.
XX
XX Claim 2; SEQ ID NO 40; 127pp; English.
XX
XX The invention relates to a novel antibody specifically binding neurokinin
XX B. An antibody of the invention has hypotensive, and gynaecological
XX activity, and may have a use in gene therapy. The antibody is useful for
XX preparing a composition for treating or preventing hypertension or pre-
XX eclampsia. The present sequence is used in the exemplification of the
XX invention.
XX
SQ Sequence 242 AA;
Query Match 100.0%; Score 66; DB 8; Length 242;
Best Local Similarity 100.0%; Pred. No. 0.006;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGGSTSNIGNNYVS 13
Db 154 SGGSTSNIGNNYVS 166
RESULT 13
ABP45916

XX ABP45916 standard; protein; 243 AA.
XX AC ABP45916;
XX DT 19-AUG-2002 (first entry)
XX DE Human Bly5 binding scFv SEQ ID 1927.
XX KW Bly5; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antineutnatic;
KW antiAIDS; vaccine; cancer; immune; autoimmue disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX OS Homo sapiens.
XX PN WO200202641-A1.
XX PD 10-JAN-2002.
XX PF 15-JUN-2001; 2001WO-US019110.
XX PR 16-JUN-2000; 2000US-0212210P.
PR 17-OCT-2000; 2000US-0240816P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WP1; 2002-114799/15.
XX DR WPI; 2002-114799/15.
XX PT Antibodies against B lymphocyte Stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.
XX PS Claim 1; Page 2700-2701; 3148pp; English.
XX XX This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte Stimulator (Bly5) polypeptides. Bly5 is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antineutnatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Bly5. The antibodies bind to Bly5
CC and so may be used to detect and quantitate the presence of Bly5 in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Bly5. They may also be
CC administered to treat diseases associated with aberrant Bly5 expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX SQ Sequence 243 AA;
XX
XX Query Match 100.0%; Score 66; DB 5; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.006;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 14
AAO31147
ID AAO31147 standard; protein; 243 AA.

OY 1 SGSTSNIGNNYVS 13
|||
Db 155 SGSTSNIGNNYVS 167

XX AAO31147;
XX AC 06-OCT-2003 (first entry)
XX DT Human CM085C11 scFv protein that specifically binds TR7.
XX DE
XX KW Human; protein coordinate data; heavy chain variable domain; VH; cancer;
KW complementarity determining region; CDR; light chain variable domain; VL;
KW TRAIL receptor 7; TR7; tumour necrosis factor; KILLER; death receptor 5;
KW DR3; TRAIL receptor 2; TRAIL-R2; TNF-related apoptosis-inducing ligand;
KW Kaposi's sarcoma; central nervous system; medulloblastoma; neuroblastoma;
KW glioblastoma; graft versus host disease; antibody therapy; neotropic;
KW AIDS; acquired immune deficiency syndrome; neurodegenerative disorder;
KW immunosuppressive; neuroprotective; antibody therapy; antibody.
XX OS Homo sapiens.
XX PN WO2003054216-A2.
XX PD 03-JUL-2003.
XX PF 19-DEC-2002; 2002WO-US040597.
XX PR 20-DEC-2001; 2001US-0341237P.
PR 05-APR-2002; 2002US-0369877P.
PR 04-JUN-2002; 2002US-0384828P.
PR 18-JUL-2002; 2002US-0396591P.
PR 15-AUG-2002; 2002US-0403370P.
PR 13-NOV-2002; 2002US-0425737P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Salcedo T, Albert VR, Rosen CA, Humphreys R, Vaughan TJ;
XX WP1; 2003-569250/53.
XX DR N-PSDB; AAL62844.
XX PT New antibody or its fragment, useful for treating, preventing or
PT ameliorating a cancer, e.g. colon, breast, uterine, pancreatic, lung or
PT gastrointestinal cancer, or Kaposi's sarcoma or, graft versus host
PT disease, AIDS.
XX PS Claim 2; Page 288; 301pp; English.
XX XX The invention relates to an isolated antibody or its fragments such as
CC VHCDR1 (heavy chain variable domain complementarity determining region),
CC VHCDR2, VHCDR3, VLCDR1 (light chain variable domain complementarity
CC determining region), VLCDR2 or VLCDR3. The antibody or its fragment
CC immunospecifically binds TRAIL (tumour necrosis factor; TNF-related
CC apoptosis-inducing ligand) receptor 7 (TR7). TR7 is also referred to as
CC TRAIL receptor 2 (TRAIL-R2), death receptor 5 (DR5) and KILLER. The
CC antibody or its fragment is useful for treating, preventing or
CC ameliorating a cancer, e.g. colon, breast, uterine, pancreatic, lung or
CC gastrointestinal cancer or Kaposi's sarcoma or cancer of the central
CC nervous system such as medulloblastoma, neuroblastoma or glioblastoma or
CC graft versus host disease, AIDS (acquired immune deficiency syndrome) or
CC a neurodegenerative disorder. The invention is useful in antibody
CC therapy. The present sequence is human scFv protein that specifically
CC binds TR7
XX SQ Sequence 243 AA;
XX
XX Query Match 100.0%; Score 66; DB 6; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.006;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SGSTSNIGNNYVS 13
|||
Db 155 SGSTSNIGNNYVS 167

RESULT 15

ID	ADG96743
AC	ADG96743 standard; protein; 243 AA.
DT	ADG96743;
XX	
DT	11-MAR-2004 (first entry)
XX	
DE	Single chain antibody that immunospecifically binds Blys Segid 1927.
XX	
KW	antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
KW	B cell proliferation; differentiation; scfv; myasthenia gravis;
KW	multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
KW	carcinoma; lymphoma; antineuritic; antirheumatic; neuroprotective;
XX	antiinflammatory; antiaesthetic; antiallergic; cytostatic.
XX	
OS	Unidentified.
XX	
PN	WO2003055979-A2.
XX	
PD	10-JUL-2003.
XX	
PE	14-NOV-2002; 2002MO-US036496.
XX	
FR	16-NOV-2001; 2001US-0331469P.
XX	
PR	19-DEC-2001; 2001US-0340817P.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
XX	
PI	Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;
XX	
DR	WPI; 2003-505530/47.
XX	
PT	Novel antibody that immunospecifically binds to a B lymphocyte stimulator
XX	(Blys), useful for detecting and treating diseases or disorders e.g.
PT	rheumatoid arthritis, asthma and leukemia.
XX	
PS	Example 1; SEQ ID NO 1927; 394pp; English.
XX	
CC	This invention relates to novel antibodies that immunospecifically bind
CC	to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
CC	chromosome 13q34 and encodes a protein that is a member of the tumour
CC	necrosis factor superfamily and induces both in vivo and in vitro B cell
CC	proliferation and differentiation. Specifically, it refers to single
CC	chain antibody molecules (scfv) derived, preferably, from the variable
CC	heavy CDR3 region that immunospecifically bind to a polypeptide, or
CC	fragment thereof, of either human, murine, rat or monkey Blys. The
CC	present invention refers to the use of such antibodies in various methods
CC	for the detection, diagnosis and prognosis of diseases related to the
CC	aberrant expression or inappropriate function of Blys or its receptor. As
CC	such, these compositions are useful for identifying immune disorders
CC	including myasthenia gravis and multiple sclerosis, inflammatory
CC	disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
CC	as AIDS and proliferative disorders including leukaemia, carcinoma and
CC	lymphoma. Accordingly, they can be described as exhibiting various
CC	activities such as antineuritic, antiarthritic, neuroprotective,
CC	antiinflammatory, antiaesthetic, antiallergic and cytostatic. This
CC	polypeptide sequence is a single chain antibody that binds Blys of the
CC	invention. NOTE: The sequence data for this patent did not form part of
CC	the printed specification, but was obtained in electronic format
XX	directly from WIPO at ftp.wipo.int/pub/published_pat_sequences.
XX	
XX	Sequence 243 AA;

```
Query Match          100.0%; Score 66; DB 7; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.006;
Matches    13; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY           1 SGSTSNIGNNYVS   13
              |||||
Db            155 SGSTSNIGNNYVS 167

RESULT 16
```

ADG34310	ID	ADG34310 standard; protein; 243 AA.
XX	AC	ADG34310;
XX	DT	26-FEB-2004 (first entry)
XX	DE	Neurokinin B antibody SEQ ID NO:33.
XX	KW	antibody; neurokinin B; hypotensive; gynaecological; gene therapy;
KM	hypertension; pre-eclampsia; NKB.	
OS	Synthetic.	
PN	WO2003102136-A2.	
XX	PD	11-DEC-2003.
XX	PF	29-MAY-2003; 2003WO-US016802.
XX	PI	(HUMA-) HUMAN GENOME SCI INC.
XX	DR	Rosen CA, Ruben SM;
XX	WI	WI: 2004-053456/05.
XX	N-PSDB	ADG34291.
PT	New antibody that specifically binds neurokinin B, useful for preparing a composition for treating or preventing hypertension or preeclampsia.	
PS	Claim 2; SEQ ID NO 33; 127bp; English.	
CC	B. The invention relates to a novel antibody specifically binding neurokinin activity, and may have a use in gene therapy. The antibody is useful for preparing a composition for treating or preventing hypertension or pre-eclampsia. The present sequence is used in the exemplification of the invention.	
CC	Sequence 243 AA;	
QY	Query Match	100.0%; Score 66; DB 8; Length 243;
Best Local Similarity	100.0%; Pred. No. 0.006;	
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
DB	155 SGSTSNIGNNYVS 167	
RESULT 17		
ADG34306	ID	ADG34306 standard; protein; 243 AA.
XX	AC	ADG34306;
XX	DT	26-FEB-2004 (first entry)
XX	DE	Neurokinin B antibody SEQ ID NO:29.
XX	KW	antibody; neurokinin B; hypotensive; gynaecological; gene therapy;
KM	hypertension; pre-eclampsia; NKB.	
OS	Synthetic.	
PN	WO2003102136-A2.	
XX	PD	11-DEC-2003.
XX	PF	29-MAY-2003; 2003WO-US016802.
XX		

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Query Match          100.0%; Score 66; DB 8; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.006;
Matches    13; Conservative    0; Mismatches    0; Indels    0; Gaps    0.

OY      1 SGSTSNIGNNNYS   13
        |||||
Db       155 SGSTSNIGNNNYS 167

RESULT 17
ADG34306
ID ADG34306 standard; protein; 243 AA.
XX AC ADG34306;
XX DT 26-FEB-2004 (first entry)
XX DE Neurokinin B antibody SEQ ID NO:29.
XX KM antibody; neurokinin B; hypotensive; gynaecological; gene therapy;
XX hypertenson; pre-eclampsia; NKB.
OS Synthetic.
XX PN WO2003102136-A2.
XX PD 11-DEC-2003.
XX PF 29-MAY-2003; 2003WO-US016802.
XX
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PR 30-MAY-2002; 2002US-0383802P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2004-053456/05.
XX
DR N-PSDB; ADG34287.
XX
PT New antibody that specifically binds neurokinin B, useful for preparing a
PT composition for treating or preventing hypertension or preeclampsia.
XX
XX Claim 2; SEQ ID NO 29; 127bp; English.
XX
XX The invention relates to a novel antibody specifically binding neurokinin
CC B. An antibody of the invention has hypotensive, and gynaecological
CC activity, and may have a use in gene therapy. The antibody is useful for
CC preparing a composition for treating or preventing hypertension or pre-
CC eclampsia. The present sequence is used in the exemplification of the
CC invention.
XX
XX Sequence 243 AA;
SQ
Query Match 100.0%; Score 66; DB 8; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.006;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGGSTNIGNNVYS 13
DB 155 SGGSTNIGNNVYS 167
|||||
RESULT 18
ADG34303
ID ADG34303 standard; protein; 244 AA.
XX
XX ADG34303;
AC
XX 26-FEB-2004 (first entry)
DT
XX
XX Neurokinin B antibody SEQ ID NO:26.
DE
XX
XX antibody; neurokinin B; hypotensive; gynaecological; gene therapy;
KM hypertension; pre-eclampsia; NKB.
XX
XX Synthetic.
OS
XX WO2003102136-A2.
PN
XX 11-DEC-2003.
PD
XX 29-MAY-2003; 2003WO-US016802.
PF
XX 30-MAY-2002; 2002US-0383802P.
PR
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX Rosen CA, Ruben SM;
PI
XX WPI; 2004-053456/05.
DR
XX N-PSDB; ADG34284.
DR
XX
XX New antibody that specifically binds neurokinin B, useful for preparing a
PT composition for treating or preventing hypertension or preeclampsia.
PT
XX
XX Claim 2; SEQ ID NO 26; 127bp; English.
XX
XX The invention relates to a novel antibody specifically binding neurokinin
CC B. An antibody of the invention has hypotensive, and gynaecological
CC activity, and may have a use in gene therapy. The antibody is useful for
CC preparing a composition for treating or preventing hypertension or pre-
CC eclampsia. The present sequence is used in the exemplification of the
CC invention.

XX
SQ Sequence 244 AA;
Query Match 100.0%; Score 66; DB 8; Length 244;
Best Local Similarity 100.0%; Pred. No. 0.006;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGGSTNIGNNVYS 13
DB 156 SGGSTNIGNNVYS 168
|||||
RESULT 19
ABP45915
ID ABP45915 standard; protein; 245 AA.
XX
XX ABP45915;
AC
XX 19-AUG-2002 (first entry)
DT
XX
XX Human Blys binding scFv SEQ ID 1926.
DE
XX
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KM tumour necrosis factor; B cell proliferation; B cell differentiation;
KM immunosuppressive; immunostimulant; immunomodulatory; antineumatic;
KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KM common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
XX Homo sapiens.
OS
XX WO200202641-A1.
PN
XX 10-JAN-2002.
PD
XX
XX 15-JUN-2001; 2001WO-US019110.
PE
XX
XX 16-JUN-2000; 2000US-0212210P.
PR
XX 17-OCT-2000; 2000US-0240816P.
PR
XX 16-MAR-2001; 2001US-0276248P.
PR
XX 21-MAR-2001; 2001US-0277379P.
PR
XX 25-MAY-2001; 2001US-0293499P.
PR
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
PI
XX WPI; 2002-114799/15.
DR
XX
XX Antibodies against B lymphocyte Stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.
PT
XX
XX Claim 1; Page 2699-2700; 3148pp; English.
XX
XX This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antineumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABR4390-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX

SO Sequence 245 AA;
Query Match 100.0%; Score 66; DB 5; Length 245;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGTSTNIGNNYVS 13
| | | | | | | | | | | | | | |
DB 157 SGTSTNIGNNYVS 169

RESULT 20
ADG96742
ID ADG96742 standard; protein; 245 AA.
XX
AC ADG96742;
XX
DT 11-MAR-2004 (first entry)
XX
DE Single chain antibody that immunospecifically binds Blys SegID 1926.
XX
KW antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
KW B cell proliferation; differentiation; scfv; myasthenia gravis;
KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
KW carcinoma; lymphoma; antineumatic; antiarthritic; neuroprotective;
KW antiinflammatory; antiasthmatic; antiallergic; cytostatic.
XX
OS Unidentified.
XX
PN WO2003055979-A2.
XX
PD 10-JUL-2003.
XX
PF 14-NOV-2002; 2002WO-US036496.
XX
PR 16-NOV-2001; 2001US-0331469P.
PR 19-DEC-2001; 2001US-0340817P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PI Ruben SM, Barash SC, Choi GH, Vaughan TV, Hilbert D;
XX
DR WPI; 2003-505530/47.
XX
PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator
PT (Blys), useful for detecting and treating diseases or disorders e.g.
PT rheumatoid arthritis, asthma and leukemia.
XX
PS Example 1; SEQ ID NO 1926; 394pp; English.
XX
CC This invention relates to novel antibodies that immunospecifically bind
CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
CC chromosome 13q34 and encodes a protein that is a member of the tumour
CC necrosis factor superfamily and induces both in vivo and in vitro B cell
CC proliferation and differentiation. Specifically, it refers to single
CC chain antibody molecules (scfvs) derived, preferably, from the variable
CC heavy CD33 region that immunospecifically bind to a polypeptide, or
CC fragment thereof, of either human, murine, rat or monkey Blys. The
CC present invention refers to the use of such antibodies in various methods
CC for the detection, diagnosis and prognosis of diseases related to the
CC aberrant expression or inappropriate function of Blys or its receptor. As
CC such, these compositions are useful for identifying immune disorders
CC including myasthenia gravis and multiple sclerosis, inflammatory
CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
CC as AIDS and proliferative disorders including leukaemia, carcinoma and
CC lymphoma. Accordingly, they can be described as exhibiting various
CC activities such as antineumatic, antiallergic, neuroprotective,
CC antiinflammatory, antiasthmatic, antiallergic and cytostatic. This
CC polypeptide sequence is a single chain antibody that binds Blys of the
CC invention. NOTE: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX

SO Sequence 245 AA;
Query Match 100.0%; Score 66; DB 7; Length 245;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGTSTNIGNNYVS 13
| | | | | | | | | | | | | | |
DB 157 SGTSTNIGNNYVS 169

RESULT 21
ADG98057
ID ADG98057 standard; protein; 245 AA.
XX
AC ADG98057;
XX
DT 11-MAR-2004 (first entry)
XX
DE TNF proliferation inducing protein ligand (APRIL) SegID 3241.
XX
KW human; B lymphocyte stimulator; Blys; tumour necrosis factor;
KW B cell proliferation; differentiation; myasthenia gravis;
KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
KW carcinoma; lymphoma; antineumatic; antiallergic; neuroprotective;
KW antiinflammatory; antiasthmatic; antiallergic; cytostatic; APRIL; TNF;
KW ligand.
XX
OS Unidentified.
XX
PN WO2003055979-A2.
XX
PD 10-JUL-2003.
XX
PF 14-NOV-2002; 2002WO-US036496.
XX
PR 16-NOV-2001; 2001US-0331469P.
PR 19-DEC-2001; 2001US-0340817P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PI Ruben SM, Barash SC, Choi GH, Vaughan TV, Hilbert D;
XX
DR WPI; 2003-505530/47.
XX
PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator
PT (Blys), useful for detecting and treating diseases or disorders e.g.
PT rheumatoid arthritis, asthma and leukemia.
XX
PS Claim 1; SEQ ID NO 3241; 394pp; English.
XX
CC This invention relates to novel antibodies that immunospecifically bind
CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
CC chromosome 13q34 and encodes a protein that is a member of the tumour
CC necrosis factor superfamily and induces both in vivo and in vitro B cell
CC proliferation and differentiation. Specifically, it refers to single
CC chain antibody molecules (scfvs) derived, preferably, from the variable
CC heavy CD33 region that immunospecifically bind to a polypeptide, or
CC fragment thereof, of either human, murine, rat or monkey Blys. The
CC present invention refers to the use of such antibodies in various methods
CC for the detection, diagnosis and prognosis of diseases related to the
CC aberrant expression or inappropriate function of Blys or its receptor. As
CC such, these compositions are useful for identifying immune disorders
CC including myasthenia gravis and multiple sclerosis, inflammatory
CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
CC as AIDS and proliferative disorders including leukaemia, carcinoma and
CC lymphoma. Accordingly, they can be described as exhibiting various
CC activities such as antineumatic, antiallergic, neuroprotective,
CC antiinflammatory, antiasthmatic, antiallergic and cytostatic. This
CC polypeptide sequence is an APRIL protein, a TNF proliferation inducing
CC ligand that can form a fusion protein with a Blys protein of the
CC invention.
XX

SQ Sequence 245 AA;
Query Match 100.0%; Score 66; DB 7; Length 245;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGSTSNIGNNYVS 13
157 SGSTSNIGNNYVS 169
Db 157 SGSTSNIGNNYVS 169
RESULT 22
ADE83862
ID ADE83862 standard; protein; 245 AA.
AC ADE83862;
XX 29-JAN-2004 (first entry)
DT 29-JAN-2004 (first entry)
DE Chemokine beta-4 binding antibody F081C09 protein SEQ ID NO:21.
XX
XX antibody; chemokine beta-4; CK-B4; single chain Fvs; scFvs;
KM antiapoptotic; dermatological; antiinflammatory; immunosuppressive;
KM antirheumatic; antiarthritic; cerebroprotective; cytostatic; anti-HIV;
KM vulnereary; dermatitis; autoimmune disease; rheumatoid arthritis;
KM systemic lupus erythematosus; autoimmune encephalitis; cancer;
KM HIV infection; wound; inflammatory disorder; human; psoriasis.
XX
OS Synthetic.
OS Homo sapiens.
XX WO2003092597-A2.
XX 13-NOV-2003.
XX 30-APR-2003; 2003WO-US013414.
XX 01-MAY-2002; 2002US-0376561P.
XX (HUMA-) HUMAN GENOME SCL INC.
XX Rosen CA, Ruben SM;
XX WPI: 2004-022614/02.
XX DR N-PSDB; ADE83845.
XX
XX New antibody that specifically binds to a chemokine beta-4 polypeptide,
PT useful for diagnosing, treating, preventing or ameliorating psoriasis,
PT rheumatoid arthritis, systemic lupus erythematosus, cancer, HIV infection
PT and wounds.
XX
XX Claim 1; SEQ ID NO 21; 181bp; English.
XX
XX The present invention describes an antibody (I) that specifically binds
CC to a chemokine beta-4 (CK-B4) polypeptide. Where (I) comprises a first
CC amino acid sequence at least 95% identical to a second amino acid
CC sequence comprising a VH complementarity determining region (CDR) or VL
CC CDR of any of the single chain Fvs (scFvs) from any of 17 fully defined
CC sequences of 245-253 amino acids (ADE83861 to ADE83877). Also described:
CC (1) a kit comprising (1); (2) an isolated nucleic acid molecule encoding
CC (1); (3) a vector comprising the isolated nucleic acid of (2); (4) a host
CC cell comprising the vector of (3); (5) a cell line engineered to express
CC (1); (6) an antibody that binds the same epitope as (1); (7) an antibody
CC that competitively inhibits the binding (1) to a CK-B4 polypeptide; (8) a
CC method for detecting aberrant expression of CK-B4 polypeptide, comprising
CC assaying the level of CK-B4 polypeptide expression in a first biological
CC sample of an individual using at least one of (1), and comparing the
CC level of CK-B4 polypeptide assayed in the biological sample with a
CC standard level of CK-B4 polypeptide expression or level of CK-B4
CC polypeptide in a second, normal biological sample, where an increase or
CC decrease in the assayed level of CK-B4 polypeptide in the first
CC biological sample compared to the standard level is indicative of
CC aberrant expression; and (9) a method of treating, preventing or

CC ameliorating psoriasis, dermatitis or an autoimmune disease, comprising
CC administering (1) to the animal. (I) has antipsoriatic, dermatological,
CC antinflammatory, immunosuppressive, antirheumatic, antiarthritic,
CC cerebroprotective, cytostatic, anti-HIV and vulnereary activities. The
CC methods and compositions of the present invention are useful for
CC diagnosing, treating, preventing or ameliorating psoriasis, dermatitis or
CC an autoimmune disease such as rheumatoid arthritis, systemic lupus
CC erythematosus and autoimmune encephalitis. They can also be used in
CC cancer, HIV infection, wounds and inflammatory disorders. The present
CC sequence is used in the exemplification of the present invention.
XX
XX Sequence 245 AA;
Query Match 100.0%; Score 66; DB 8; Length 245;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGSTSNIGNNYVS 13
157 SGSTSNIGNNYVS 169
Db 157 SGSTSNIGNNYVS 169
RESULT 23
ADG34308
ID ADG34308 standard; protein; 245 AA.
XX ADG34308;
XX 26-FEB-2004 (first entry)
DT 26-FEB-2004 (first entry)
DE Neurokinin B antibody SEQ ID NO:31.
XX
XX antibody; neurokinin B; hypotensive; gynaecological; gene therapy;
KM hypertension; pre-eclampsia; NKB.
XX
OS Synthetic.
OS WO2003102136-A2.
XX 11-DEC-2003.
XX 29-MAY-2003; 2003WO-US016802.
XX 30-MAY-2002; 2002US-0383802P.
XX (HUMA-) HUMAN GENOME SCL INC.
XX Rosen CA, Ruben SM;
XX WPI: 2004-053456/05.
XX DR N-PSDB; ADG34289.
XX
XX New antibody that specifically binds neurokinin B, useful for preparing a
PT composition for treating or preventing hypertension or preeclampsia.
PT
XX Claim 2; SEQ ID NO 31; 127bp; English.
XX
XX The invention relates to a novel antibody specifically binding neurokinin
CC B. An antibody of the invention has hypotensive, and gynaecological
CC activity, and may have a use in gene therapy. The antibody is useful for
CC preparing a composition for treating or preventing hypertension or pre-
CC eclampsia. The present sequence is used in the exemplification of the
CC invention.
XX
XX Sequence 245 AA;
Query Match 100.0%; Score 66; DB 8; Length 245;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGSTSNIGNNYVS 13
157 SGSTSNIGNNYVS 169
Db 157 SGSTSNIGNNYVS 169

RESULT 24
ADG34313
ID ADG34313 standard; protein; 245 AA.
XX
AC ADG34313;
XX
XX 26-FEB-2004 (first entry)
XX
XX Neurokinin B antibody SEQ ID NO:36.
DE
XX
XX antibody; neurokinin B; hypotensive; gynaecological; gene therapy;
KM hyperextension; pre-eclampsia; NKB.
XX
XX Synthetic.
OS
XX WO2003102136-A2.
XX
XX 11-DEC-2003.
PD
XX
XX 29-MAY-2003; 2003WO-US016802.
PF
XX
XX 30-MAY-2002; 2002US-0383802P.
PR
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX Rosen CA, Ruben SM,
PI
XX
XX WPI; 2004-053456/05.
DR
XX
XX N-PSDB; ADG34294.
DR
XX
XX New antibody that specifically binds neurokinin B, useful for preparing a
PT composition for treating or preventing hypertension or preeclampsia.
PS
XX
XX Claim 2; SEQ ID NO 36; 127bp; English.
XX
XX The invention relates to a novel antibody specifically binding neurokinin
CC B. An antibody of the invention has hypotensive, and gynaecological
CC activity, and may have a use in gene therapy. The antibody is useful for
CC preparing a composition for treating or preventing hypertension or pre-
CC eclampsia. The present sequence is used in the exemplification of the
CC invention.
CC
XX
SQ Sequence 245 AA;
Query Match 100.0%; Score 66; DB 8; Length 245;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGGSTSNIGNNVYS 13
Db 157 SGGSTSNIGNNVYS 169

RESULT 25
ABP45902
ID ABP45902 standard; protein; 246 AA.
XX
XX
AC ABP45902;
XX
XX 19-AUG-2002 (first entry)
DT
XX
XX Human Blys binding scFv SEQ ID 1913.
DE
XX
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KM tumour necrosis factor; B cell proliferation; B cell differentiation;
KM immunosuppressive; immunostimulant; immunomodulatory; antitumour;
KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KM common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.

XX
XX WO200202641-A1.
XX
XX 10-JAN-2002.
XX
XX 15-JUN-2001; 2001WO-US019110.
XX
XX 16-JUN-2000; 2000US-0212210P.
XX
XX 17-OCT-2000; 2000US-0240816P.
XX
XX 16-MAR-2001; 2001US-0276248P.
XX
XX 21-MAR-2001; 2001US-0277379P.
XX
XX 25-MAY-2001; 2001US-0293499P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX (CAME-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
XX WPI; 2002-114799/15.
XX
XX
XX Antibodies against B lymphocyte stimulating polypeptides, useful for the
XX diagnosis and treatment of cancers and immune disorders.
XX
XX
XX Claim 1; Page 2683-2684; 3148bp; English.
XX
XX This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC antitumour, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP4728 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
CC
XX
SQ Sequence 246 AA;
Query Match 100.0%; Score 66; DB 5; Length 246;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGGSTSNIGNNVYS 13
Db 158 SGGSTSNIGNNVYS 170

RESULT 26
ABP45906
ID ABP45906 standard; protein; 246 AA.
XX
XX
AC ABP45906;
XX
XX 19-AUG-2002 (first entry)
DT
XX
XX Human Blys binding scFv SEQ ID 1917.
DE
XX
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KM tumour necrosis factor; B cell proliferation; B cell differentiation;
KM immunosuppressive; immunostimulant; immunomodulatory; antitumour;
KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KM common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.


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PN WO200202641-A1.
XX
XX 10-JAN-2002.
XX
XX 15-JUN-2001; 2001WO-US019110.
XX
XX 16-JUN-2000; 2000US-0212210P.
XX 17-OCT-2000; 2000US-0240816P.
XX 16-MAR-2001; 2001US-0276248P.
XX 21-MAR-2001; 2001US-0277379P.
XX 25-MAY-2001; 2001US-0293499P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX (CAME-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX Ruben SM, Baraeh SC, Choi GH, Vaughan T, Hilbert D;
XX WPI; 2002-114799/15.
XX
XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
XX diagnosis and treatment of cancers and immune disorders.
XX
XX Claim 1; Page 2688-2689; 3148pp; English.
XX
XX This invention describes novel antibodies that immunospecifically bind to
XX B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
XX tumour necrosis factor (TNF) super family and induces B cell
XX proliferation and differentiation. The antibodies of the invention have
XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
XX antirheumatic and antiAIDS activity and can be used in vaccines to
XX inhibit the expression and activity of Blys. The antibodies bind to Blys
XX and so may be used to detect and quantitate the presence of Blys in
XX biological samples and may be used in this way to diagnose disease
XX associated with aberrant expression of Blys. They may also be
XX administered to treat diseases associated with aberrant Blys expression
XX and activity such as cancer, immune, and autoimmune disorders and
XX diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
XX immunodeficiency (e.g. common variable immunodeficiency (CVID) and
XX acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
XX the antibodies and fragments of the antibodies described in the method of
XX the invention
XX
XX SQ Sequence 246 AA;
XX
XX Query Match 100.0%; Score 66; DB 5; Length 246;
XX Best Local Similarity 100.0%; Pred. No. 0.0061;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SGSTSNIGNNYVS 13
XX |||||
XX 158 SGSTSNIGNNYVS 170
XX
XX RESULT 27
XX ADG96733
XX ID ADG96733 standard; protein; 246 AA.
XX
XX AC ADG96733;
XX
XX DT 11-MAR-2004 (first entry)
XX
XX DE Single chain antibody that immunospecifically binds Blys SegID 1917.
XX
XX KW antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
XX B cell proliferation; differentiation; scfv; myasthenia gravis;
XX multiple sclerosis; aschma; rheumatoid arthritis; AIDS; leukaemia;
XX carcinoma; lymphoma; antirheumatic; antiallergic; neuroprotective;
XX antiinflammatory; antiasthmatic; antiallergic; cyostatic.
XX
XX OS Unidentified.
XX
XX PN WO2003055979-A2.
XX

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PD 10-JUL-2003.
XX
XX 14-NOV-2002; 2002WO-US036496.
XX
XX 16-NOV-2001; 2001US-0331469P.
XX 19-DEC-2001; 2001US-0340817P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Baraeh SC, Choi GH, Vaughan TV, Hilbert D;
XX WPI; 2003-505530/47.
XX
XX Novel antibody that immunospecifically binds to a B lymphocyte stimulator
XX (Blys), useful for detecting and treating diseases or disorders e.g.
XX rheumatoid arthritis, asthma and leukemia.
XX
XX Example 1; SEQ ID NO 1917; 394pp; English.
XX
XX This invention relates to novel antibodies that immunospecifically bind
XX to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
XX chromosome 13q34 and encodes a protein that is a member of the tumour
XX necrosis factor superfamily and induces both in vivo and in vitro B cell
XX proliferation and differentiation. Specifically, it refers to single
XX chain antibody molecules (scfvs) derived, preferably, from the variable
XX heavy CDR3 region that immunospecifically bind to a polypeptide, or
XX fragment thereof, of either human, murine, rat or monkey Blys. The
XX present invention refers to the use of such antibodies in various methods
XX for the detection, diagnosis and prognosis of diseases related to the
XX aberrant expression or inappropriate function of Blys or its receptor. As
XX such, these compositions are useful for identifying immune disorders
XX including myasthenia gravis and multiple sclerosis, inflammatory
XX disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
XX as AIDS and proliferative disorders including leukaemia, carcinoma and
XX lymphoma. Accordingly, they can be described as exhibiting various
XX activities such as antirheumatic, antiallergic, neuroprotective,
XX antiinflammatory, antiasthmatic, antiallergic and cyostatic. This
XX polypeptide sequence is a single chain antibody that binds Blys of the
XX invention. NOTE: The sequence data for this patent did not form part of
XX the printed specification, but was obtained in electronic format
XX directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
XX SQ Sequence 246 AA;
XX
XX Query Match 100.0%; Score 66; DB 7; Length 246;
XX Best Local Similarity 100.0%; Pred. No. 0.0061;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SGSTSNIGNNYVS 13
XX |||||
XX 158 SGSTSNIGNNYVS 170
XX
XX RESULT 28
XX ADG96729
XX ID ADG96729 standard; protein; 246 AA.
XX
XX AC ADG96729;
XX
XX DT 11-MAR-2004 (first entry)
XX
XX DE Single chain antibody that immunospecifically binds Blys SegID 1913.
XX
XX KW antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
XX B cell proliferation; differentiation; scfv; myasthenia gravis;
XX multiple sclerosis; aschma; rheumatoid arthritis; AIDS; leukaemia;
XX carcinoma; lymphoma; antirheumatic; antiallergic; neuroprotective;
XX antiinflammatory; antiasthmatic; antiallergic; cyostatic.
XX
XX OS Unidentified.
XX
XX PN WO2003055979-A2.
XX

```

PD 10-JUL-2003.
XX
XX 14-NOV-2002; 2002WO-US036496.
XX
XX 16-NOV-2001; 2001US-0311469P.
PR 19-DEC-2001; 2001US-0340817P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Barash SC, Choi GH, Vaughan TV, Hilbert D,
PI WPI; 2003-505530/47.
XX
XX Novel antibody that immunospecifically binds to a B lymphocyte stimulator
PT (Blys), useful for detecting and treating diseases or disorders e.g.
PT rheumatoid arthritis, asthma and leukemia.
XX
XX Example 1; SEQ ID NO 1913; 394dp; English.
XX
XX This invention relates to novel antibodies that immunospecifically bind
CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
CC chromosome 13q34 and encodes a protein that is a member of the tumour
CC necrosis factor superfamily and induces both in vivo and in vitro B cell
CC proliferation and differentiation. Specifically, it refers to single
CC chain antibody molecules (scFvs) derived, preferably, from the variable
CC heavy CD3 region that immunospecifically bind to a polypeptide, or
CC fragment thereof, of either human, murine, rat or monkey Blys. The
CC present invention refers to the use of such antibodies in various methods
CC for the detection, diagnosis and prognosis of diseases related to the
CC aberrant expression or inappropriate function of Blys or its receptor. As
CC such, these compositions are useful for identifying immune disorders
CC including myasthenia gravis and multiple sclerosis, inflammatory
CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
CC as AIDS and proliferative disorders including leukaemia, carcinoma and
CC lymphoma. Accordingly, they can be described as exhibiting various
CC activities such as antirheumatic, antiarthritic, neuroprotective,
CC antiinflammatory, antistimatic, antiallergic and cytoprotective. This
CC polypeptide sequence is a single chain antibody that binds Blys of the
CC invention. NOTE: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 246 AA:
SQ
Query Match 100.0%; Score 66; DB 7; Length 246;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGGSTNIGNNYVS 13
DB 158 SGGSTNIGNNYVS 170
RESULT 29
ADE83872
ID ADE83872 standard; protein; 246 AA.
XX
XX ADE83872;
XX
XX 29-JAN-2004 (first entry)
XX
XX Chemokine beta-4 binding antibody F002C08 protein SEQ ID NO:31.
XX
XX antibody; chemokine beta-4; CK-B4; single chain Fvs; scFvs;
XX antiapoptotic; dermatological; antiinflammatory; immunosuppressive;
XX antiinflammatory; antiallergic; cerebroprotective; cytoprotective; anti-HIV;
XX vulnary; dermatitis; autoimmune disease; rheumatoid arthritis;
XX systemic lupus erythematosus; autoimmune encephalitis; cancer;
XX HIV infection; wound; inflammatory disorder; human; psoriasis.
XX
XX Synthetic.
OS Homo sapiens.
XX

PN M02003092597-A2.
XX
XX 13-NOV-2003.
XX
XX 30-APR-2003; 2003WO-US013414.
XX
XX 01-MAY-2002; 2002US-0376561P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM,
PI WPI; 2004-022614/02.
XX
XX N-PSDB; ADE83855.
XX
XX New antibody that specifically binds to a chemokine beta-4 polypeptide,
PT useful for diagnosing, treating, preventing or ameliorating psoriasis,
PT rheumatoid arthritis, systemic lupus erythematosus, cancer, HIV infection
PT and wounds.
XX
XX Claim 1; SEQ ID NO 31; 181pp; English.
XX
XX The present invention describes an antibody (1) that specifically binds
CC to a chemokine beta-4 (CK-B4) polypeptide, where (1) comprises a first
CC amino acid sequence at least 95% identical to a second amino acid
CC sequence comprising a VH complementarily determining region (CDR) or VL
CC CDR of any of the single chain Fvs (scFvs) from any of 17 fully defined
CC sequences of 245-253 amino acids (ADE83861 to ADE83877). Also described:
CC (1) a kit comprising (1); (2) an isolated nucleic acid molecule encoding
CC (1); (3) a vector comprising the isolated nucleic acid of (2); (4) a host
CC cell comprising the vector of (3); (5) a cell line engineered to express
CC (1); (6) an antibody that binds the same epitope as (1); (7) an antibody
CC that competitively inhibits the binding (1) to a CK-B4 polypeptide; (8) a
CC method for detecting aberrant expression of CK-B4 polypeptide, comprising
CC assaying the level of CK-B4 polypeptide expression in a first biological
CC sample of an individual using at least one of (1), and comparing the
CC level of CK-B4 polypeptide assayed in the biological sample with a
CC standard level of CK-B4 polypeptide expression or level of CK-B4
CC polypeptide in a second, normal biological sample, where an increase or
CC decrease in the assayed level of CK-B4 polypeptide in the first
CC biological sample compared to the standard level is indicative of
CC aberrant expression; and (9) a method of treating, preventing or
CC ameliorating psoriasis, dermatitis or an autoimmune disease, comprising
CC administering (1) to the animal. (1) has antiapoptotic, dermatological,
CC antiinflammatory, immunosuppressive, antirheumatic, antiallergic,
CC cerebroprotective, cytoprotective, anti-HIV and vulnary activities. The
CC methods and compositions of the present invention are useful for
CC diagnosing, treating, preventing or ameliorating psoriasis, dermatitis or
CC an autoimmune disease such as rheumatoid arthritis, systemic lupus
CC erythematosus and autoimmune encephalitis. They can also be used in
CC cancer, HIV infection, wounds and inflammatory disorders. The present
CC sequence is used in the exemplification of the present invention.
XX
XX Sequence 246 AA:
SQ
Query Match 100.0%; Score 66; DB 8; Length 246;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGGSTNIGNNYVS 13
DB 158 SGGSTNIGNNYVS 170
RESULT 30
ABP45671
ID ABP45671 standard; protein; 247 AA.
XX
XX ABP45671;
XX
XX 19-AUG-2002 (first entry)
XX
XX Human Blys binding scFv SEQ ID 1682.
DE

KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.
 OS Homo sapiens.
 XX
 XX WO200202641-A1.
 PN
 PD 10-JAN-2002.
 XX
 XX 15-JUN-2001; 2001WO-US019110.
 PF
 XX 16-JUN-2000; 2000US-0212210P.
 PR 17-OCT-2000; 2000US-0240816P.
 PR 16-MAR-2001; 2001US-0276248P.
 PR 21-MAR-2001; 2001US-0277379P.
 PR 25-MAY-2001; 2001US-0293499P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 XX WPI; 2002-114799/15.
 DR
 XX
 XX Antibodies against B lymphocyte stimulating polypeptides, useful for the
 PT diagnosis and treatment of cancers and immune disorders.
 XX
 XX Claim 1; Page 2439-2440; 3148pp; English.
 PS
 XX This invention describes novel antibodies that immunospecifically bind to
 CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antineuronic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys
 CC and so may be used to detect and quantitate the presence of Blys in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of Blys. They may also be
 CC administered to treat diseases associated with aberrant Blys expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method of
 CC the invention
 CC
 XX
 XX Sequence 247 AA;
 SQ
 QY 1 SGSTSNIGNNYS 13
 |||||
 Db 159 SGSTSNIGNNYS 171
 Query Match 100.0%; Score 66; DB 5; Length 247;
 Best Local Similarity 100.0%; Pred. No. 0.0061;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 35
 ABP45888
 ID ABP45888 standard; protein; 247 AA.
 XX
 XX ABR45888;
 AC
 XX 19-AUG-2002 (first entry)
 DT
 XX
 XX Human Blys binding scFv SEQ ID 1899.
 DE
 XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antineuronic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 OS Homo sapiens.
 XX

KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.
 OS Homo sapiens.
 XX
 XX WO200202641-A1.
 PN
 PD 10-JAN-2002.
 XX
 XX 15-JUN-2001; 2001WO-US019110.
 PF
 XX 16-JUN-2000; 2000US-0212210P.
 PR 17-OCT-2000; 2000US-0240816P.
 PR 16-MAR-2001; 2001US-0276248P.
 PR 21-MAR-2001; 2001US-0277379P.
 PR 25-MAY-2001; 2001US-0293499P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 XX WPI; 2002-114799/15.
 DR
 XX
 XX Antibodies against B lymphocyte stimulating polypeptides, useful for the
 PT diagnosis and treatment of cancers and immune disorders.
 XX
 XX Claim 1; Page 2667-2668; 3148pp; English.
 PS
 XX This invention describes novel antibodies that immunospecifically bind to
 CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antineuronic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys
 CC and so may be used to detect and quantitate the presence of Blys in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of Blys. They may also be
 CC administered to treat diseases associated with aberrant Blys expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method of
 CC the invention
 CC
 XX
 XX Sequence 247 AA;
 SQ
 QY 1 SGSTSNIGNNYS 13
 |||||
 Db 159 SGSTSNIGNNYS 171
 Query Match 100.0%; Score 66; DB 5; Length 247;
 Best Local Similarity 100.0%; Pred. No. 0.0061;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 36
 ADG30413
 ID ADG30413 standard; protein; 247 AA.
 XX
 XX ADG30413;
 AC
 XX 26-FEB-2004 (first entry)
 DT
 XX
 XX Human GMBC609 scFv protein.
 DE
 XX GMAD; VH; CDR; complementarity determining region; VL; scFv;
 KW single chain antibody; antidiabetic; type II diabetes; human; GMBC609.
 KW Homo sapiens.
 OS
 XX

CC aberrant expression or inappropriate function of Blys or its receptor. As
 CC such, these compositions are useful for identifying immune disorders
 CC including myasthenia gravis and multiple sclerosis, inflammatory
 CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
 CC as AIDS and proliferative disorders including leukemia, carcinoma and
 CC lymphoma. Accordingly, they can be described as exhibiting various
 CC activities such as antirheumatic, antiarthritic, neuroprotective,
 CC antiinflammatory, antiallergic and cytostatic. This
 CC polypeptide sequence is a single chain antibody that binds Blys of the
 CC invention. NOTE: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX
 SO Sequence 247 AA;

Query Match 100.0%; Score 66; DB 7; Length 247;
 Best Local Similarity 100.0%; Pred. No. 0.0061;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SGSTSNIGNNYS 13
 |||||
 Db 159 SGSTSNIGNNYS 171

Search completed: March 31, 2005, 12:02:30
 Job time : 101.75 secs

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OM protein - protein search, using SW model

Run on: March 31, 2005, 11:51:44 ; Search time 25.3906 Seconds
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Title: US-10-614-959-13
Perfect score: 66
Sequence: 1 SGSTSNIGNNVYS 13

Scoring table: BLOSUM62
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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

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3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep: *
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5: /cgn2_6/ptodata/1/1aa/PTUS_COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	66	100.0	13	US-09-383-667-13	Sequence 13, Appl
2	62	93.9	98	US-08-665-202-37	Sequence 37, Appl
3	62	93.9	98	US-09-315-574-37	Sequence 37, Appl
4	62	93.9	111	US-08-665-202-36	Sequence 36, Appl
5	62	93.9	111	US-08-665-202-42	Sequence 42, Appl
6	62	93.9	111	US-08-665-202-43	Sequence 43, Appl
7	62	93.9	111	US-08-983-607-35	Sequence 35, Appl
8	62	93.9	111	US-09-315-574-36	Sequence 36, Appl
9	62	93.9	111	US-09-315-574-42	Sequence 42, Appl
10	62	93.9	112	US-09-315-574-43	Sequence 43, Appl
11	62	93.9	112	US-08-665-202-39	Sequence 39, Appl
12	62	93.9	112	US-08-983-607-31	Sequence 31, Appl
13	62	93.9	112	US-09-025-7698-18	Sequence 18, Appl
14	62	93.9	112	US-09-315-574-39	Sequence 39, Appl
15	62	93.9	112	US-09-490-070A-18	Sequence 18, Appl
16	62	93.9	112	US-09-490-153-18	Sequence 18, Appl
17	62	93.9	112	US-09-490-324-18	Sequence 18, Appl
18	62	93.9	114	US-09-240-274-62	Sequence 62, Appl
19	62	93.9	234	US-09-377-425A-4	Sequence 4, Appl
20	62	93.9	258	US-08-665-202-5	Sequence 5, Appl
21	62	93.9	258	US-09-315-574-5	Sequence 5, Appl
22	62	93.9	262	US-09-069-821-4	Sequence 4, Appl
23	62	93.9	262	US-09-956-086-4	Sequence 4, Appl
24	62	93.9	262	US-09-956-087-4	Sequence 4, Appl
25	62	93.9	282	US-09-420-592A-7	Sequence 7, Appl
26	62	93.9	282	US-09-985-442-7	Sequence 7, Appl
27	62	93.9	282	US-09-983-580-7	Sequence 7, Appl

28	61	92.4	111	2	US-08-652-816A-15	Sequence 15, Appl
29	58	87.9	111	2	US-08-665-202-40	Sequence 40, Appl
30	58	87.9	111	4	US-09-315-574-40	Sequence 40, Appl
31	58	87.9	113	1	US-08-211-202-112	Sequence 112, App
32	57	86.4	109	3	US-09-240-274-55	Sequence 55, Appl
33	57	86.4	109	3	US-09-025-7698-32	Sequence 32, Appl
34	57	86.4	109	3	US-09-025-7698-51	Sequence 51, Appl
35	57	86.4	109	4	US-09-490-070A-32	Sequence 32, Appl
36	57	86.4	109	4	US-09-490-070A-51	Sequence 51, Appl
37	57	86.4	109	4	US-09-490-153-32	Sequence 32, Appl
38	57	86.4	109	4	US-09-490-153-51	Sequence 51, Appl
39	57	86.4	109	4	US-09-490-324-32	Sequence 32, Appl
40	57	86.4	109	4	US-09-490-324-51	Sequence 51, Appl
41	55	83.3	110	1	US-08-199-911-2	Sequence 2, Appl
42	53	80.3	98	1	US-08-211-202-111	Sequence 111, App
43	53	80.3	98	2	US-08-665-202-38	Sequence 38, Appl
44	53	80.3	98	4	US-09-315-574-38	Sequence 38, Appl
45	53	80.3	109	3	US-09-240-274-59	Sequence 59, Appl

ALIGNMENTS

RESULT 1
US-09-383-667-13
Sequence 13, Application US/09383667
Patent No. 6624295
GENERAL INFORMATION:
APPLICANT: Adams, Camellia W.
APPLICANT: Devaux, Brigitte
APPLICANT: Eaton, Dan L.
APPLICANT: Haas, Philip E.
APPLICANT: Judice, J. Kevin
APPLICANT: Kirchofer, Daniel
APPLICANT: Suggest, Shelley
TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
FILE REFERENCE: P1661R2
CURRENT APPLICATION NUMBER: US/09/383, 667
CURRENT FILING DATE: 1999-08-26
EARLIER APPLICATION NUMBER: US 60/098, 233
EARLIER FILING DATE: 1998-08-28
EARLIER APPLICATION NUMBER: US 60/122, 767
EARLIER FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 32
SEQ ID NO 13
LENGTH: 13
TYPE: PRT
ORGANISM: Homo sapiens
US-09-383-667-13
Query Match 100.0%; Score 66; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.000; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 0;
Cy 1 SGSTSNIGNNVYS 13
Db 1 SGSTSNIGNNVYS 13
RESULT 2
US-08-665-202-37
Sequence 37, Application US/08665202
Patent No. 5977322
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco

STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-665-202-37

Query Match 93.3%; Score 62; DB 2; Length 98;
Best Local Similarity 92.3%; Pred. No. 0.007;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTSNIGNNYVS 13
Db 23 SGGSSNIGNNYVS 35

RESULT 3
US-09-315-574-37
Sequence 37, Application US/09315574
Patent No. 6512097
GENERAL INFORMATION:
APPLICANT: Marks, James D.
TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Majestic, Parsons, Siebert & Haue P.C.
STREET: Four Embarcadero Center, Suite 1100
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-315-574-37

Query Match 93.3%; Score 62; DB 4; Length 98;
Best Local Similarity 92.3%; Pred. No. 0.007;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGTSNIGNNYVS 13
Db 23 SGGSSNIGNNYVS 35

RESULT 4
US-08-665-202-36
Sequence 36, Application US/08665202
Patent No. 5977322
GENERAL INFORMATION:
APPLICANT: Marks, James D.
TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid

STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-665-202-36

Query Match 93.9%; Score 62; DB 2; Length 111;
Best Local Similarity 92.3%; Pred. No. 0.0079;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
|||:|||||||
DB 23 SSSSNIGNNYVS 35

RESULT 5
US-08-665-202-42
Sequence 42, Application US/08665202
Patent No. 5977322
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 5977322e1 High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-665-202-42

Query Match 93.9%; Score 62; DB 2; Length 111;
Best Local Similarity 92.3%; Pred. No. 0.0079;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
|||:|||||||
DB 23 SSSSNIGNNYVS 35

RESULT 6
US-08-665-202-43

Sequence 43, Application US/08665202
Patent No. 5977322
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 5977322e1 High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-665-202-43

Query Match 93.9%; Score 62; DB 2; Length 111;
Best Local Similarity 92.3%; Pred. No. 0.0079;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
|||:|||||||
DB 23 SSSSNIGNNYVS 35

RESULT 7
US-08-983-607-35
Sequence 35, Application US/08983607
Patent No. 6140470
GENERAL INFORMATION:
APPLICANT: Alan Garen
APPLICANT: Xiaohong Cai
TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
TITLE OF INVENTION: bodies
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Department of Molecular Biophysics
ADDRESSEE: and Biochemistry, Yale University
STREET: 266 Whitney Avenue
CITY: New Haven
STATE: Connecticut
COUNTRY: United States of America
ZIP: 06520-8114

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER: IBM PC
OPERATING SYSTEM: MS DOS
SOFTWARE: Word Processing
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/983,607
FILING DATE: April 27, 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB96/01032
FILING DATE: June 28, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mary M. Kinsky
REGISTRATION NUMBER: 32423
REFERENCE/DOCKET NUMBER: OCR-679
TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-773-9544
TELEFAX: 203-773-1183
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 residues
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: polypeptide
ORIGINAL SOURCE:
ORGANISM: Homo sapiens (melanoma patient immu-
ORGANISM: nized with autologous tumor cells)
INDIVIDUAL ISOLATE: peripheral blood lymphocytes
IMMEDIATE SOURCE:
LIBRARY: DM414 scFv antibodies obtained from
LIBRARY: fUSB5 fusion phage construct
CLONE: V373
FEATURE:
NAME/KEY: light chain
US-08-983-607-35

Query Match 93.9%; Score 62; DB 3; Length 111;
Best Local Similarity 92.3%; Pred. No. 0.0079;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
|||:|||||||
Db 23 SGSSSNIGNNYVS 35

RESULT 8
US-09-315-574-36
Sequence 36, Application US/09315574
Patent No. 6512097
GENERAL INFORMATION:
APPLICANT: Marks, James D.
TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Majestic, Parsons, Siebert & Haue P.C.
STREET: Four Embarcadero Center, Suite 1100
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574

FILING DATE: 20-MAY-99
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-315-574-36

Query Match 93.9%; Score 62; DB 4; Length 111;
Best Local Similarity 92.3%; Pred. No. 0.0079;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
|||:|||||||
Db 23 SGSSSNIGNNYVS 35

RESULT 9
US-09-315-574-42
Sequence 42, Application US/09315574
Patent No. 6512097
GENERAL INFORMATION:
APPLICANT: Marks, James D.
TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Majestic, Parsons, Siebert & Haue P.C.
STREET: Four Embarcadero Center, Suite 1100
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom

REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-315-574-42

Query Match 93.9%; Score 62; DB 4; Length 111;
Best Local Similarity 92.3%; Pred. No. 0.0079;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
|||:|||||
Db 23 SGSSSNIGNNYVS 35

RESULT 10
US-09-315-574-43
Sequence 43, Application US/09315574
Patent No. 6512097
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Majestic, Parsons, Siebert & Haue P.C.
STREET: Four Embarcadero Center, Suite 1100
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: US 60/000,238
APPLICATION DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-315-574-43

Query Match 93.9%; Score 62; DB 4; Length 111;
Best Local Similarity 92.3%; Pred. No. 0.0079;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
|||:|||||
Db 23 SGSSSNIGNNYVS 35

RESULT 11
US-08-665-202-39
Sequence 39, Application US/08665202
Patent No. 5977322
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-665-202-39

Query Match 93.9%; Score 62; DB 2; Length 112;
Best Local Similarity 92.3%; Pred. No. 0.008;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
|||:|||||
Db 23 SGSSSNIGNNYVS 35

RESULT 12
US-08-983-607-31
Sequence 31, Application US/08983607
Patent No. 6140470
GENERAL INFORMATION:
APPLICANT: Alan Garen

APPLICANT: Xiaohong Cai
TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
NUMBER OF INVENTION: bodies
CORRESPONDENCE ADDRESSES: 51
ADDRESS: Department of Molecular Biophysics
ADDRESSEE: and Biochemistry, Yale University
STREET: 266 Whitney Avenue
CITY: New Haven
STATE: Connecticut
COUNTRY: United States of America
ZIP: 06520-8114
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER: IBM PC
OPERATING SYSTEM: MS DOS
SOFTWARE: Word Processing
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/983,607
FILING DATE: April 27, 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB96/01032
FILING DATE: June 28, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mary M. Kinney
REGISTRATION NUMBER: 32423
REFERENCE/DOCKET NUMBER: OCR-679
TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-773-9544
TELEFAX: 203-773-1183
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 residues
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: polypeptide
DESCRIPTION: polypeptide
ORIGINAL SOURCE:
ORGANISM: Homo sapiens (melanoma patient immu-
ORGANISM: nized with autologous tumor cells)
INDIVIDUAL ISOLATE: peripheral blood lymphocytes
IMMEDIATE SOURCE:
LIBRARY: DM414 scFv antibodies obtained from
LIBRARY: fuses fusion phage construct
CLONE: V73
FEATURE:
NAME/KEY: light chain
US-08-983-607-31

Query Match 93.9%; Score 62; DB 3; Length 112;
Best Local Similarity 92.3%; Pred. No. 0.008;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGSTNIGNNYVS 13
|||:|||||||
Db 24 SGGSTNIGNNYVS 36

RESULT 13
US-09-025-769B-18
Sequence 18, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCE ADDRESSES: 373
CORRESPONDENCE ADDRESSES:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30 (ERO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-18

Query Match 93.9%; Score 62; DB 3; Length 112;
Best Local Similarity 92.3%; Pred. No. 0.008;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGSTNIGNNYVS 13
|||:|||||||
Db 23 SGGSTNIGNNYVS 35

RESULT 14
US-09-315-574-39
Sequence 39, Application US/09315574
Patent No. 6512097
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Majestic, Parsons, Siebert & Heue P.C.
STREET: Four Embarcadero Center, Suite 1100
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-315-574-39

Query Match 93.9%; Score 62; DB 4; Length 112;
Best Local Similarity 92.3%; Pred. No. 0.008;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
DB 23 SGSSSNIGNNYVS 35

RESULT 15
US-09-490-070A-18
Sequence 18, Application US/09490070A
Patent No. 6696248
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: Colin G. Sandercok, Esq. c/o Heller Ehtman
White & McAuillie
STREET: 1666 K Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercok, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids

TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-490-070A-18

Query Match 93.9%; Score 62; DB 4; Length 112;
Best Local Similarity 92.3%; Pred. No. 0.008;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
DB 23 SGSSSNIGNNYVS 35

RESULT 16
US-09-490-153-18
Sequence 18, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-490-153-18

Query Match 93.9%; Score 62; DB 4; Length 112;
Best Local Similarity 92.3%; Pred. No. 0.008;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
DB 23 SGSSSNIGNNYVS 35

RESULT 17
US-09-490-324-18
Sequence 18, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vito
Ge, Liming
Moroney, Simon
Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-490-324-18
Query Match 93.9%; Score 62; DB 4; Length 112;
Best Local Similarity 92.3%; Pred. No. 0.008;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGGSTNIGNNVYS 13
|||:|||||||
Db 23 SGGSSNIGNNVYS 35
RESULT 18
US-09-240-274-62
Sequence 62, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380

EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 62
LENGTH: 114
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain N02
US-09-240-274-62
Query Match 93.9%; Score 62; DB 3; Length 114;
Best Local Similarity 92.3%; Pred. No. 0.0082;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGGSTNIGNNVYS 13
|||:|||||||
Db 22 SGGSSNIGNNVYS 34
RESULT 19
US-09-372-425A-4
Sequence 4, Application US/09372425A
Patent No. 6475749
GENERAL INFORMATION:
APPLICANT: Sherie L. Morrison
TITLE OF INVENTION: Improved Rh Antibody
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oppenheimer Wolff & Donnelly LLP
STREET: 2029 Century Park East, Suite 3800
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 98
SOFTWARE: MS Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/372,425A
FILING DATE: August 11, 1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Oldenkamp, David J.
REGISTRATION NUMBER: 29,421
REFERENCE/DOCKET NUMBER: 510015-223
TELECOMMUNICATION INFORMATION:
TELEPHONE: (310) 788-5000
TELEFAX: (310) 788-5100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Light chain - AA
US-09-372-425A-4
Query Match 93.9%; Score 62; DB 4; Length 234;
Best Local Similarity 92.3%; Pred. No. 0.017;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGGSTNIGNNVYS 13
|||:|||||||
Db 41 SGGSSNIGNNVYS 53

RESULT 20
US-08-665-202-5
Sequence 5, Application US/08665202
Patent No. 5877322
GENERAL INFORMATION:
APPLICANT: Maika, James D.
APPLICANT: Schlier, Robert
TITLE OF INVENTION: No. 5977322e1 High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 258 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-665-202-5

Query Match 93.9%; Score 62; DB 2; Length 258;
Best Local Similarity 92.3%; Pred. No. 0.019;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
Db 167 SGSSSNIGNNYVS 179

RESULT 21
US-09-315-574-5
Sequence 5, Application US/09315574
Patent No. 6512097
GENERAL INFORMATION:
APPLICANT: Maika, James D.
APPLICANT: Schlier, Robert
TITLE OF INVENTION: No. 6512097e1 High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Majestic, Parsons, Siebert & Haue P.C.
STREET: Four Embarcadero Center, Suite 1100
CITY: San Francisco
STATE: California

COUNTRY: USA
ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 258 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-315-574-5

Query Match 93.9%; Score 62; DB 4; Length 258;
Best Local Similarity 92.3%; Pred. No. 0.019;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
Db 167 SGSSSNIGNNYVS 179

RESULT 22
US-09-069-821-4
Sequence 4, Application US/09069821
Patent No. 6323322
GENERAL INFORMATION:
APPLICANT: FILIPULA, DAVID
APPLICANT: WANG, MAOLANG
APPLICANT: SHORR, ROBERT
APPLICANT: WHITLOW, MARC
APPLICANT: LEE, LHSYNG S.
TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
TITLE OF INVENTION: CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/069,821
FILING DATE: 30-APR-1998
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/067,341
FILING DATE: 02-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/063,074
FILING DATE: 27-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/050,472
FILING DATE: 23-JUN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/044,449
FILING DATE: 30-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 0977,2280003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 262 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-09-069-821-4

Query Match 93.9%; Score 62; DB 3; Length 262;
Best Local Similarity 92.3%; Pred. No. 0.019;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 SGSTSNIGNNYVS 13
|||:|||||
Db 23 SGSSSNIGNNYVS 35

RESULT 23
US-09-956-086-4
Sequence 4, Application US/09956086
Patent No. 6743696
GENERAL INFORMATION:
APPLICANT: FILIPULA, DAVID
WANG, MAOLIANG
SHORR, ROBERT
WHITLOW, MARC
LEE, LISHYNG S.
TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/956,086
FILING DATE: 20-SEP-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/069,821
FILING DATE: <Unknown>
APPLICATION NUMBER: US 60/063,074
FILING DATE: 27-OCT-1997
APPLICATION NUMBER: US 60/050,472
FILING DATE: 23-JUN-1997

APPLICATION NUMBER: US 60/044,449
FILING DATE: 30-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 0977,2280003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 262 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: No. 6743896 Relevant
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-956-086-4

Query Match 93.9%; Score 62; DB 4; Length 262;
Best Local Similarity 92.3%; Pred. No. 0.019;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 SGSTSNIGNNYVS 13
|||:|||||
Db 23 SGSSSNIGNNYVS 35

RESULT 24
US-09-956-087-4
Sequence 4, Application US/09956087
Patent No. 6743908
GENERAL INFORMATION:
APPLICANT: FILIPULA, DAVID
WANG, MAOLIANG
SHORR, ROBERT
WHITLOW, MARC
LEE, LISHYNG S.
TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/956,087
FILING DATE: 20-SEP-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/069,821
FILING DATE: 1998-04-30
APPLICATION NUMBER: US 60/063,074
FILING DATE: 27-OCT-1997
APPLICATION NUMBER: US 60/050,472
FILING DATE: 23-JUN-1997
APPLICATION NUMBER: US 60/044,449
FILING DATE: 30-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 0977,2280003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540

;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 262 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: not relevant
;; MOLECULE TYPE: peptide
;; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-956-087-4

Query Match 93.9%; Score 62; DB 4; Length 262;
Best Local Similarity 92.3%; Pred. No. 0.019;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
|||:|||||
DB 23 SGSSSNIGNNYVS 35

RESULT 25
US-09-420-592A-7
; Sequence 7, Application US/09420592A
; Patent No. 633396
; GENERAL INFORMATION:
; APPLICANT: Filpula, David R.
; APPLICANT: Wang, Maoliang
; APPLICANT: Whitlow, Marc D.
; TITLE OF INVENTION: No. 6333396el Method for Targeted Delivery of Nucleic Acids
; FILE REFERENCE: 0977.2300001
; CURRENT APPLICATION NUMBER: US/09/420,592A
; CURRENT FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/104,949
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: C6.5/218 sfv
US-09-420-592A-7

Query Match 93.9%; Score 62; DB 3; Length 282;
Best Local Similarity 92.3%; Pred. No. 0.021;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
|||:|||||
DB 23 SGSSSNIGNNYVS 35

RESULT 26
US-09-985-442-7
; Sequence 7, Application US/09985442
; Patent No. 6692942
; GENERAL INFORMATION:
; APPLICANT: Filpula, David R.
; APPLICANT: Wang, Maoliang
; APPLICANT: Whitlow, Marc D.
; TITLE OF INVENTION: No. 6692942el Method for Targeted Delivery of Nucleic Acids
; FILE REFERENCE: 0977.2300003
; CURRENT APPLICATION NUMBER: US/09/985,442
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 09/420,592
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/104,949
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 282
; TYPE: PRT

;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: C6.5/218 sfv
US-09-985-442-7;

Query Match 93.9%; Score 62; DB 4; Length 282;
Best Local Similarity 92.3%; Pred. No. 0.021;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
|||:|||||
DB 23 SGSSSNIGNNYVS 35

RESULT 27
US-09-983-580-7
; Sequence 7, Application US/09983580
; Patent No. 6764853
; GENERAL INFORMATION:
; APPLICANT: Filpula, David R.
; APPLICANT: Wang, Maoliang
; APPLICANT: Whitlow, Marc D.
; TITLE OF INVENTION: No. 6764853el Method for Targeted Delivery of Nucleic Acids
; FILE REFERENCE: 0977.2300002
; CURRENT APPLICATION NUMBER: US/09/983,580
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: 09/420,592
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/104,949
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: C6.5/218 sfv
US-09-983-580-7

Query Match 93.9%; Score 62; DB 4; Length 282;
Best Local Similarity 92.3%; Pred. No. 0.021;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
|||:|||||
DB 23 SGSSSNIGNNYVS 35

RESULT 28
US-08-652-816A-15
; Sequence 15, Application US/08652816A
; Patent No. 5872215
; GENERAL INFORMATION:
; APPLICANT: Oebourn, JK
; APPLICANT: Allen, DJ
; APPLICANT: McCafferty, JG
; TITLE OF INVENTION: Specific binding members, materials and
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,816A

;; FILING DATE: 23-MAY-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: GB 9125579.4
;; FILING DATE: 02-DEC-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: GB 9125579.8
;; FILING DATE: 02-DEC-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: GB 9206318.9
;; FILING DATE: 24-MAR-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: GB 9206372.6
;; FILING DATE: 23-SEP-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: GB 9525004.9
;; FILING DATE: 07-DEC-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: GB 9610824.6
;; FILING DATE: 23-MAY-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/GB92/02240
;; FILING DATE: 02-DEC-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/244,597
;; FILING DATE: 01-JUN-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: David W. Clough
;; REGISTRATION NUMBER: 36,107
;; REFERENCE/DOCKET NUMBER: 2811/33308
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312-474-6300
;; INFORMATION FOR SEQ ID NO: 15:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 111 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
US-08-652-816A-15

Query Match 92.4%; Score 61; DB 2; Length 111;
Best Local Similarity 92.3%; Pred. No. 0.011;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNYVS 13
Db 23 SGSTPNIGNNYVS 35

RESULT 29
US-08-665-202-40
Sequence 40, Application US/08665202
Patent No. 5977322
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 5977322e1 High Affinity Human Antibodies to
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 60/000,238
;; FILING DATE: 14-JUN-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 60/000,250
;; FILING DATE: 15-JUN-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hunter, Tom
;; REGISTRATION NUMBER: 38,498
;; REFERENCE/DOCKET NUMBER: 02307E-061410
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 40:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 111 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-665-202-40

Query Match 87.9%; Score 58; DB 2; Length 111;
Best Local Similarity 84.6%; Pred. No. 0.035;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNYVS 13
Db 23 SGSTPNIGNNYVS 35

RESULT 30
US-09-315-574-40
Sequence 40, Application US/09315574
Patent No. 6512097
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 6512097e1 High Affinity Human Antibodies to
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Majestic, Parsons, Siebert & Heue P.C.
STREET: Four Embarcadero Center, Suite 1100
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-315-574-40

Query Match 87.9%; Score 58; DB 4; Length 111;
Best Local Similarity 84.6%; Pred. No. 0.035;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
||:|||||
Db 23 SGSTSNIGNNYVS 35

RESULT 31
US-08-211-202-112
Sequence 112, Application US/08211202
Patent No. 5565332

GENERAL INFORMATION:
APPLICANT: HOOGENBOOM, Hendricus Reneerus Jacobus Matheus
APPLICANT: BAIER, Michael
APPLICANT: JESPEERS, Laurent Stephane Anne Therese
APPLICANT: WINTER, Gregory Paul
TITLE OF INVENTION: Production of chimeric antibodies - a
TITLE OF INVENTION: combinatorial approach
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
ADDRESS: Botun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211.202
FILING DATE: 23-SEP-1992
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120252.3
FILING DATE: 23-SEP-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120377.8
FILING DATE: 25-SEP-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 24-MAR-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992

ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/31960

TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-211-202-112

Query Match 87.9%; Score 58; DB 1; Length 113;
Best Local Similarity 91.7%; Pred. No. 0.035;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYV 12
||:|||||
Db 23 SGSSNIGNNYV 34

RESULT 32
US-09-240-274-55
Sequence 55, Application US/09240274
Patent No. 6253455

GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THERMOF
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240.274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 55
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain I03
US-09-240-274-55

Query Match 86.4%; Score 57; DB 3; Length 109;
Best Local Similarity 84.6%; Pred. No. 0.049;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
||:|||||
Db 22 SGSSNIGNNYVS 34

RESULT 33
US-09-025-769B-32
Sequence 32, Application US/09025769B
Patent No. 6300064

GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Haiming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,7698
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-7698-32

Query Match 86.4%; Score 57; DB 3; Length 109;
Best Local Similarity 84.6%; Pred. No. 0.049;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
|||:||||:||||
Db 23 SGSSSNIGNNYVS 35

RESULT 34
US-09-025-7698-51
Sequence 51, Application US/090257698
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, VIC
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,7698
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-7698-51

Query Match 86.4%; Score 57; DB 3; Length 109;
Best Local Similarity 84.6%; Pred. No. 0.049;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
|||:||||:||||
Db 23 SGSSSNIGNNYVS 35

RESULT 35
US-09-490-070A-32
Sequence 32, Application US/09490070A
Patent No. 6696248
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, VIC
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
White & McAuliffe
STREET: 1666 K Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000

INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 32:

US-09-490-070A-32

Query Match 86.4%; Score 57; DB 4; Length 109;
Best Local Similarity 84.6%; Pred. No. 0.049;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
|||:||||:||||
Db 23 SGSSSNIGNNYVS 35

RESULT 36
US-09-490-070A-51

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; Sequence 51, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Illag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckhuhn, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
; White & McLaughlin
; STREET: 1666 K Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,070A
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Colin G. Sandercock, Esq.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37629-0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 912-2000
; TELEFAX: (202) 912-2020
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-09-490-070A-51

Query Match      86.4%; Score 57; DB 4; Length 109;
Best Local Similarity 84.6%; Pred. No. 0.049;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 SGSTSNIGNNYVS 13
DB      23 SSSSSNIGNNYVS 35

RESULT 37
US-09-490-153-32
; Sequence 32, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Illag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckhuhn, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York

```

```

; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,153
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-09-490-153-32

Query Match      86.4%; Score 57; DB 4; Length 109;
Best Local Similarity 84.6%; Pred. No. 0.049;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 SGSTSNIGNNYVS 13
DB      23 SSSSSNIGNNYVS 35

RESULT 38
US-09-490-153-51
; Sequence 51, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Illag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckhuhn, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,153
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0

```

FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-09-490-153-51

Query Match 86.4%; Score 57; DB 4; Length 109;
Best Local Similarity 84.6%; Pred. No. 0.049;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
|||:|||||
Db 23 SGSSSNIGNNYVS 35

RESULT 39
US-09-490-324-32
Sequence 32, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Moroney, Simon
Ge, Liming
Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-09-490-324-32

Query Match 86.4%; Score 57; DB 4; Length 109;
Best Local Similarity 84.6%; Pred. No. 0.049;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
|||:|||||
Db 23 SGSSSNIGNNYVS 35

RESULT 40
US-09-490-324-51
Sequence 51, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Moroney, Simon
Ge, Liming
Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-09-490-324-51

Query Match 86.4%; Score 57; DB 4; Length 109;
Best Local Similarity 84.6%; Pred. No. 0.049;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
|||:|||||
Db 23 SGSSSNIGNNYVS 35

Search completed: March 31, 2005, 12:13:27
Job time : 26.3906 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 31, 2005, 12:10:00 ; Search time 72.7188 Seconds
(without alignments)
59.279 Million cell updates/sec

Title: US-10-614-959-13
Perfect score: 66
Sequence: 1 SGSTSNIGNMYVS 13

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1413372 seqs, 31592847 residues

Total number of hits satisfying chosen parameters: 1413372

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications_AA:*
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20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	66	100.0	240	15	US-10-293-418-1898 Sequence 1898, Ap
3	66	100.0	243	10	US-09-880-748-1897 Sequence 1927, Ap
4	66	100.0	243	14	US-10-322-673-53 Sequence 53, Ap1
5	66	100.0	243	15	US-10-293-418-1927 Sequence 1927, Ap
6	66	100.0	245	10	US-09-880-748-1926 Sequence 1926, Ap
7	66	100.0	245	15	US-10-293-418-1926 Sequence 1926, Ap
8	66	100.0	245	15	US-10-293-418-1926 Sequence 1926, Ap
9	66	100.0	246	10	US-09-880-748-1913 Sequence 1913, Ap
10	66	100.0	246	10	US-09-880-748-1917 Sequence 1917, Ap
11	66	100.0	246	15	US-10-293-418-1913 Sequence 1913, Ap
12	66	100.0	246	15	US-10-293-418-1917 Sequence 1917, Ap
13	66	100.0	247	10	US-09-880-748-1443 Sequence 1443, Ap

14	66	100.0	247	10	US-09-880-748-1682 Sequence 1682, Ap
15	66	100.0	247	10	US-09-880-748-1707 Sequence 1707, Ap
16	66	100.0	247	10	US-09-880-748-1899 Sequence 1899, Ap
17	66	100.0	247	10	US-09-880-748-1928 Sequence 1928, Ap
18	66	100.0	247	10	US-09-880-748-1934 Sequence 1934, Ap
19	66	100.0	247	15	US-10-293-418-1443 Sequence 1443, Ap
20	66	100.0	247	15	US-10-293-418-1682 Sequence 1682, Ap
21	66	100.0	247	15	US-10-293-418-1707 Sequence 1707, Ap
22	66	100.0	247	15	US-10-293-418-1899 Sequence 1899, Ap
23	66	100.0	247	15	US-10-293-418-1928 Sequence 1928, Ap
24	66	100.0	247	15	US-10-293-418-1934 Sequence 1934, Ap
25	66	100.0	249	10	US-09-880-748-1419 Sequence 1419, Ap
26	66	100.0	249	10	US-09-880-748-1618 Sequence 1618, Ap
27	66	100.0	249	10	US-09-880-748-2049 Sequence 2049, Ap
28	66	100.0	249	15	US-10-293-418-1419 Sequence 1419, Ap
29	66	100.0	249	15	US-10-293-418-1618 Sequence 1618, Ap
30	66	100.0	249	15	US-10-293-418-2049 Sequence 2049, Ap
31	66	100.0	251	10	US-09-880-748-1309 Sequence 1309, Ap
32	66	100.0	251	10	US-09-880-748-1671 Sequence 1671, Ap
33	66	100.0	251	10	US-09-880-748-1809 Sequence 1809, Ap
34	66	100.0	251	15	US-10-293-418-1309 Sequence 1309, Ap
35	66	100.0	251	15	US-10-293-418-1671 Sequence 1671, Ap
36	66	100.0	251	15	US-10-293-418-1809 Sequence 1809, Ap
37	66	100.0	252	10	US-09-880-748-988 Sequence 988, Ap
38	66	100.0	252	10	US-09-880-748-1698 Sequence 1698, Ap
39	66	100.0	252	15	US-10-293-418-988 Sequence 988, Ap
40	66	100.0	252	15	US-10-293-418-1698 Sequence 1698, Ap
41	66	100.0	253	10	US-09-880-748-935 Sequence 935, Ap
42	66	100.0	253	10	US-09-880-748-939 Sequence 939, Ap
43	66	100.0	253	10	US-09-880-748-939 Sequence 939, Ap
44	66	100.0	253	10	US-09-880-748-1611 Sequence 1611, Ap
45	66	100.0	253	10	US-09-880-748-1936 Sequence 1936, Ap

ALIGNMENTS

RESULT 1
US-09-880-748-1898
; Sequence 1898, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P6523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1898
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1898

Query Match 100.0%; Score 66; DB 10; Length 240;
Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNMYVS 13
DB 153 SGSTSNIGNMYVS 165

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RESULT 2
US-10-293-418-1898
; Sequence 1898, Application US/10293418
; Publication No. US200302396A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P2
; CURRENT FILING DATE: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1898
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1898

Query Match          100.0%; Score 66; DB 15; Length 240;
Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SGTSTNIGNNYVS 13
Db      153 SGTSTNIGNNYVS 165

RESULT 3
US-09-880-748-1927
; Sequence 1927, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1927
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1927

Query Match          100.0%; Score 66; DB 10; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SGTSTNIGNNYVS 13
Db      155 SGTSTNIGNNYVS 167

RESULT 4
US-10-322-673-53
; Sequence 53, Application US/10322673
; Publication No. US20030180296A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PFS85
; CURRENT APPLICATION NUMBER: US/10/322,673
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 53
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: CM085C11 scFv
US-10-322-673-53

Query Match          100.0%; Score 66; DB 14; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SGTSTNIGNNYVS 13
Db      155 SGTSTNIGNNYVS 167

RESULT 5
US-10-293-418-1927
; Sequence 1927, Application US/10293418
; Publication No. US200302396A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
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; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1927
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1927

Query Match 100.0%; Score 66; DB 15; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNVYS 13
Db 155 SGSTSNIGNNVYS 167

RESULT 6
US-09-880-748-1926
; Sequence 1926, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1926
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1926

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Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNVYS 13
Db 157 SGSTSNIGNNVYS 169

RESULT 7
US-10-293-418-1926
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; Publication No. US2003022396A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379

; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1926
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1926

Query Match 100.0%; Score 66; DB 15; Length 245;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNVYS 13
Db 157 SGSTSNIGNNVYS 169

RESULT 8
US-10-293-418-3241
; Sequence 3241, Application US/10293418
; Publication No. US2003022396A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 3241
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-3241

Query Match 100.0%; Score 66; DB 15; Length 245;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNVYS 13
Db 157 SGSTSNIGNNVYS 169

RESULT 9
US-09-880-748-1913
; Sequence 1913, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523

;; CURRENT APPLICATION NUMBER: US/09/880,748
;; CURRENT FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/212,210
;; PRIOR FILING DATE: 2000-06-15
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; NUMBER OF SEQ ID NOS: 3239
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 1913
;; LENGTH: 246
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-880-748-1913

Query Match 100.0%; Score 66; DB 10; Length 246;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SGSTSNIGNNVYS 13
Db 158 SGSTSNIGNNVYS 170

RESULT 10
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;; Publication No. US2003005937A1
;; GENERAL INFORMATION:
;; APPLICANT: Ruben et al.
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
;; FILE REFERENCE: P5523
;; CURRENT APPLICATION NUMBER: US/09/880,748
;; CURRENT FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/212,210
;; PRIOR FILING DATE: 2000-06-15
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; NUMBER OF SEQ ID NOS: 3239
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 1917
;; LENGTH: 246
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-880-748-1917

Query Match 100.0%; Score 66; DB 10; Length 246;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SGSTSNIGNNVYS 13
Db 158 SGSTSNIGNNVYS 170

RESULT 11
US-10-293-418-1913
;; Sequence 1913, Application US/10293418
;; Publication No. US20030223996A1
;; GENERAL INFORMATION:
;; APPLICANT: Ruben et al.
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

;; FILE REFERENCE: P5523P2
;; CURRENT APPLICATION NUMBER: US/10/293,418
;; CURRENT FILING DATE: 2002-11-27
;; PRIOR APPLICATION NUMBER: 60/331,469
;; PRIOR FILING DATE: 2001-11-16
;; PRIOR APPLICATION NUMBER: 60/340,817
;; PRIOR FILING DATE: 2001-12-19
;; PRIOR APPLICATION NUMBER: 09/880,748
;; PRIOR FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; PRIOR APPLICATION NUMBER: 60/212,210
;; PRIOR FILING DATE: 2000-06-16
;; NUMBER OF SEQ ID NOS: 3247
;; SEQ ID NO 1913
;; LENGTH: 246
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-293-418-1913

Query Match 100.0%; Score 66; DB 15; Length 246;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SGSTSNIGNNVYS 13
Db 158 SGSTSNIGNNVYS 170

RESULT 12
US-10-293-418-1917
;; Sequence 1917, Application US/10293418
;; Publication No. US20030223996A1
;; GENERAL INFORMATION:
;; APPLICANT: Ruben et al.
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
;; FILE REFERENCE: P5523P2
;; CURRENT APPLICATION NUMBER: US/10/293,418
;; CURRENT FILING DATE: 2002-11-27
;; PRIOR APPLICATION NUMBER: 60/331,469
;; PRIOR FILING DATE: 2001-11-16
;; PRIOR APPLICATION NUMBER: 60/340,817
;; PRIOR FILING DATE: 2001-12-19
;; PRIOR APPLICATION NUMBER: 09/880,748
;; PRIOR FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; PRIOR APPLICATION NUMBER: 60/212,210
;; PRIOR FILING DATE: 2000-06-16
;; NUMBER OF SEQ ID NOS: 3247
;; SEQ ID NO 1917
;; LENGTH: 246
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-293-418-1917

Query Match 100.0%; Score 66; DB 15; Length 246;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SGSTSNIGNNVYS 13

Db 158 SGSTSNIGNNVYS 170

RESULT 13
US-09-880-748-1443
; Sequence 1443, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1443
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1443

Query Match 100.0%; Score 66; DB 10; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNVYS 13
Db 159 SGSTSNIGNNVYS 171

RESULT 14
US-09-880-748-1682
; Sequence 1682, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1682
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1682

Query Match 100.0%; Score 66; DB 10; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNVYS 13
Db 159 SGSTSNIGNNVYS 171

RESULT 15
US-09-880-748-1707
; Sequence 1707, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1707
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1707

Query Match 100.0%; Score 66; DB 10; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNVYS 13
Db 159 SGSTSNIGNNVYS 171

RESULT 16
US-09-880-748-1899
; Sequence 1899, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1899
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1899

Query Match 100.0%; Score 66; DB 10; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
Db 159 SGSTSNIGNNYVS 171

RESULT 17

US-09-880-748-1928
; Sequence 1928, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1928
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1928

Query Match 100.0%; Score 66; DB 10; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
Db 159 SGSTSNIGNNYVS 171

RESULT 18
US-09-880-748-1934
; Sequence 1934, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1934
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1934

Query Match 100.0%; Score 66; DB 10; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.0054;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGSTSNIGNNYVS 13
Db 159 SGSTSNIGNNYVS 171

RESULT 19

US-10-293-418-1443
; Sequence 1443, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1443
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1443

Query Match 100.0%; Score 66; DB 15; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
Db 159 SGSTSNIGNNYVS 171

RESULT 20
US-10-293-418-1682
; Sequence 1682, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17

```

; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1682
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1682

Query Match      100.0%; Score 66; DB 15; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 SGSTSNIGNNVYS 13
        |||||
Db      159 SGSTSNIGNNVYS 171

RESULT 21
US-10-293-418-1707
; Sequence 1707, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1707
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1707

Query Match      100.0%; Score 66; DB 15; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 SGSTSNIGNNVYS 13
        |||||
Db      159 SGSTSNIGNNVYS 171

RESULT 22
US-10-293-418-1899
; Sequence 1899, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817

```

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; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1899
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1899

Query Match      100.0%; Score 66; DB 15; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 SGSTSNIGNNVYS 13
        |||||
Db      159 SGSTSNIGNNVYS 171

RESULT 23
US-10-293-418-1928
; Sequence 1928, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1928
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1928

Query Match      100.0%; Score 66; DB 15; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 SGSTSNIGNNVYS 13
        |||||
Db      159 SGSTSNIGNNVYS 171

RESULT 24
US-10-293-418-1934

```

```
; Sequence 1934, Application US/10293418
; Publication No. US2003022396A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1934
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1934
```

```
Query Match          100.0%; Score 66; DB 10; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SGSTSNIGNNYVS 13
Db      159 SGSTSNIGNNYVS 171
```

```
RESULT 25
US-09-880-748-1419
; Sequence 1419, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1419
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1419
```

```
Query Match          100.0%; Score 66; DB 10; Length 249;
Best Local Similarity 100.0%; Pred. No. 0.0055;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SGSTSNIGNNYVS 13
```

```
Db      161 SGSTSNIGNNYVS 173
```

```
RESULT 26
US-09-880-748-1618
; Sequence 1618, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1618
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1618
```

```
Query Match          100.0%; Score 66; DB 10; Length 249;
Best Local Similarity 100.0%; Pred. No. 0.0055;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SGSTSNIGNNYVS 13
Db      161 SGSTSNIGNNYVS 173
```

```
RESULT 27
US-09-880-748-2049
; Sequence 2049, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2049
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2049
```

```
Query Match          100.0%; Score 66; DB 10; Length 249;
Best Local Similarity 100.0%; Pred. No. 0.0055;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```


OY 1 SGSTSNIGNNYVS 13
Db 161 SGSTSNIGNNYVS 173

RESULT 28
US-10-293-418-1419

; Sequence 1419, Application US/10293418
; Publication No. US20030223996A1

; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

; FILE REFERENCE: PF523P2

; CURRENT APPLICATION NUMBER: US/10/293,418

; CURRENT FILING DATE: 2002-11-27

; PRIOR APPLICATION NUMBER: 60/331,469

; PRIOR FILING DATE: 2001-11-16

; PRIOR APPLICATION NUMBER: 60/340,817

; PRIOR FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 09/880,748

; PRIOR FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: 60/293,499

; PRIOR FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: 60/277,379

; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/276,248

; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/240,816

; PRIOR FILING DATE: 2000-10-17

; PRIOR APPLICATION NUMBER: 60/212,210

; PRIOR FILING DATE: 2000-06-16

; NUMBER OF SEQ ID NOS: 3247

; SEQ ID NO 1419

; LENGTH: 249

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-10-293-418-1419

Query Match 100.0%; Score 66; DB 15; Length 249;
Best Local Similarity 100.0%; Pred. No. 0.0055;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SGSTSNIGNNYVS 13
Db 161 SGSTSNIGNNYVS 173

RESULT 29
US-10-293-418-1618

; Sequence 1618, Application US/10293418

; Publication No. US20030223996A1

; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

; FILE REFERENCE: PF523P2

; CURRENT APPLICATION NUMBER: US/10/293,418

; CURRENT FILING DATE: 2002-11-27

; PRIOR APPLICATION NUMBER: 60/331,469

; PRIOR FILING DATE: 2001-11-16

; PRIOR APPLICATION NUMBER: 60/340,817

; PRIOR FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 09/880,748

; PRIOR FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: 60/293,499

; PRIOR FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: 60/277,379

; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/276,248

; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/240,816

; PRIOR FILING DATE: 2000-10-17

; PRIOR APPLICATION NUMBER: 60/212,210

; PRIOR FILING DATE: 2000-06-16

; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1618
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1618

Query Match 100.0%; Score 66; DB 15; Length 249;
Best Local Similarity 100.0%; Pred. No. 0.0055;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SGSTSNIGNNYVS 13
Db 161 SGSTSNIGNNYVS 173

RESULT 30
US-10-293-418-2049

; Sequence 2049, Application US/10293418

; Publication No. US20030223996A1

; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

; FILE REFERENCE: PF523P2

; CURRENT APPLICATION NUMBER: US/10/293,418

; CURRENT FILING DATE: 2002-11-27

; PRIOR APPLICATION NUMBER: 60/331,469

; PRIOR FILING DATE: 2001-11-16

; PRIOR APPLICATION NUMBER: 60/340,817

; PRIOR FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 09/880,748

; PRIOR FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: 60/293,499

; PRIOR FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: 60/277,379

; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/276,248

; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/240,816

; PRIOR FILING DATE: 2000-10-17

; PRIOR APPLICATION NUMBER: 60/212,210

; PRIOR FILING DATE: 2000-06-16

; NUMBER OF SEQ ID NOS: 3247

; SEQ ID NO 2049

; LENGTH: 249

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-10-293-418-2049

Query Match 100.0%; Score 66; DB 15; Length 249;
Best Local Similarity 100.0%; Pred. No. 0.0055;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SGSTSNIGNNYVS 13
Db 161 SGSTSNIGNNYVS 173

RESULT 31
US-09-880-748-1309

; Sequence 1309, Application US/09880748

; Publication No. US2003005937A1

; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

; FILE REFERENCE: PF523

; CURRENT APPLICATION NUMBER: US/09/880,748

; CURRENT FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: 60/212,210

; PRIOR FILING DATE: 2000-06-15

; PRIOR APPLICATION NUMBER: 60/240,816

; PRIOR FILING DATE: 2000-10-17

; PRIOR APPLICATION NUMBER: 60/276,248

```

? PRIOR FILING DATE: 2001-03-16
? PRIOR APPLICATION NUMBER: 60/227,379
? PRIOR FILING DATE: 2001-03-21
? PRIOR APPLICATION NUMBER: 60/293,459
? PRIOR FILING DATE: 2001-05-25
? NUMBER OF SEQ ID NOS: 3239
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 1309
? LENGTH: 251
? TYPE: PR1
? ORGANISM: Homo sapiens
? US-09-860-748-1309

```

Query Match	100.0%;	Score 66;	DB 10;	Length 251;
Best Local Similarity	100.0%;	Pred. No. 0.0055;		
Matches 13;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	SGSTSNIGNNYVS	13
Db	163	SGSTSNIGNNYVS	175

```

RESULT 32
US-09-880-748-1671
; Sequence 1671, Application US/09880748
; Publication NO. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blyss
; FILE REFERENCE: PFS23
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1671
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1671

```

Query Match	100.0%	Score 66;	DB 10;	Length 251;
Best Local Similarity	100.0%	Pred. No. 0.0055;		
Matches 13; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	SGSTSNIGNNYVS	13
Db	163	SGSTSNIGNNYVS	175

RESULT 33
US-09-880-748-1809
Sequence 1809, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind HIV/S
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17

```

?
? PRIOR APPLICATION NUMBER: 60/276,248
? PRIOR FILING DATE: 2001-03-16
? PRIOR APPLICATION NUMBER: 60/277,379
? PRIOR FILING DATE: 2001-03-21
? PRIOR APPLICATION NUMBER: 60/293,499
? PRIOR FILING DATE: 2001-05-25
? NUMBER OF SEQ ID NOS: 3229
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 1809
?
? LENGTH: 251
? TYPE: DRT
? ORGANISM: Homo sapiens
US-03-880-748-1809

```

Query Match	100.0%;	Score 66;	DB 10;	length 251;
Best Local Similarity	100.0%;	Pred. No. 0.0055;		
Matches 13;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	SGSTSNIGNNYVS	13
Db	163	SGSTSNIGNNYVS	175

```

RESULT 34
US-10-293-418-1309
; Sequence 1309, Application US/10293418
; Publication No. US20030223996A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
FILE REFERENCE: PEP52392
CURRENT APPLICATION NUMBER: US/10/293,418
PRIORITY FILING DATE: 2002-11-27
PRIORITY FILING DATE: 2002-11-27
PRIORITY FILING DATE: 2001-11-16
PRIORITY FILING DATE: 2001-11-16
PRIORITY FILING DATE: 2001-12-19
PRIORITY FILING DATE: 2001-12-19
PRIORITY FILING DATE: 2001-06-15
PRIORITY FILING DATE: 2001-06-15
PRIORITY FILING DATE: 2001-05-25
PRIORITY FILING DATE: 2001-05-25
PRIORITY FILING DATE: 2001-03-21
PRIORITY FILING DATE: 2001-03-21
PRIORITY FILING DATE: 2001-03-16
PRIORITY FILING DATE: 2001-03-16
PRIORITY FILING DATE: 2000-10-17
PRIORITY FILING DATE: 2000-10-17
PRIORITY FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1309
LENGTH: 251
TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-418-1309

```

Query Match	100.0%	Score 66;	DB 15;	length 251;
Best Local Similarity	100.0%;	Pred. No. 0.0055;		
Matches 13; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	SGSTSNIGNNYVS	13
Db	163	SGSTSNIGNNYVS	175

RESULT 35
US-10-293-418-1671
; Sequence 1671, Application US/10293418
; Publication No. US2003022396A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunoselectively Bind Bly5
; FILE REFERENCE: P5523P2

```

; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1671
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1671

Query Match      100.0%; Score 66; DB 15; Length 251;
Best Local Similarity 100.0%; Pred. No. 0.0055;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SGSTSNIGNNVYS 13
|||||
Db      163 SGSTSNIGNNVYS 175

RESULT 36
US-10-293-418-1809
; Sequence 1809, Application US/10293418
; Publication No. US2003022396A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1809
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1809

Query Match      100.0%; Score 66; DB 15; Length 251;
Best Local Similarity 100.0%; Pred. No. 0.0055;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SGSTSNIGNNVYS 13
|||||
Db      163 SGSTSNIGNNVYS 175
```

```

Db      163 SGSTSNIGNNVYS 175

RESULT 37
US-09-880-748-988
; Sequence 988, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 988
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-988

Query Match      100.0%; Score 66; DB 10; Length 252;
Best Local Similarity 100.0%; Pred. No. 0.0056;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SGSTSNIGNNVYS 13
|||||
Db      163 SGSTSNIGNNVYS 175

RESULT 38
US-09-880-748-1698
; Sequence 1698, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1698
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1698

Query Match      100.0%; Score 66; DB 10; Length 252;
Best Local Similarity 100.0%; Pred. No. 0.0056;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SGSTSNIGNNVYS 13
|||||
```

Db 164 SGSTSNIGNNYVS 176

RESULT 39

US-10-293-418-988
; Sequence 988, Application US/10293418
; Publication No. US2003023996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: p5523p2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 988
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-988

Query Match 100.0%; Score 66; DB 15; Length 252;
Best Local Similarity 100.0%; Pred. No. 0.0056;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SGSTSNIGNNYVS 13
Db 163 SGSTSNIGNNYVS 175

RESULT 40

US-10-293-418-1698
; Sequence 1698, Application US/10293418
; Publication No. US2003023996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: p5523p2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247

; SEQ ID NO 1698
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1698

Query Match 100.0%; Score 66; DB 15; Length 252;
Best Local Similarity 100.0%; Pred. No. 0.0056;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SGSTSNIGNNYVS 13
Db 164 SGSTSNIGNNYVS 176

Search completed: March 31, 2005, 12:46:09
Job time : 73.7188 secs

GenCore version 5.1.6
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OM protein - protein search, using bw model

Run on: March 31, 2005, 11:51:19 ; Search time 18.4844 Seconds
(without alignments)
67.669 Million cell updates/sec

Title: US-10-614-959-13
Perfect score: 66
Sequence: 1 SGSTSNIGNNYVS 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR.79:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	62	93.9	98 2 S36050	Ig lambda chain -
2	62	93.9	111 2 S47009	Ig lambda chain V1
3	62	93.9	111 2 S19664	Ig lambda chain V
4	62	93.9	113 2 A29700	Ig lambda chain V
5	62	93.9	232 2 S25742	Ig lambda chain -
6	62	93.9	235 2 S05270	Ig lambda chain pr
7	59	89.4	130 2 S09712	Ig lambda chain V
8	57	86.4	130 1 LIHUBL	Ig lambda chain pr
9	56	84.8	111 2 S47185	Ig lambda chain pr
10	55	84.8	111 2 S24321	Ig lambda chain pr
11	55	83.3	111 1 LIHUNW	Ig lambda chain -
12	53	80.3	98 2 S36048	Ig lambda chain -
13	53	80.3	111 1 LIHUNG	Ig lambda chain V-
14	53	80.3	129 2 S78058	Ig lambda chain pr
15	53	80.3	130 2 S78057	Ig lambda chain pr
16	52	78.8	109 1 LIHUEP	Ig lambda chain V-
17	50	75.8	98 2 S36046	Ig lambda chain -
18	49	74.2	234 2 S25757	Ig lambda chain -
19	48	72.7	112 2 C44151	Ig lambda chain V
20	46	69.7	216 2 A42193	Ig lambda chain (B
21	45	68.2	98 2 S36047	Ig lambda chain -
22	45	68.2	110 2 S36258	Ig lambda chain V
23	45	68.2	112 2 D44151	Ig lambda chain pr
24	45	68.2	117 2 S23627	Ig lambda chain pr
25	45	68.2	233 2 S25752	Ig lambda chain -
26	44	66.7	112 2 A44151	Ig lambda chain V
27	44	66.7	112 2 B44151	Ig lambda chain V
28	44	66.7	235 2 S25754	Ig lambda chain -
29	43.5	65.9	235 2 S14675	Ig lambda chain -

30	43	65.2	95	2	S49571	Ig lambda chain pr
31	43	65.2	149	2	S23626	Ig lambda chain V
32	43	65.2	2272	2	T18572	gag, pol and env p
33	43	65.2	2500	2	G71609	hypothetical protei
34	42	63.6	110	2	S57428	Ig light chain V-J
35	42	63.6	110	2	S57408	Ig lambda chain V-
36	42	63.6	233	2	S25744	Ig lambda chain -
37	42	63.6	348	2	F96997	uncharacterized co
38	41	62.1	99	2	S36054	Ig lambda chain -
39	41	62.1	107	2	B46516	Ig lambda chain V
40	41	62.1	111	1	L6HUT	Ig lambda chain V-
41	41	62.1	112	1	LIHUMT	Ig lambda chain V-
42	41	62.1	414	2	A71646	5-aminoLevulinate
43	40	60.6	109	1	LIHWA	Ig lambda chain V-
44	40	60.6	112	1	LIHWA	Ig lambda chain V-
45	40	60.6	217	2	JB0246	Ig lambda chain NI

ALIGNMENTS

RESULT 1

S36050
Ig lambda chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
C:Accession: S36050
R:Williams, S.C.
Submitted to the EMBL Data Library, April 1993
A:Reference number: S36046
A:Accession: S36050
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 198 <Wtl>
A:Cross-references: EMBL:Z22191; NID:G312298; PIDN:CAA80201.1; PTD:G312299
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-91/Domain: immunoglobulin homology <IMM>

Query Match 93.9%; Score 62; DB 2; Length 98;
Best Local Similarity 92.3%; Pred. No. 0.001; Mismatches 0; Gaps 0;

Matches 12; Conservative 1; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
DB 23 SGSSNIGNNYVS 35
|||||

RESULT 2

S47009
Ig lambda chain V1-J3 region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C:Accession: S47009
R:Mamoudi, M.; Gaayna, E.; Denomme, G.; Edwards, J.; Bell, D.; Cairns, E.
Submitted to the EMBL Data Library, July 1994
A:Description: The role of the immunoglobulin heavy chain in human anti-DNA antibody bin
A:Reference number: S47009
A:Accession: S47009
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-111 <MAH>
A:Cross-references: EMBL:Z35495; NID:G517346; PIDN:CAA84629.1; PTD:G517347
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-91/Domain: immunoglobulin homology <IMM>

Query Match 93.9%; Score 62; DB 2; Length 111;
Best Local Similarity 92.3%; Pred. No. 0.001; Mismatches 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
|||||

Db 23 SGSSSNIGNNVYS 35

RESULT 3

S19664

Ig lambda chain V region (clone alpha-phoX15) - human

C/Species: Homo sapiens (man)

C/Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000

C/Accession: S19664; S24444

R/Markes: U.D.; Hoogenboom, H.R.; Bonner, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991

A/Title: By-passing immunization. Human antibodies from V-gene libraries displayed on ph

A/Reference number: S19663; MUID:92085276; PMID:1748994

A/Accession: S19664

A/Molecule type: mRNA

A/Residues: 1-111 <MAR>

A/Cross-references: EMBL:X61641

A/Status: preliminary; translation not shown

Submitted to the EMBL Data Library, October 1991

A/Accession: S24442

A/Molecule type: mRNA

A/Residues: 1-110, 'W' <DON>

A/Cross-references: EMBL:X61641; NID:G35458; PIDN:CAA43822.1; PID:G1335271

C/Suprafamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/15-91/Domain: immunoglobulin homology <IMM>

Query Match 93.9%; Score 62; DB 2; Length 111;

Best Local Similarity 92.3%; Pred. No. 0.0011;

Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNVYS 13

Db 23 SGSSSNIGNNVYS 35

RESULT 4

A29700

Ig lambda chain V region (zim) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 21-Jan-2000

C/Accession: A29700

R/Bulter, M.; Breuer, M.; Linke, R.P.

Biol. Chem. Hoppe-Seyler 368, 863-870, 1987

A/Title: Is the formation of Al-type amyloid promoted by structural peculiarities of im

A/Reference number: A29700; MUID:87299022; PMID:3620114

A/Accession: A29700

A/Molecule type: protein

A/Residues: 1-113 <EUL>

C/Suprafamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/14-90/Domain: immunoglobulin homology <IMM>

Query Match 93.9%; Score 62; DB 2; Length 113;

Best Local Similarity 92.3%; Pred. No. 0.0012;

Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNVYS 13

Db 22 SGSSSNIGNNVYS 34

RESULT 5

S25742

Ig lambda chain - human

C/Species: Homo sapiens (man)

C/Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C/Accession: S25742

R/Combrato, G.; Klobbeck, H.G.

Eur. J. Immunol. 21, 1513-1522, 1991

A/Title: V(lambda) and J(lambda) gene segments of the human immunoglobulin lan

A/Reference number: S16439; MUID:91257162; PMID:1904362

A/Accession: S25742

A/Status: preliminary; translation not shown

A/Molecule type: mRNA

A/Residues: 1-232 <COM>

A/Cross-references: EMBL:X57806; NID:G33709; PIDN:CAA40944.1; PID:G33710

C/Suprafamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/147-215/Domain: immunoglobulin homology <IMM>

Query Match 93.9%; Score 62; DB 2; Length 232;

Best Local Similarity 92.3%; Pred. No. 0.0025;

Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNVYS 13

Db 39 SGSSSNIGNNVYS 51

RESULT 6

S05270

Ig lambda chain precursor - human

C/Species: Homo sapiens (man)

C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000

C/Accession: S05270; S04601

R/Kishimoto, T.

Submitted to the EMBL Data Library, March 1989

A/Reference number: S05270

A/Accession: S05270

A/Molecule type: mRNA

A/Residues: 1-235 <KIS1>

A/Cross-references: EMBL:X14583; NID:G33394; PIDN:CAA32725.1; PID:G33395

R/Kishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M.

Nucleic Acids Res. 17, 4385, 1989

A/Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains of

A/Reference number: S04601; MUID:89296497; PMID:2500644

A/Accession: S04601

A/Molecule type: mRNA

A/Residues: 1-130 <KIS2>

A/Cross-references: EMBL:X14583

C/Suprafamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/1-20/Domain: signal sequence #status predicted <SIG>

F/150-218/Domain: immunoglobulin homology <IMM>

Query Match 93.9%; Score 62; DB 2; Length 235;

Best Local Similarity 92.3%; Pred. No. 0.0025;

Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNVYS 13

Db 42 SGSSSNIGNNVYS 54

RESULT 7

S09712

Ig lambda chain V region - human

C/Species: Homo sapiens (man)

C/Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C/Accession: S09712

R/Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coatswell, J.

Biochem. J. 268, 135-140, 1990

A/Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domains of

A/Reference number: S09710; MUID:90262535; PMID:2111699

A/Accession: S09712

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-130 <HUG>

A/Cross-references: GB:X52109; NID:G31454; PIDN:CAA36343.1; PID:G31455

C/Suprafamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F/34-110/Domain: immunoglobulin homology <IMM>

Query Match 89.4%; Score 59; DB 2; Length 130;
 Best Local Similarity 84.6%; Pred. No. 0.0045;
 Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 SGSTSNIGNNYVS 13
 ||:|||||
 Db 42 SGTSSNIGNNYVS 54

RESULT 8

L1HNB.L

Ig lambda chain precursor V-I region (BL2) - human

C/Species: Homo sapiens (man)

C/Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004

C/Accession: A01966

R/Tsujimoto, Y.; Croce, C.M.

Nucleic Acids Res. 12, 8407-8414, 1984

A/Title: Molecular cloning of a human immunoglobulin lambda chain variable sequence.

A/Reference number: A01966; MUID:85062823; PMID:6095199

A/Accession: A01966

A/Molecule type: mRNA

A/Residues: 1-130 <TSU>

A/Cross-references: UNIPROT:P06316; GB:X01147; NID:G33335; PIDN:CAA5598.1; PID:G758087

C/Genetics:

A/Gene: GDB:IGLV@

A/Cross-references: GDB:119342; OMIM:147240

A/Map position: 22q11.2-22q11.2

C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap

hain disulfide bonds. In some cases, such as Iga and Igm, the subunits associate into 1a

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/1-19/Domain: signal sequence #status predicted <SIG>

F/20-130/Product: Ig lambda chain V-I region (BL2) #status predicted <MAT>

F/34-110/Domain: immunoglobulin homology <IMM>

F/116-130/Region: J segment

F/41-108/Disulfide bonds: #status predicted

Query Match 86.4%; Score 57; DB 1; Length 130;

Best Local Similarity 84.6%; Pred. No. 0.01;

Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 SGSTSNIGNNYVS 13
 ||:|||||
 Db 42 SGTSSNIGNNYVS 54

RESULT 9

S47185

Ig lambda chain - human

C/Species: Homo sapiens (man)

C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000

C/Accession: S47185

R/McIntosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.

submitted to the EMBL Data Library, June 1994

A/Description: Cloning and analysis of Igm anti-chryoglobulin autoantibodies from patien

A/Reference number: S47181

A/Accession: S47185

A/Status: Preliminary

A/Molecule type: mRNA

A/Residues: 1-111 <MCi>

A/Cross-references: EMBL:X79782; NID:G506428; PIDN:CAA56178.1; PID:G506429

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/14-90/Domain: immunoglobulin homology <IMM>

Query Match 84.8%; Score 56; DB 2; Length 111;

Best Local Similarity 84.6%; Pred. No. 0.013;

Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 SGSTSNIGNNYVS 13
 ||:|||||
 Db 22 SGTSSNIGNNYVS 34

RESULT 10

S24321

Ig lambda chain precursor - human

C/Species: Homo sapiens (man)

C/Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C/Accession: S24321

R/Aucourtier, P.; Khamlichi, A.A.; Preud'homme, J.L.; Bauwens, M.; Touchard, G.; Cogne,

Biochem. J. 285, 149-152, 1992

A/Title: Complementary DNA sequence of human amyloidogenic immunoglobulin light-chain pr

A/Reference number: S24319; MUID:92344562; PMID:1379039

A/Accession: S24321

A/Status: Preliminary

A/Molecule type: mRNA

A/Residues: 1-131 <AUC>

A/Cross-references: EMBL:X64134; NID:932808; PIDN:CAA5495.1; PID:G32809

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/34-110/Domain: immunoglobulin homology <IMM>

Query Match 84.8%; Score 56; DB 2; Length 131;

Best Local Similarity 84.6%; Pred. No. 0.015;

Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 SGSTSNIGNNYVS 13
 ||:|||||
 Db 42 SGTSSNIGNNYVS 54

RESULT 11

L1HUNW

Ig lambda chain V-I region (New) - human

C/Species: Homo sapiens (man)

C/Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004

C/Accession: A01964

R/Langer, B.; Steinmetz-Kayne, M.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 349, 945-951, 1968

A/Title: The complete amino acid sequence of Bence-Jones protein New (lambda type). Subg

A/Reference number: A01964; MUID:65060892; PMID:4177823

A/Accession: A01964

A/Molecule type: Protein

A/Residues: 1-111 <LAN>

A/Cross-references: UNIPROT:P01701

C/Comment: This is a Bence Jones protein.

C/Genetics:

A/Gene: GDB:IGLV@

A/Cross-references: GDB:119342; OMIM:147240

A/Map position: 22q11.2-22q11.2

C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap

hain disulfide bonds. In some cases, such as Iga and Igm, the subunits associate into 1a

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: blocked amino end; heterotetramer

F/15-91/Domain: immunoglobulin homology <IMM>

F/12-89/Disulfide bonds: #status predicted

Query Match 83.3%; Score 55; DB 1; Length 111;

Best Local Similarity 76.9%; Pred. No. 0.019;

Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 SGSTSNIGNNYVS 13
 ||:|||||
 Db 23 SGTSSNIGNNYVS 35

RESULT 12

S36048

Ig lambda chain - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000

C/Accession: S36048; S36049

R.Williams, S.C.

submitted to the EMBL Data Library, April 1993
A:Reference number: S36046

A:Accession: S36046
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <MW>
A:Cross-references: EMBL:Z22189; NID:9312294; PIDN:CAA8019.1; PID:9312295; EMBL:Z22190
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-91/Domain: immunoglobulin homology <IMM>

Query Match 80.3%; Score 53; DB 2; Length 98;
Best Local Similarity 83.3%; Pred. No. 0.037;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNV 12
|||:||||:
Db 23 SGSSSNIGNNV 34

RESULT 13

L1HUNG

Ig lambda chain V-I region (Nig-64) - human (tentative sequence)
C:Species: Homo sapiens (man)
C>Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 09-Jul-2004
C:Accession: A01965
R:Kamezani, F.; Takayasu, T.; Suzuki, S.; Shinoda, T.; Okuyama, T.; Shimizu, A.
J. Biochem. 93, 421-429, 1983
A:Title: Comparative studies on the structure of the light chains of human immunoglobulin
A:Reference number: A91970; MUID:83186114; PMID:6404900
A:Accession: A01965
A:Molecule type: protein
A:Residues: 1-111 <KAM>
A:Cross-references: UNIPROT:P01702
C:Genetics:
A:Gene: GDB:IGLV@
A:Cross-references: GDB:119342; OMIM:147240
A:Map position: 22q11.2-22q11.2
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1d
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: blocked amino end; heterotetramer
F:15-91/Domain: immunoglobulin homology <IMM>
F:1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #stratu
F:22-89/Disulfide bonds: #status predicted

Query Match 80.3%; Score 53; DB 1; Length 111;
Best Local Similarity 76.9%; Pred. No. 0.042; 0; Indels 0; Gaps 0;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNV 13
|||:||||:
Db 23 SGSSSNIGNNV 35

RESULT 14

S78058

Ig lambda chain precursor V-J region (clone mAb 67VL) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C:Accession: S78058; S23723
R:Harindranath, N.
Submitted to the EMBL Data Library, August 1990
A:Reference number: S78058
A:Accession: S78058
A:Molecule type: mRNA
A:Residues: 1-129 <HAR>
A:Cross-references: EMBL:X5446; NID:937923; PIDN:CAA8313.1; PID:9330121
R:Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Bursatello, S.E.; Wilder, R.L.; Nockins
Int. Immunol. 3, 865-875, 1991
A:Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h
patient.
A:Reference number: S23716; MUID:92031262; PMID:1718404

A:Accession: S23723
A:Molecule type: mRNA

A:Residues: 19-129 <HAR>
A:Cross-references: EMBL:X5446
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:1-18/Domain: signal sequence (fragment) #status predicted <SIG>
F:19-129/Product: Ig lambda chain (fragment) #status predicted <MAT>
F:33-109/Domain: immunoglobulin homology <IMM>

Query Match 80.3%; Score 53; DB 2; Length 129;
Best Local Similarity 83.3%; Pred. No. 0.049;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNV 12
|||:||||:
Db 41 SGSSSNIGNNV 52

RESULT 15

S78057

Ig lambda chain precursor V-J region (Eps) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C:Accession: S78057; S23722
R:Harindranath, N.
Submitted to the EMBL Data Library, August 1990
A:Reference number: S78051
A:Accession: S78057
A:Molecule type: mRNA
A:Residues: 1-130 <HAR>
A:Cross-references: EMBL:X54438; NID:937920; PIDN:CAA8307.1; PID:937921
R:Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Bursatello, S.E.; Wilder, R.L.; Nockins,
Int. Immunol. 3, 865-875, 1991
A:Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h
patient.
A:Reference number: S23716; MUID:92031262; PMID:1718404
A:Accession: S23722
A:Molecule type: mRNA
A:Residues: 20-130 <HAR>
A:Cross-references: EMBL:X54438
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-130/Product: Ig lambda chain (fragment) #status predicted <MAT>
F:34-110/Domain: immunoglobulin homology <IMM>

Query Match 80.3%; Score 53; DB 2; Length 130;
Best Local Similarity 83.3%; Pred. No. 0.049; 0; Indels 0; Gaps 0;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNV 12
|||:||||:
Db 42 SGSSSNIGNNV 53

RESULT 16

L1HVEP

Ig lambda chain V-I region (Eps) - human (tentative sequence)
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C:Accession: A24656
R:Toft, K.G.; Sletten, K.; Huseby, G.
Biol. Chem. Hoppe-Seyler 366, 617-625, 1985
A:Title: The amino-acid sequence of the variable region of a carbohydrate-containing anti
A:Reference number: A24656; MUID:86000126; PMID:3529803
A:Accession: A24656
A:Molecule type: protein
A:Residues: 1-109 <TOF>
A:Cross-references: UNIPROT:P06888
A:Note: Residues 1-2, 56-62, and 74-78 and the sequenced peptides were positioned by hom
C:Genetics:
A:Gene: GDB:IGLV@

A/Cross-references: GDB:119342; OMIM:147240
A/Map position: 22q11.2-22q11.2
C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (Kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 18 C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: amyloid; blocked amino end; glycoprotein; heterotetramer; immunoglobulin F/15-91/Domain: immunoglobulin homology <IMM>
F/1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #status F/22-89/Disulfide bonds: #status predicted
F/104/Binding site: carbohydrate (asn) (covalent) #status experimental

Query Match 78.8%; Score 52; DB 1; Length 109;
Best Local Similarity 83.3%; Pred. No. 0.061;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGGSTNIGNNYVS 12
DB 23 SGGSSNIGNNAVN 34

RESULT 17
Ig lambda chain - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
R/Williams, S.C.
Submitted to the EMBL Data Library, April 1993
A/Reference number: S36046
A/Accession: S36046
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-98 <MIL>
A/Cross-references: EMBL:Z22187; NID:G31212; PIDN:CAA80197.1; PID:G31213
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

Query Match 75.8%; Score 50; DB 2; Length 98;
Best Local Similarity 76.9%; Pred. No. 0.12;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGGSTNIGNNYVS 13
DB 23 SGGSSNIGNNAVN 35

RESULT 18
Ig lambda chain - human (fragment)
S25757
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S25757
R/Combario, G.; Klobbeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A/Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lambda A/Reference number: S16439; MUID:91257162; PMID:1904362
A/Accession: S25757
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-234 <COM>
A/Cross-references: EMBL:X57822; NID:G33743; PIDN:CAA40959.1; PID:G33744
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/149-217/Domain: immunoglobulin homology <IMM>

Query Match 74.2%; Score 49; DB 2; Length 234;
Best Local Similarity 76.9%; Pred. No. 0.46;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGGSTNIGNNYVS 13
DB 41 SGGSTNIGNNYVN 53

RESULT 19
C44151
Ig lambda chain V region (BO-10) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 21-Jan-2000
C/Accession: C44151
R/Zepede, S.L.; Barbas III, C.F.; Hom, Y.L.; Caotlien, R.H.; Graff, R.; Degraw, J.; Pya Proc. Natl. Acad. Sci. U.S.A. 89, 3175-3179, 1992
A/Title: Human combinatorial antibody libraries to hepatitis B surface antigen.
A/Reference number: A44151; MUID:9228746; PMID:1373487
A/Accession: C44151
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-112 <ZEB>
A/Note: nucleotide translation not given
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/14-90/Domain: immunoglobulin homology <IMM>

Query Match 72.7%; Score 48; DB 2; Length 112;
Best Local Similarity 76.9%; Pred. No. 0.31;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SGGSTNIGNNYVS 13
DB 22 SGGSTNIGNNYVN 34

RESULT 20
A42193
Ig lambda chain (BJP-DIA) - human
N/Alternate names: amyloid fibril protein AL-DIA; Bence Jones protein; Ig lambda chain (C/Species: Homo sapiens (man)
C/Date: 03-Mar-1994 #sequence_revision 07-Apr-1994 #text_change 21-Jan-2000
C/Accession: A42193; S18297
R/Klafl, H.W.; Kratzin, H.D.; Pick, A.I.; Eckart, K.; Karas, M.; Hilschmann, N. Biochemistry 31, 3265-3272, 1992
A/Title: Complete amino acid sequence determinations demonstrate identity of the urinary A/Reference number: A42193; MUID:92207944; PMID:1554711
A/Accession: A42193
A/Molecule type: protein
A/Residues: 1-216 <KLA>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin; pyroglytamic acid
F/131-199/Domain: immunoglobulin homology <IMM>
F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 69.7%; Score 46; DB 2; Length 216;
Best Local Similarity 69.2%; Pred. No. 1.4;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGGSTNIGNNYVS 13
DB 23 SGGSSNIGNNYVT 35

RESULT 21
S36047
Ig lambda chain - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
C/Accession: S36047
R/Williams, S.C.
Submitted to the EMBL Data Library, April 1993
A/Reference number: S36046
A/Accession: S36047
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-98 <MIL>
A/Cross-references: EMBL:Z22186; NID:G312291; PIDN:CAA80198.1; PID:G312292
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

F;15-91/Domain: immunoglobulin homology <IMM>

Query Match 68.2%; Score 45; DB 2; Length 98;
Best Local Similarity 69.2%; Pred. No. 0.9;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNVYS 13
|||:||||:|:
Db 23 SSSSSNIGSNVTN 35

RESULT 22

S36258

Ig lambda chain V region (clone alpha-CD4-74) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000

C;Accession: S36258

R;GiFFfthh, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.

EMBO J. 12, 725-734, 1993

A;Title: Human anti-self antibodies with high specificity from phage display libraries.

A;Reference number: S36256; MUID:93178448; PMID:7679990

A;Accession: S36258

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-110 <GRI>

A;Cross-references: EMBL:Z18849

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-91/Domain: immunoglobulin homology <IMM>

Query Match 68.2%; Score 45; DB 2; Length 110;
Best Local Similarity 76.9%; Pred. No. 1;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNVYS 13
|||:||||:|:
Db 23 SSSSSNIGSNVYS 35

RESULT 23

D44151

Ig lambda chain V region (BO-12) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 21-Jan-2000

C;Accession: D44151

R;Zebedee, S.L.; Barbas III, C.F.; Hom, Y.L.; Caothien, R.H.; Graff, R.; Degraw, J.; Pyat

Proc. Natl. Acad. Sci. U.S.A. 89, 3175-3179, 1992

A;Title: Human combinatorial antibody libraries to hepatitis B surface antigen.

A;Reference number: A44151; MUID:9228746; PMID:1373487

A;Accession: D44151

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-112 <ZEB>

A;Note: nucleotide translation is not given

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;14-90/Domain: immunoglobulin homology <IMM>

Query Match 68.2%; Score 45; DB 2; Length 112;
Best Local Similarity 69.2%; Pred. No. 1;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNVYS 13
|||:||||:|:
Db 22 SSSSSNIGSNVTN 34

RESULT 24

S23627

Ig lambda chain precursor - human

C;Species: Homo sapiens (man)

C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C;Accession: S23627

R;Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Dettos, M.; Kozin, F.; Carson, D.A.; C

J. Exp. Med. 175, 831-842, 1992

A;Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from tv

A;Reference number: S23623; MUID:92156804; PMID:1740665

A;Accession: S23627

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-117 <OLE>

A;Cross-references: EMBL:X59707; NID:G34426; PIDN:CAA42228.1; PID:G34427

C;Genetics:

A;Intons: 16/1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;34-110/Domain: immunoglobulin homology <IMM>

Query Match 68.2%; Score 45; DB 2; Length 117;
Best Local Similarity 69.2%; Pred. No. 1.1;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNVYS 13
|||:||||:|:
Db 42 SSSSSNIGSNVTN 54

RESULT 25

S25752

Ig lambda chain - human

C;Species: Homo sapiens (man)

C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C;Accession: S25752

R;Combrato, G.; Klobbeck, H.G.

Eur. J. Immunol. 21, 1513-1522, 1991

A;Title: V(Lambda) and J(Lambda) gene segments of the human immunoglobulin lamt

A;Reference number: S16439; MUID:91257162; PMID:1904362

A;Accession: S25752

A;Status: preliminary; translation not shown

A;Molecule type: mRNA

A;Residues: 1-233 <COM>

A;Cross-references: EMBL:X57817; NID:G33733; PIDN:CAA40954.1; PID:G33734

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;148-216/Domain: immunoglobulin homology <IMM>

Query Match 68.2%; Score 45; DB 2; Length 233;
Best Local Similarity 69.2%; Pred. No. 2.3;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNVYS 13
|||:||||:|:
Db 40 SSSSSNIGSNVTN 52

RESULT 26

A44151

Ig lambda chain V region (BO-08) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 21-Jan-2000

C;Accession: A44151

R;Zebedee, S.L.; Barbas III, C.F.; Hom, Y.L.; Caothien, R.H.; Graff, R.; Degraw, J.; Pyat

Proc. Natl. Acad. Sci. U.S.A. 89, 3175-3179, 1992

A;Title: Human combinatorial antibody libraries to hepatitis B surface antigen.

A;Reference number: A44151; MUID:9228746; PMID:1373487

A;Accession: A44151

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-112 <ZEB>

A;Note: nucleotide translation not given

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;14-90/Domain: immunoglobulin homology <IMM>

Query Match 66.7%; Score 44; DB 2; Length 112;
Best Local Similarity 69.2%; Pred. No. 1.6;

Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 SGTSTNIGNNYVS 13
 |||:|||||:
 Db 22 SGTSSNIGNTVNV 34

RESULT 27

Ig lambda chain V region (BO-09) - human (fragment)
 B44151
 C/Species: Homo sapiens (man)
 C/Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 21-Jan-2000
 C/Accession: B44151
 R/Zabedee, S.L.; Barbas III, C.F.; Hom, Y.L.; Caethoven, R.H.; Graff, R.; Degraw, J.; Pya
 Proc. Natl. Acad. Sci. U.S.A. 89, 3175-3179, 1992
 A/Title: Human combinatorial antibody libraries to hepatitis B surface antigen.
 A/Reference number: A44151; MUID:92228746; PMID:1373487
 A/Accession: B44151
 A/Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
 A/Molecule type: mRNA
 A/Residues: 1-112 <ZEB>
 A/Cross-references: GB:M88310; NID:g183954; PIDN:AAA5968.1; PID:g183955
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F:14-90/Domain: immunoglobulin homology <IMM>

Query Match 66.7%; Score 44; DB 2; Length 112;
 Best Local Similarity 69.2%; Pred. No. 1.6;
 Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 SGTSTNIGNNYVS 13
 |||:|||||:
 Db 22 SGTSSNIGNTVNV 34

RESULT 28

Ig lambda chain - human (fragment)
 S25754
 C/Species: Homo sapiens (man)
 C/Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C/Accession: S25754
 R/Combratio, G.; Klobeck, H.G.
 Eur. J. Immunol. 21, 1513-1522, 1991
 A/Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lan
 A/Reference number: S16439; MUID:91257162; PMID:1904362
 A/Accession: S25754
 A/Status: preliminary; translation not shown
 A/Molecule type: mRNA
 A/Residues: 1-235 <COM>
 A/Cross-references: EMBL:X57819; NID:g33737; PIDN:CAA40956.1; PID:g33738
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F:150-218/Domain: immunoglobulin homology <IMM>

Query Match 66.7%; Score 44; DB 2; Length 235;
 Best Local Similarity 69.2%; Pred. No. 3.4;
 Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 SGTSTNIGNNYVS 13
 |||:|||||:
 Db 41 SGTSSNIGNTVNV 53

RESULT 29

Ig lambda chain - human
 S14675
 C/Species: Homo sapiens (man)
 C/Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 09-Jul-2004
 C/Accession: S14675; S12445
 R/Vasick, T.J.
 submitted to the EMBL Data Library, February 1990
 A/Reference number: S14675
 A/Accession: S14675

A/Molecule type: DNA
 A/Residues: 1-235 <VAS1>
 A/Cross-references: UNIPROT:Q8WUK4; EMBL:X51754
 R/Vasick, T.J.; Leder, P.
 J. Exp. Med. 172, 609-620, 1990
 A/Title: Structure and expression of the human immunoglobulin lambda genes.
 A/Reference number: S12440; MUID:90324881; PMID:2115572
 A/Accession: S12445
 A/Molecule type: DNA
 A/Residues: 1-129 <VAS2>
 A/Cross-references: EMBL:X51754
 C/Genetics:
 A/Intons: 16/1; 130/1
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F:150-218/Domain: immunoglobulin homology <IMM>

Query Match 65.9%; Score 43.5; DB 2; Length 235;
 Best Local Similarity 71.4%; Pred. No. 4.2;
 Matches 10; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY 1 SGTSTNIGNNYVS 13
 |||:|||||:
 Db 42 SGTSSDIGNNYVS 55

RESULT 30

Ig lambda chain precursor V region - human (fragment)
 S49571
 C/Species: Homo sapiens (man)
 C/Date: 05-Mar-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999
 C/Accession: S49571
 R/Giachino, C.; Padovan, E.; Lanzavecchia, A.
 submitted to the EMBL Data Library, November 1994
 A/Description: K+1+ dual receptor B cells are present in the human peripheral repertoire
 A/Reference number: S49571
 A/Accession: S49571
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-95 <G1A>
 A/Cross-references: EMBL:Z46625; NID:g575259; PIDN:CAA6595.1; PID:g575260
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin

Query Match 65.2%; Score 43; DB 2; Length 95;
 Best Local Similarity 75.0%; Pred. No. 1.9;
 Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGTSTNIGNNYV 12
 |||:|||||:
 Db 9 SGTSSNIGSNV 20

RESULT 31

Ig lambda chain V region - human (fragment)
 S23626
 C/Species: Homo sapiens (man)
 C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
 C/Accession: S23626
 R/Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Defos, M.; Kozin, F.; Carson, D.A.;
 J. Exp. Med. 175, 831-842, 1992
 A/Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from t
 A/Reference number: S23623; MUID:92156804; PMID:1740665
 A/Accession: S23626
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-149 <OLE>
 A/Cross-references: EMBL:X59706; NID:g34204; PIDN:CAA42227.1; PID:g34205
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F:34-110/Domain: immunoglobulin homology <IMM>

Query Match 65.2%; Score 43; DB 2; Length 149;

A;Status: Preliminary

РЕСПИТ 27

F96997

uncharacterized conserved protein of probably eukaryotic origin CAC0793 [Imported] - CID
 C/Species: Clostridium acetobutylicum
 C/Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
 C/Accession: F96997
 R/Molling, J.; Bretton, G.; Omeichenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
 J. Bacteriol. 183, 4823-4838, 2001
 A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium CID
 A/Reference number: A96900; MUID:21359325; PMID:21359325
 A/Accession: F96997
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-348 <KIR>
 A/Cross-references: UNIPROT:Q97KX3; GB:AE001437; PIDN:AAK78769.1; PID:g15023680; GSPDB:C
 A/Experimental source: Clostridium acetobutylicum ATCC824
 C/Genetics:
 A/Gene: CAC0793

Query Match 63.6%; Score 42; DB 2; Length 348;
 Best Local Similarity 88.9%; Pred. No. 12;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3 STSNTGNV 11
 |||||
 Db 158 STSNTGNV 166

RESULT 38
 Ig lambda chain - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
 C/Accession: S36054
 R/Williams, S.C. EMBL Data Library, April 1993
 Submitted to the EMBL Data Library, April 1993
 A/Reference number: S36046
 A/Accession: S36054
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-99 <MIT>
 A/Cross-references: EMBL:Z22195; NID:g312310; PIDN:CAA80205.1; PID:g312311
 C/Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C/Keywords: heterotrimer; immunoglobulin
 F/15-92/Domain: immunoglobulin homology <IMM>

Query Match 62.1%; Score 41; DB 2; Length 99;
 Best Local Similarity 66.7%; Pred. No. 4.5;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 SGSTNIGNV 12
 :||:|||||
 Db 23 TGSSNIGAGV 34

RESULT 39
 B46516
 Ig lambda chain V region - horse (fragment)
 C/Species: Equus caballus (domestic horse)
 C/Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
 C/Accession: B46516
 R/Home, W.A.; Ford, J.E.; Gibson, D.M.
 J. Immunol. 149, 3927-3936, 1992
 A/Title: L chain isotype regulation in horse. I. Characterization of Ig lambda genes.
 A/Reference number: A46516; MUID:93094587; PMID:1460283
 A/Accession: B46516
 A/Status: preliminary; not compared with conceptual translation
 A/Molecule type: nucleic acid
 A/Residues: 1-107 <HOM>
 A/Experimental source: spleen
 A/Note: sequence extracted from NCBI backbone (NCBI:120369)
 C/Superfamily: Immunoglobulin V region; Immunoglobulin homology
 F/23-101/Domain: immunoglobulin homology <IMM>

Query Match 62.1%; Score 41; DB 2; Length 107;
 Best Local Similarity 72.7%; Pred. No. 4.9;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGSTNIGNV 11
 |||||
 Db 31 SGSSNIGSY 41

RESULT 40
 Ig lambda chain V-VI region (WLT) - human
 C/Species: Homo sapiens (man)
 C/Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
 C/Accession: A01989
 R/Dwulet, F.E.; Strako, K.; Benson, M.D.
 Scand. J. Immunol. 22, 653-660, 1985
 A/Title: Amino acid sequence of a lambda VI primary (AL) amyloid protein (WLT).
 A/Reference number: A01989; MUID:8612267; PMID:4089539
 A/Accession: A01989
 A/Molecule type: protein
 A/Residues: 1-111 <DMU>
 A/Cross-references: UNIPROT:P06318
 C/Genetics:
 A/Gene: GDB:IGLV@
 A/Cross-references: GDB:119342; OMIM:147240
 A/Map position: 22q11.2-22q11.2
 C/Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kappa)
 chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la
 C/Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C/Keywords: heterotrimer; immunoglobulin
 F/1-22/Region: framework 1
 F/15-93/Domain: immunoglobulin homology <IMM>
 F/23-35/Region: complementarity-determining 1
 F/36-50/Region: framework 2
 F/51-57/Region: complementarity-determining 2
 F/58-91/Region: framework 3
 F/92-101/Region: complementarity-determining 3
 F/102-111/Region: framework 4
 F/122-91/Disulfide bonds: #status predicted

Query Match 62.1%; Score 41; DB 1; Length 111;
 Best Local Similarity 58.3%; Pred. No. 5.1;
 Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 QY 1 SGSTNIGNV 12
 :||:|||||
 Db 23 TGSSGIGSNV 34

Search completed: March 31, 2005, 12:11:15
 Job time : 18.4844 secs

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OM protein - protein search, using sw model

Run on: March 31, 2005, 11:42:54 ; Search time 86.3281 Seconds
(without alignments)
77.113 Million cell updates/sec

Title: US-10-614-959-13
Perfect score: 66
Sequence: 1 SGSTSNIGNNYVS 13

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	86.4	130	1 LV1G_HUMAN	P06316 homo sapien
2	56	84.8	101	2 O81ZD8	O81ZD8 homo sapien
3	55	83.3	110	2 O8TE63	O8TE63 homo sapien
4	55	83.3	111	1 LV1C_HUMAN	P01701 homo sapien
5	53	80.3	108	2 Q96S80	Q96S80 homo sapien
6	53	80.3	111	1 LV1D_HUMAN	P01702 homo sapien
7	52	78.8	109	1 LV1D_HUMAN	P06888 homo sapien
8	52	78.8	235	2 O6IN99	O6IN99 homo sapien
9	51	77.3	236	2 O8NEJ1	O8NEJ1 homo sapien
10	49	74.2	237	2 O6DHW4	O6DHW4 homo sapien
11	45	68.2	221	2 O6GMW6	O6GMW6 homo sapien
12	44	66.7	221	2 O87LH3	O87LH3 vibrio para
13	44	66.7	326	2 Q7SCJ5	Q7SCJ5 neurospora
14	44	66.7	441	2 O8JRX2	O8JRX2 phthorimaea
15	43	65.2	1170	2 O7WZM9	O7WZM9 pseudomonas
16	43	65.2	1357	2 Q9W4M4	Q9W4M4 drosophila
17	43	65.2	2186	1 YU52_CAEEL	P34431 caenorhabdi
18	43	65.2	2270	2 O17329	O17329 plasmodium
19	43	65.2	2502	2 O96223	O96223 plasmodium
20	42	63.6	236	2 O6GMV7	O6GMV7 homo sapien
21	42	63.6	348	2 O97KX3	O97KX3 clostridium
22	42	63.6	633	1 ACES_ELEEL	O42275 electrophor
23	41	62.1	111	1 LV6D_HUMAN	P06318 homo sapien
24	41	62.1	112	1 LV1H_HUMAN	Q9V8W7 drosophila
25	41	62.1	388	2 Q9VRW7	Q9VRW7 homo sapien
26	41	62.1	414	1 HEM1_RICPR	O9ZCB8 rickettsia
27	41	62.1	414	2 O6BVS3	O6BVS3 rickettsia
28	41	62.1	847	2 O6BVS9	O6BVS9 debaryomyce
29	41	62.1	958	2 Q7RRT8	Q7RRT8 plasmodium
30	41	62.1	1272	2 Q9S5G4	Q9S5G4 drosophila
31	41	62.1	1272	2 Q9W117	Q9W117 drosophila

32	41	62.1	1298	2 O81IE2	O81IE2 drosophila
33	41	62.1	1336	2 O81IA0	O81IA0 drosophila
34	41	62.1	1701	2 O81IS0	O81IS0 plasmodium
35	40	60.6	109	1 LV1F_HUMAN	P04208 homo sapien
36	40	60.6	112	1 LV1B_HUMAN	P01700 homo sapien
37	40	60.6	159	2 O8GFE2	O8GFE2 photorhabdu
38	40	60.6	314	2 O76611	O76611 caenorhabdi
39	40	60.6	315	2 O8W1R8	O8W1R8 lycopersico
40	40	60.6	410	2 O8F1Z5	O8F1Z5 escherichia
41	40	60.6	415	2 O9FJF2	O9FJF2 arabidopsis
42	40	60.6	514	2 Q47936	Q47936 francisella
43	40	60.6	561	2 Q7R259	Q7R259 neurospora
44	40	60.6	569	2 Q7Q967	Q7Q967 anopheles g
45	40	60.6	715	1 CLPB_MYCPN	P75247 mycoplasma

ALIGNMENTS

RESULT 1

LV1G_HUMAN STANDARD; PRT; 130 AA.
ID P06316;
AC 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-I region BL2 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85062823; PubMed=6095199;
RA Tsujimoto Y., Croce C.M.;
RT "Molecular cloning of a human immunoglobulin lambda chain variable
sequence."
RL Nucleic Acids Res. 12:8407-8414(1984).
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DR EMBL; X01147; CAA25598.1; -.
DR PIR; A01966; L1HUBL.
DR HSSP; P01703; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SMO0406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 20 130 Ig lambda chain V-I region BL2.
FT DOMAIN 20 115 V segment.
FT DOMAIN 116 130 J segment.
FT DISULFID 41 108 By similarity.
FT NON_TER 130
SQ SEQUENCE 130 AA; 13564 MW; FA44BBI7D3A55EBF CRC64;

Query Match 86.4%; Score 57; DB 1; Length 130;
Best Local Similarity 84.6%; Pred. No. 0.069;

Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
|||||

Db 42 SGGSSNIGNDYVS 54

RESULT 2

Q81ZD8 PRELIMINARY; PRT; 101 AA.

AC Q81ZD8; 01-MAR-2003 (TREMblrel. 23, Created)

DT 01-MAR-2003 (TREMblrel. 23, Last sequence update)

DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)

DE Anti-chyroglobulin light chain variable region (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OC NCBI_TaxID=9606;

RE NCBI_TaxID=9606;

RA Jang Y.-J., Chung J., Park J.-Y.,

RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY145444; AAN64328.1; -

DR HSP; P01703; 7PAB.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_v.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PSS0835; IG_LIKE; 1.

FT NON_TER 1

FT NON_TER 101

SEQUENCE 101 AA; 10374 MW; 1506C2D9AACBA793 CRC64;

Query Match 84.8%; Score 56; DB 2; Length 101;

Best Local Similarity 84.6%; Pred. No. 0.079; Indels 0; Gaps 0;

Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGGSTNIGNNYVS 13

Db 13 SGGSSNIGNNYVS 25

RESULT 3

Q8TE63 PRELIMINARY; PRT; 110 AA.

AC Q8TE63; 01-JUN-2002 (TREMblrel. 21, Created)

DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)

DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)

DE Immunoglobulin light chain variable region (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OC NCBI_TaxID=9606;

RE NCBI_TaxID=9606;

RA MEDLINE=95007525; PubMed=7923137;

RA Hall B.L., Murray J.H., Haspel M.V., Kobrin B.J.;

RT "Establishment, molecular rescue, and expression of 123AV16-1, a

RT tumor-reactive human monoclonal antibody.";

RT Cancer Res. 54:5178-5185 (1994).

DR EMBL; L33985; AAL68704.1; -

DR HSP; P01703; 7PAB.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_v.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PSS0835; IG_LIKE; 1.

FT NON_TER 1

FT NON_TER >110

SEQUENCE 110 AA; 11479 MW; 559D1628F8F5437C CRC64;

Query Match 83.3%; Score 55; DB 2; Length 110;

Best Local Similarity 76.9%; Pred. No. 0.13; Indels 0; Gaps 0;

Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGSTNIGNNYVS 13

Db 23 SGGSTNIGNNYVS 35

RESULT 4

ID LVIC_HUMAN STANDARD; PRT; 111 AA.

AC P01701; 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Ig lambda chain V-I region NEM.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OC NCBI_TaxID=9606;

RE NCBI_TaxID=9606;

RA MEDLINE=6906082; PubMed=4177823;

RA Langer B., Steinmetz-Kayne M., Hilschmann N.;

RT "The complete amino acid sequence of Bence Jones protein New (lambda-

RT type). Subgroups in the variable part of immunoglobulin L-chains of

RT the lambda-type.";

RT Hoppe-Seyler's Z. physiol. Chem. 349:945-951 (1968).

CC -1 MISCELLANEOUS: This is a Bence-Jones protein.

CC -1 SIMILARITY: Contains 1 immunoglobulin-like domain.

DR HSP; P01703; 7PAB.

DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0003823; F:antigen binding; NAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; IGV; 1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PSS0835; IG_LIKE; 1.

KW Bence-Jones protein; Direct protein sequencing;

KW Immunoglobulin V region; Pyrolydione carboxylic acid.

FT DOMAIN 1 105

FT MOD RES 1 1

FT DISULFID 22 89

FT NON_TER 111

SEQUENCE 111 AA; 11453 MW; AABCECA3C49F2AD3 CRC64;

Query Match 83.3%; Score 55; DB 1; Length 111;

Best Local Similarity 76.9%; Pred. No. 0.13; Indels 0; Gaps 0;

Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGGSTNIGNNYVS 13

Db 23 SGGSTNIGNNYVS 35

RESULT 5

Q96SBO PRELIMINARY; PRT; 108 AA.

AC Q96SBO; 01-DEC-2001 (TREMblrel. 19, Created)

DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)

DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)

DE Anti-streptococcal/anti-myosin immunoglobulin lambda light chain

DE variable region (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OC NCBI_TaxID=9606;

RE NCBI_TaxID=9606;

RA MEDLINE=98375893; PubMed=9712075;

RA Adderson E.E., Shikman A.R., Ward K.E., Cunningham M.W.;

RT "Molecular analysis of polyreactive monoclonal antibodies from

RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin


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RT antibody V region genes.",
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; U96394; AAB68783.1; -.
DR PDB; 1KU4; Model; L=1-108.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; Ig-LIKE; 1.
FT NON TER 1
SQ SEQUENCE 108 AA; 11594 MW; FABSDC478A043F48 CRC64;

Query Match 80.3%; Score 53; DB 2; Length 108;
Best Local Similarity 83.3%; Pred. No. 0.28;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNVY 12
DB 23 SGSSNIGNNVY 34

RESULT 6
LYVD HUMAN STANDARD; PRT; 111 AA.
ID LYVD_HUMAN STANDARD; PRT; 111 AA.
AC P01702;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig lambda chain V-I region NIG-64.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=83186114; PubMed=6404900;
RA Kamezani F., Takayasu T., Suzuki S., Shinoda T., Okuyama T.,
RA Shimizu A.;
RT "Comparative studies on the structure of the light chains of human
RT immunoglobulins. IV. Assignment of a subgroup.",
RL J. Biochem. 93:421-429(1983).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A01965; LIHONG.
DR HSSP; P01703; 7PAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; Ig-LIKE; 1.
KW Immunoglobulin V region.
KM Immunoglobulin V region.
FT DOMAIN 1 105
FT DISULFID 22 89
FT NON TER 111
SQ SEQUENCE 111 AA; 11454 MW; A21C6121C18A61E0 CRC64;

Query Match 80.3%; Score 53; DB 1; Length 111;
Best Local Similarity 76.9%; Pred. No. 0.29;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNVY 13
DB 23 SGSSNIGNDNFVS 35

RESULT 7
LYVI HUMAN STANDARD; PRT; 109 AA.
ID LYVI_HUMAN STANDARD; PRT; 109 AA.
AC P06888;
DT 01-JAN-1988 (Rel. 06, Created)
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DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig lambda chain V-I region EPS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=86000126; PubMed=3929803;
RA Toft K.G., Stetten K., Husby G.;
RT "The amino-acid sequence of the variable region of a carbohydrate-
RT containing amyloid fibril protein EPS (immunoglobulin light chain,
RT type lambda).";
RL Biol. Chem. Hoppe-Seyler 366:617-625 (1985).
CC -1- MISCELLANEOUS: Residues 1-2, 56-62, and 74-78 and the sequenced
CC peptides were positioned by homology.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A24656; LIHUP.
DR HSSP; P01703; 7PAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; Ig-LIKE; 1.
KW Amyloid; Direct protein sequencing; Glycoprotein;
KM Immunoglobulin V region.
FT DOMAIN 1 105
FT DISULFID 22 89
FT NON TER 109
SQ SEQUENCE 109 AA; 11414 MW; 556A313E24D3AC73 CRC64;

Query Match 78.8%; Score 52; DB 1; Length 109;
Best Local Similarity 83.3%; Pred. No. 0.42;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNVY 12
DB 23 SGSSNIGNNVY 34

RESULT 8
O6IN99 PRELIMINARY; PRT; 235 AA.
ID O6IN99 PRELIMINARY; PRT; 235 AA.
AC O6IN99;
DT 05-JUL-2004 (TRENBLREL. 27, Created)
DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLREL. 27, Last annotation update)
DE IGLC2 protein.
GN Name=IGLC2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RP TISSUE=Pancreas;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhac N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.D., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguercio N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
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DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF07654; C1-sec; 1.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00409; Ig; 2.
 DR SMART; SM00407; IGc1; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 DR Hypothetical protein; 237 AA; 25108 MW; 6814170F7E784825 CRC64;
 SQ SEQUENCE

Query Match 74.2%; Score 49; DB 2; Length 237;
 Best Local Similarity 83.3%; Pred. No. 3;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGSTSNIGNYV 12
 DB 42 SGSSNIGNYV 53

RESULT 11

Q6GMW6 PRELIMINARY; PRT; 235 AA.
 AC Q6GMW6;
 DT 05-JUL-2004 (TRENBLREL. 27, Created)
 DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)
 DT 05-JUL-2004 (TRENBLREL. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 NCBI_TaxID=9606;

SEQUENCE FROM N.A.

RC TISSUE=Primary B-Cells;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marisina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshtycki S., Carninci P., Prange C.,
 RA Raha S.S., Loggiano N.A., Peters G.J., Abramson R.D., Muliyil S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallajon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Paine J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
 RA Jones S.J., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RA Strausberg R.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC073784; AAH73784.1; -.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF07654; C1-sec; 1.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00409; Ig; 2.
 DR SMART; SM00407; IGc1; 1.
 DR SMART; SM00406; IGV; 1.
 DR SMART; SM00406; IGV; 1.

DR PROSITE; PSS0835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 DR Hypothetical protein;
 SQ SEQUENCE 235 AA; 24803 MW; 058B05F6118F1B8 CRC64;

Query Match 68.2%; Score 45; DB 2; Length 235;
 Best Local Similarity 69.2%; Pred. No. 14;
 Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGSTSNIGNYV 13
 DB 42 SGSSNIGNYV 54

RESULT 12

Q87LH3 PRELIMINARY; PRT; 221 AA.
 ID Q87LH3;
 DT 01-JUN-2003 (TRENBLREL. 24, Created)
 DT 01-JUN-2003 (TRENBLREL. 24, Last sequence update)
 DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
 DE Putative short-chain dehydrogenase.
 GN OrderedLocustNames=VP2639;
 OS Vibrio parahaemolyticus.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrrio.
 NCBI_TaxID=670;
 RN [1]

SEQUENCE FROM N.A.

RP STRAIN=RIMD 2210633 / Serotype O3:K6;
 RC MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
 RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
 RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
 RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
 RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
 distinct from that of V. cholerae";
 RL Lancet 361:743-749(2003).
 DR EMBL; AP005082; BAC6902.1; -.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0080152; P:metabolism; IEA.
 DR InterPro; IPR002198; Adh_short.
 DR InterPro; IPR002347; Adh_short_C2.
 DR Pfam; PF00106; adh_short; 1.
 DR PRINTS; PR00081; GDBRHH.
 KM Complete proteome.
 SQ SEQUENCE 221 AA; 23803 MW; D545E953C9AB3A2P CRC64;

Query Match 66.7%; Score 44; DB 2; Length 221;
 Best Local Similarity 66.7%; Pred. No. 20;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GSSTNIGNYV 13
 DB 203 GALANIGNYV 214

RESULT 13

Q7SCU5 PRELIMINARY; PRT; 326 AA.
 ID Q7SCU5;
 DT 01-MAR-2004 (TRENBLREL. 26, Created)
 DT 01-MAR-2004 (TRENBLREL. 26, Last sequence update)
 DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
 DE Hypothetical protein.
 GN Name=NCU00836.1;
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
 NCBI_TaxID=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OR74A;
 RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,

RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
 RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endtizzi M.,
 RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
 RA Seltrenikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
 RA Koche G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
 RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Guere S.,
 RA Kamal M., Kamysseis M., Mauceli E., Bielke C., Rudd S., Frisman D.,
 RA Krysotova S., Kasumussen C., Metzberg R.L., Perkins D.D., Kroken S.,
 RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmani S.A.,
 RA Desouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
 RA Yarden O., Plamann M., Seltzer S., Dunlap J., Radford A., Aramayo R.,
 RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
 RA Paulsen I., Sachs M.S., Lander E.S., Nisbaum C., Birren B.,
 RT "The Genome Sequence of the Filamentous Fungus *Neurospora crassa*,"
 RL Nature 0:0-0(2003).
 CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC EMBL: AABX0100101; EAA34466.1; -;
 DR GO: GO:0005576; C:extracellular; IEA.
 DR GO: GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . ; IEA.
 DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro: IPR000254; CBD_fungal.
 DR InterPro: IPR005103; Glyco_hydro_61.
 DR Pfam: PF00734; CBM_1; 1.
 DR Pfam: PF03443; Glyco_hydro_61; 1.
 DR PROSITE: PS00562; CBD_FUNGAL; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 326 AA; 33269 MW; 61BC539A292B599F CRC64;

Query Match 66.7%; Score 44; DB 2; Length 326;
 Best Local Similarity 61.5%; Pred. No. 30;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 SGSTNIGNNVVS 13
 Db 311 SGSTCKGVNDYVS 323

RESULT 14
 ID Q9W4M4 PRELIMINARY; PRT; 441 AA.
 AC Q9W4M4;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Late expression factor 4.
 GN Name=PhogV087;
 OS Phthorimea operculella granulovirus.
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Granulovirus.
 OC NCBI_TaxID=192584;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Croizier L., Taha A., Croizier G., Lopez Ferber M.,
 RL Submitted (Apr-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL: A9495956; AAM70285.1; -;
 DR GO: GO:0030528; F:transcription regulator activity; IEA.
 DR GO: GO:0045449; P:regulation of transcription; IEA.
 DR InterPro: IPR007790; LEF-4.
 DR Pfam: PF05098; LEF-4; 1.
 SQ SEQUENCE 441 AA; 51639 MW; DC7B3982232B3550 CRC64;

Query Match 66.7%; Score 44; DB 2; Length 441;
 Best Local Similarity 66.7%; Pred. No. 41;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SGSTNIGNNVV 12
 Db 264 SGNTLFGNIGNVYL 275

RESULT 15
 Q7W2N9

ID Q7W2N9 PRELIMINARY; PRT; 1170 AA.
 AC Q7W2N9;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Pili1;
 GN Name=pili1;
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 CC Pseudomonadaceae; Pseudomonas.
 CC NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PA14;
 RC PubMed=14983043; DOI=10.1073/pnas.0304622101;
 RA He J., Baldini R.L., Dezell E., Sautier M., Zhang Q., Liberati N.T.,
 RA Lee D., Urbach J., Goodman H.M., Rahme L.G.,
 RT "The broad host range pathogen *Pseudomonas aeruginosa* strain PA14
 RT carries two pathogenicity islands harboring plant and animal virulence
 RT genes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:2530-2535(2004).
 DR EMBL: AY273871; AAP81276.1; -;
 DR InterPro: IPR008707; Nucleoside_P1C.
 DR Pfam: PF05567; Nucleoside_P1C; 1.
 DR Pfam: PF05567; Nucleoside_P1C; 1.
 SQ SEQUENCE 1170 AA; 128118 MW; 9F4CDF6D681B62F3 CRC64;

Query Match 65.2%; Score 43; DB 2; Length 1170;
 Best Local Similarity 70.0%; Pred. No. 16+02;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 GSTNLSNNY 11
 Db 139 GSTNLSNNY 148

RESULT 16
 ID Q9W4M4 PRELIMINARY; PRT; 1357 AA.
 AC Q9W4M4;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE CG15570-PA.
 GN ORFNames=CG15570;
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidae; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananatzides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazek R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 RA Abril J.F., Aghayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu N., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
 RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieres S., Fleischmann W.,
 RA Fostel C., Gabrielian A.B., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
 RA Idali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasako P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., Moleod M.P., Mobergson D.,
 RA Merklov G., Mishina N.V., Mobergson D., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusken D.R., Pacleb J.M.,
 RA Palazolo M., Peltan G.S., Fan S., Pollard J., Port V., Reese M.G.,
 RA Rine B.C., Siden-Klamis I., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamis I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Strickas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodger, Morley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "the genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celinker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe W., Dugan S.P., Friese E., Hodgson A.,
 RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
 RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Sylvestras R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 RT "finishing a whole-genome shotgun: Release 3 of the *Drosophila*
 RT melanogaster euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svitskas R.,
 RA Patel S., Friese E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celinker S.E.;
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
 RT a genomics perspective.";
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Betencourt B.R., Celinker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX FLYBASE;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RX FLYBASE;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE003430; AAFA5927.1; -;
 DR FLYBASE; FBgn002697; CG15570.
 SQ SEQUENCE 1357 AA; 136890 MW; C282DC6F34A61A CRC64;

YL52 CAEEL STANDARD; PRT; 2166 AA.
 ID YL52 CAEEL
 AC P34431; P34432;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Hypothetical protein P44E2.2 in chromosome III.
 GN ORFNames=F44E2.2/F44E2.1;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STEADY-BRISTOL N2;
 RL MEDLINE=94150718; PubMed=7906398; DOI=10.1038/368032a0;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
 RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
 RA Johnston L., Jones M., Kershaw J., Kireten J., Laister N.,
 RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Riken L., Roopra A., Saunders D., Showkeen R.,
 RA Sims M., Smalton N., Smith A., Smith W., Sonhammer B., Staden R.,
 RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
 RA Waterston R., Watson A., Weinstein L., Wilkinson-Sproat J.,
 RA Wohldman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of *C.*
 RT elegans.";
 RL Nature 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STEADY-BRISTOL N2;
 RL MEDLINE=99069613; PubMed=9851916;
 RG The C. elegans sequencing consortium;
 RT "Genome sequence of the nematode *C. elegans*: a platform for
 RT investigating biology.";
 RL Science 282:2012-2018(1998).
 RN [3]
 RP REVISIONS, AND ALTERNATIVE SPLICING.
 RA Waterston R.;
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- ALTERNATIVE PRODUCTS;
 CC Name=b;
 CC IsoId=P34431-1; Sequence=Displayed;
 CC Name=a;
 CC IsoId=P34431-2; Sequence=VSP_005225;
 CC Note=No experimental confirmation available;
 CC -1- SIMILARITY: Contains 1 CCHC-type zinc finger.
 CC -1- SIMILARITY: Contains 1 peptidase A1 domain.
 CC -1- SIMILARITY: Contains 1 reverse transcriptase domain.
 CC -----
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 CC -----
 DR EMBL; L23646; AAA28035.2; -;
 DR EMBL; L23646; AAL02516.1; -;
 DR HSSP; P03366; 1HMV.
 DR WormBase; WBgene00018416; P44B2.2.
 DR WormPep; P44B2.2a; CE07254.
 DR WormPep; P44B2.2b; CE29321.
 DR InterPro; IPR001969; Pept_Asp_AS.
 DR InterPro; IPR001584; RVE.
 DR InterPro; IPR000477; RVTse.
 DR InterPro; IPR001878; Znf_CCHC.
 DR Pfam; PF00665; tve; 1.
 DR Pfam; PF00078; RVT; 1.

RESULT 17

DR Pfam: PF00098; zfcCHC; 1.
DR PRINTS; PR00939; C2HCZNFINGER.
DR SMART; SM00343; Znf_C2HC; 1.
DR PROSITE; PS00141; ASP_PROTEASE; 1.
DR PROSITE; PS50878; RT_POL; 1.
DR PROSITE; PS50158; ZF_CCHC; 1.
KM Alternative splicing; Aspartyl protease; Hydrolyase;
KM Hypothetical protein; RNA-directed DNA polymerase; Transferase;
KM Zinc-finger.
FT ZNF_RING 589 606 CCHC-type.
FT DOMAIN 966 1145 Reverse transcriptase.
FT ACT_SITE 664 664 Protease (By similarity).
FT VARSPIC 91 101 Missing (in isoform a).
FT /Ftrd-VSP 005225.
SQ SEQUENCE 2186 AA; 249691 MW; 29C5A10F81FB3DB6 CRC64;
Query Match 65.2%; Score 43; DB 1; Length 2186;
Best Local Similarity 80.0%; Pred. No. 3e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 3 STSNIGNNV 12
Db 219 STSNVGNVV 228
RESULT 18
Q17329 PRELIMINARY; PRT; 2272 AA.
ID Q17329
AC Q17329
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Gag, pol and env protein.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peleodermidae; Caenorhabditis.
OX NCBI_Taxid=6239;
[1]
RP SEQUENCE FROM N.A.
RC TRANSPOSON=Cer1 retrotransposon;
RX MEDLINE=94150718; PubMed=7906398; DOI=10.1038/368032a0;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kistlen J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkhen R.,
RA Smalton N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Spratt J., Wohlman P.,
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans";
RL Nature 368:32-38(1994).
[2]
RP SEQUENCE FROM N.A.
RC TRANSPOSON=Cer1 retrotransposon;
RX MEDLINE=9218156; PubMed=1538779; DOI=10.1038/356037a0;
RA Sulston J., Du Z., Thomas K., Wilson R., Hillier L., Staden R.,
RA Halloran N., Green P., Thierry-Mieg J., Qiu L., Dear S., Coulson A.,
RA Craxton M., Durbin R., Berks M., Metzstein M., Hawkins T.,
RA Ainscough R., Waterston R.,
RT "The C. elegans genome sequencing project: a beginning (see
RT comments)";
RL Nature 356:37-41(1992).
[3]
RP SEQUENCE FROM N.A.
RC TRANSPOSON=Cer1 retrotransposon;
RA Britten R.J.;
RT "Active gypsy/Ty3 retrotransposons or retroviruses in Caenorhabditis
RT elegans";
RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0(1994).
[4]

RP SEQUENCE FROM N.A.
RC TRANSPOSON=Cer1 retrotransposon;
RA Britten R.J.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U15406; AAA50456.1; -.
DR PIR; S44816; S44816.
DR PIR; T18572; T18572.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO; GO:0016740; F:transcriptase activity; IEA.
DR GO; GO:0006310; P:DNA recombination; IEA.
DR GO; GO:0006278; P:RNA-dependent DNA replication; IEA.
DR InterPro; IPR001969; Pept_Asp_AS.
DR InterPro; IPR001584; Rve.
DR InterPro; IPR00477; RVTse.
DR InterPro; IPR001878; Znf_CCHC.
DR Pfam; PF00078; RVT_1; 1.
DR Pfam; PF00098; ZF_CCHC; 1.
DR SMART; SM00343; Znf_C2HC; 1.
DR PRINTS; PR00939; C2HCZNFINGER.
DR PROSITE; PS00141; ASP_PROTEASE; UNKNOWN_1.
DR PROSITE; PS50158; ZF_CCHC; 1.
KM RNA-directed DNA polymerase; Transferase.
SQ SEQUENCE 2272 AA; 259695 MW; 47034F67AC3DA2B0 CRC64;
Query Match 65.2%; Score 43; DB 2; Length 2272;
Best Local Similarity 80.0%; Pred. No. 3.2e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 3 STSNIGNNV 12
Db 305 STSNVGNVV 314
RESULT 19
O96223 PRELIMINARY; PRT; 2500 AA.
ID O96223
AC O96223
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Hypothetical protein PFB0650w.
GN Name=PFB0650w;
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_Taxid=36329;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99021743; PubMed=9804551; DOI=10.1126/science.282.5391.1126;
RA Gardner M.J., Tetteh H., Carucci D.J., Cummings L.M., Aravind L.,
RA Koonin E.V., Shallow S., Mason T., Yu K., Fujii C., Pedersen J.,
RA Shen K., Jing J., Aston C., Lai Z., Schwartz D.C., Perera M.,
RA Salzberg S., Zhou L., Sutton G.G., Clayton R., White O., Smith H.O.,
RA Fraser C.M., Adams M.D., Venter J.C., Hoffman S.L.;
RT "Chromosome 2 sequence of the human malaria parasite Plasmodium
RT falciparum";
RL Science 282:1126-1132(1998).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=2225705; PubMed=12368864; DOI=10.1038/nature01097;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.-S., Nene V., Shallow S.J., Sub B., Peterson J., Angioli S.,
RA Birta M., Allen J., Selengut J., Haft D., Mether M.W., Vaidya A.B.,
RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrett B.;
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum";

RL Nature 419:498-511 (2002).
 DR EMBL; AB001408; AAC71919.1; -
 DR PIR; G71609; G71609.
 KM Hypothetical protein.
 SQ SEQUENCE 2500 AA; 293866 MW; B91DB801ED521221 CRC64;

Query Match 65.2%; Score 43; DB 2; Length 2500;
 Best Local Similarity 70.0%; Pred. No. 3.5e+02;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 STSNIGNNVY 12
 DB 594 STNNMNNM 603

RESULT 20

Q6GMV7 PRELIMINARY; PRT; 236 AA.

AC Q6GMV7; 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NC NCBI_Taxid=9606;
 RN [1]

SEQUENCE FROM N.A.

RC TISSUE=Spleen;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gumaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalins D.B., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RL [2]

SEQUENCE FROM N.A.

RC TISSUE=Spleen;

RA Strauberg R.;
 RT Submitted (JUN-2004) to the EMBL/Genbank/DBJ databases.

DR EMBL; BC073795; AAH73795.1; -

DR InterPro; IPR003599; IG-like.

DR InterPro; IPR003597; IG-cl.

DR InterPro; IPR003596; IG-MHC.

DR InterPro; IPR003596; IG-V.

DR Pfam; PF07654; CI-set; 1.

DR Pfam; PF00047; IG; 2.

DR SMART; SM00409; IG; 2.

DR SMART; SM00406; IG; 1.

DR SMART; SM00406; IG; 1.

DR PROSITE; PS50835; IG-LIKE; 2.

DR PROSITE; PS00290; IG-MHC; UNKNOWN_1.

KW Hypothetical protein_

SQ SEQUENCE 236 AA; 24950 MW; 3B0477247847E930 CRC64;

Query Match 63.6%; Score 42; DB 2; Length 236;

Best Local Similarity 69.2%; Pred. No. 48;
 Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 SGSTNIGNNVYS 13
 DB 42 SGSSNIGNNVN 54

RESULT 21

Q97KX3 PRELIMINARY; PRT; 348 AA.

AC Q97KX3; 01-OCT-2001 (TREMBlrel. 18, Created)
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Uncharacterized conserved protein of probably eukaryotic origin.
 GN Ordered locus names=CAC0793;
 OS Clostridium acetobutylicum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 NC NCBI_Taxid=1486;
 RN [1]

SEQUENCE FROM N.A.

RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;

RX MEDLINE=21359325; PubMed=1146286;

RX DOI=10.1128/JB.183.16.4823-4838.2001;

RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng O.,
 RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
 RA Tatusov R.L., Sabatne F., Doucette-Stamm L.A., Soucaille P.,
 RA Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.;

RT "Genome sequence and comparative analysis of the solvent-producing
 RT bacterium Clostridium acetobutylicum.";

RL J. Bacteriol. 183:4823-4838 (2001).

DR EMBL; AB007594; AAH78769.1; -

DR PIR; F96997; F96997.

DR InterPro; IPR01220; Lectin legB.

DR PROSITE; PS00307; LECTIN_LEGUME_BETA; UNKNOWN_1.

KW Complete proteome.

SQ SEQUENCE 348 AA; 39594 MW; 592731AED6573DF9 CRC64;

QY 3 STSNIGNNVY 11
 DB 158 STSNIGNNVY 166

RESULT 22

ACNES_ELEBL STANDARD; PRT; 633 AA.

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Acetylcholinesterase precursor (BC 3.1.1.7) (AChE).

OS Electrophorus electricus (Electric eel).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Gymnalliformes;

OC Electrophoridae; Electrophorus.

NC NCBI_Taxid=8005;

SEQUENCE FROM N.A.

RC MEDLINE=96070504; PubMed=9407087; DOI=10.1074/jbc.272.52.33045;

RA Simon S., Massoulié J.;

RT "Cloning and expression of acetylcholinesterase from Electrophorus.
 RT Splicing pattern of the 3' exons in vivo and in transfected mammalian
 RT cells.";

RL J. Biol. Chem. 272:33045-33055 (1997).

CC -1- FUNCTION: Rapidly hydrolyzes choline released into the synapse.

CC -1- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.

CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/11pase family.

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CC -----
DR EMBL AF030422; AAB86606.1; -
DR HSSP; P04058; 1H23.
DR InterPro; IPR002018; CarboxylesteraseB.
DR InterPro; IPR000997; Cholinesterase.
DR InterPro; IPR000379; Ser esterase.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PR00878; CHOLINESTERASE.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KM Glycoprotein; Hydrolyase; Membrane; Neurotransmitter degradation;
KM Serine esterase; Signal; Synapse.
FT SIGNAL 1 23 Potential.
FT CHAIN 24 633 Acetylcholinesterase.
FT ACT_SITE 225 225 Acyl-ester intermediate (By similarity).
FT ACT_SITE 352 352 Charge relay system (By similarity).
FT ACT_SITE 494 494 Charge relay system (By similarity).
FT DISULFID 91 118 By similarity.
FT DISULFID 279 290 By similarity.
FT DISULFID 427 579 By similarity.
FT DISULFID 630 630 Interchain (By similarity).
FT CARBOHYD 133 133 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 184 184 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 283 283 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 368 368 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 511 511 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 591 591 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 633 AA; 71814 MW; FC92FE7E4ADB84C3 CRC64;

Query Match 63.6%; Score 42; DB 1; Length 633;
Best Local Similarity 62.2%; Pred. No. 1.3e+02;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SGGSTNIGNNVY 13
DB 459 SGGSSNIGNNVY 471

RESULT 23
LV6D HUMAN STANDARD; PRT; 111 AA.
AC P06318;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig lambda chain V-VI region WLT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=86122667; PubMed=4089539;
RA Dvulet F.E., Strako K., Benson M.D.;
RT "Amino acid sequence of a lambda VI primary (AL) amyloid protein
RT (WLT).";
RL Scand. J. Immunol. 22:653-660(1985).
DR HSSP; P06317; 1CD0.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.

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DR SMART; SM00406; IGV; 1.
KM PROSITE; PSS0835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 22 Framework-1.
FT DOMAIN 23 35 Complementarity-determining-1.
FT DOMAIN 36 50 Framework-2.
FT DOMAIN 51 57 Complementarity-determining-2.
FT DOMAIN 58 91 Framework-3.
FT DOMAIN 92 101 Framework-4.
FT DOMAIN 102 111 Complementarity-determining-3.
FT DISULFID 22 91 Framework-4.
FT NON_TER 111 By similarity.
SQ SEQUENCE 111 AA; 11966 MW; 0C8B82FE378CE24F CRC64;

Query Match 62.1%; Score 41; DB 1; Length 111;
Best Local Similarity 58.3%; Pred. No. 33;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGGSTNIGNNVY 12
DB 23 TSSSGSISNVY 34

RESULT 24
LV1H HUMAN STANDARD; PRT; 112 AA.
AC P06887;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig lambda chain V-1 region MEM.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=85257662; PubMed=2410269;
RA Minaeo E., Roy U.P., Congy N., Perran-Rivat L., Minaeo C.;
RT "The amino acid sequence of a lambda light chain presenting abnormal
RT physicochemical and antigenic features.";
RL Eur. J. Biochem. 150:349-357(1985).
CC -1- MISCELLANEOUS: Residues 33-36 and some of the sequenced peptides
CC were positioned by homology.
CC -1- MISCELLANEOUS: The C region of this chain has the Mcg+ and Kern+
CC markers.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A25479; L1HMM.
DR HSSP; P01703; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region;
KW Monoclonal antibody; Pyrolydione carboxylic acid.
FT DOMAIN 1 106 Ig-like.
FT MOD_RES 1 1 Pyrolydione carboxylic acid.
FT DISULFID 22 90 By similarity.
FT NON_TER 112 By similarity.
SQ SEQUENCE 112 AA; 11789 MW; 748124F079CFEBE4 CRC64;

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Query Match 62.1%; Score 41; DB 1; Length 112;
Best Local Similarity 70.0%; Pred. No. 33;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGGSTNIGNNV 10
DB 23 SGGSSNIGNNV 32

```


RESULT 25
 Q9VRW7 PRELIMINARY; PRT; 388 AA.
 AC Q9VRW7;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE CG13300-PA.
 GN ORFNames=CG13300;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pelecygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_Taxid=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blaise R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 RA April J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
 RA Borkov D., Botchan M.R., Boulton J., Brokstein P., Brotter P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo S., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup I.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heilmann T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy L., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier B., Spradlin A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodgerf, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.W., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.N., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Friese B., Hodson A.,
 RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
 RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstock G., Wheeler S.E., Myers B.W., Gibbs R.A., Rubin G.M.,
 RT "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*.
 RT melanogaster eukaryotic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminier J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,
 RA Patel S., Friese B., Wheeler D.A., Lewis S.E., Rubin G.M.,

RA Ashburner M., Celniker S.E.;
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
 RT a genomics perspective.";
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Miara S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminier J.S., Milburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Bernan B.P.,
 RA Bettencourt B.R., Celniker S.E., de Grey A.D., Dysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX FLYbase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RG FLYbase;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB003563; AAF50665.1; -;
 DR INTCAT; Q9VRW7; -;
 DR FLYbase; FBgn0035699; CG13300.
 SO SEQUENCE 388 AA; 41664 MW; 2F8F5E96584B1F38 CRC64;
 Qy 1 SGGTSNIGNNV 12
 Db 224 NGSSNNINNH 235
 Query Match 62.1%; Score 41; DB 2; Length 388;
 Best Local Similarity 58.3%; Pred. No. 1.2e+02;
 Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 RESULT 26
 ID1 HEMI RICPR STANDARD; PRT; 414 AA.
 AC Q9ZCB8;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DE 5-aminolevulinate synthase (EC 2.3.1.37) (5-aminolevulinic acid
 synthase) (delta-aminolevulinic synthase) (Delta-ALA synthetase).
 GN Name=hemA; OrderedLocNames=RP841;
 OS Rickettsia prowazekii.
 CC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
 CC Rickettsiaceae; Rickettsiae; Rickettsia.
 CC NCBI_Taxid=782;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Madrid E;
 RX MEDLINE=99039499; PubMed=9823893; DOI=10.1038/24094;
 RA Anderson S.G.E., Zomrodipour A., Anderson J.O.,
 RA Scharitz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
 RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
 RT "The genome sequence of *Rickettsia prowazekii* and the origin of
 RT mitochondria.";
 RL Nature 396:133-140(1998).
 CC -1- CATALYTIC ACTIVITY: Succinyl-CoA + glycine = 5-aminolevulinic acid +
 CC COA + CO(2).
 CC -1- COFACTOR: Pyridoxal phosphate.
 CC -1- PATHWAY: Heme biosynthesis; first (rate-limiting) step.
 CC -1- SIMILARITY: Belongs to the class-II pyridoxal-phosphate-dependent
 CC aminotransferase family.
 CC -----
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 DR EMBL; AJ235273; CAA15265.1; -.
 DR PIR; A71646; A71646.
 DR InterPro; IPR010961; Saminolev_synth.
 DR InterPro; IPR003408; Ala_synthase.
 DR InterPro; IPR004839; Aminotrans_1/IT.
 DR InterPro; IPR01917; Aminotrans_11.
 DR Pfam; PF02490; Ala_synthase; 1.
 DR Pfam; PF00155; Aminotran_1.2; 1.
 DR TIGRFAMs; TIGR01822; 2am3keto_COA; 1.
 DR TIGRFAMs; TIGR01821; Saminolev_synth; 1.
 DR TIGRFAMs; TIGR01825; Gly_Cac_Trel; 1.
 DR PROSITE; PS00599; AA_TRANSFER_CLASS_2; 1.
 KM Acyltransferase; Complete proteome; Heme biosynthesis;
 KM Pyridoxal phosphate; Transferase.
 PT BINDING 244
 SQ SEQUENCE 414 AA; 46516 MW; 9763C4E196A2822 CRC64.

Query Match 62.1%; Score 41; DB 1; Length 414;
 Best Local Similarity 61.5%; Pred. No. 1.3e+02;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNYVS 13
 Db 76 SGGTRNIGNNIS 88

RESULT 27
 Q68VS3 PRELIMINARY; PRT; 414 AA.
 AC Q68VS3 (TREMblrel. 28, Created)
 DT 25-OCT-2004 (TREMblrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMblrel. 28, Last annotation update)
 DE 5-aminolevulinic acid synthase (EC 2.3.1.37).
 GN Name=hema; OrderedLocNames=RT0829;
 OS Rickettsia typhi.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
 OC Rickettsiaceae; Rickettsiae; Rickettsia.
 OX NCBI_TaxId=785;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Williamston;
 RX PubMed=15311790; DOI=10.1128/JB.186.17.5842-5855.2004;
 RA McLeod M.P., Qin X., Karpach S.E., Giola J., Highlander S.K.,
 RA Fox G.B., McNeill T.Z., Jiang H., Muzny D., Jacob L.S., Hawes A.C.,
 RA Sodergren E., Gill R., Hume J., Morgan M., Fan G., Amin A.G.,
 RA Gibbs R.A., Hong C., Yu X.-J., Walker D.H., Weinstein G.M.;
 RT "Complete genome sequence of Rickettsia typhi and comparison with
 RT sequences of other Rickettsiae.";
 RL J. Bacteriol. 186:5842-5855(2004).
 DR EMBL; AE017197; AA004283.1; -.
 DR GO; GO:0008415; F:acyltransferase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR InterPro; IPR010961; Saminolev_synth.
 DR InterPro; IPR003408; Ala_synthase.
 DR InterPro; IPR004839; Aminotrans_1/IT.
 DR InterPro; IPR01917; Aminotrans_11.
 DR Pfam; PF02490; Ala_synthase; 1.
 DR Pfam; PF00155; Aminotran_1.2; 1.
 DR TIGRFAMs; TIGR01821; Saminolev_synth; 1.
 DR PROSITE; PS00599; AA_TRANSFER_CLASS_2; UNKNOWN 1.
 KM Acyltransferase; Complete proteome; Transferase;
 SQ SEQUENCE 414 AA; 46460 MW; 50293078A98D56D CRC64;

Query Match 62.1%; Score 41; DB 2; Length 414;
 Best Local Similarity 61.5%; Pred. No. 1.3e+02;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNYVS 13
 Db 76 SGGTRNIGNNIS 88

RESULT 28
 Q6BK59 PRELIMINARY; PRT; 847 AA.
 AC Q6BK59 (TREMblrel. 28, Created)
 DT 25-OCT-2004 (TREMblrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMblrel. 28, Last annotation update)
 DE Similar to trl09C019 Candida albicans CanAg6 protein.
 GN ORFNames=DEHA0F261149;
 OS Debaryomyces hanseni CBS767.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Debaryomycetes.
 OX NCBI_TaxId=284592;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CBS767;
 RG Genolevures;
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
 RA Lafontaine I., de Montigny J., Marck C., Neugeglisse C., Talla E.,
 RA Goffard N., Frangeul L., Aigle M., Anthonard V., Babour A., Barbe V.,
 RA Barney S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
 RA Boistrasse A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
 RA Hantreay F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Koszul R., Lemaître M., Lesur I., Ma L., Müller H.,
 RA Nicoud J.M., Nikolski M., Oztas S., Ozler-Kalogeropoulos O.,
 RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
 RA Swemene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
 RA Wincker P., Souciet J.L.;
 RT "Genome evolution in yeasts.";
 RL Nature 430:35-44(2004).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CBS767;
 RA Genoscope;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CR382138; CAG89823.1; -.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR InterPro; IPR008803; RHD3.
 DR Pfam; PF05879; RHD3; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN 1.
 SQ SEQUENCE 847 AA; 96135 MW; 66D78C51CB4B6ACD CRC64;

Query Match 62.1%; Score 41; DB 2; Length 847;
 Best Local Similarity 72.7%; Pred. No. 2.6e+02;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNY 11
 Db 59 STSSSDIGNNY 69

RESULT 29
 Q7RRT8 PRELIMINARY; PRT; 958 AA.
 AC Q7RRT8 (TREMblrel. 26, Created)
 DT 01-MAR-2004 (TREMblrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
 DE 01-MAR-2004 (TREMblrel. 26, Last annotation update)
 DE Aapargagine-rich protein, putative.
 GN Name=PY00629;
 OS Plasmodium yoelii yoelii.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxId=13239;
 RN [1]
 RP SEQUENCE FROM N.A.

Query Match 62.1%; Score 41; DB 2; Length 847;
 Best Local Similarity 72.7%; Pred. No. 2.6e+02;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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RC STRAIN=17XNT1;
RX PubMed=1368865; DOI=10.1038/nature01099;
RA Carlson J.M., Angiuoli S.V., Suh B.B., Koof T.W., Pertea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bickell S.L.,
RA Shallem S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabli A., Cummings L.M.,
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.B., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Jense C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii."
RL Nature 419:512-519(2002).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB10100170; EAA17409.1; -.
DR InterPro; IPR011591; Botulinum.
DR ProDom; PD001963; Botulinum; 1.
SQ SEQUENCE 958 AA; 108049 MW; 134FC37BF03E088B CRC64;

Query Match 62.1%; Score 41; DB 2; Length 958;
Best Local Similarity 66.7%; Pred. No. 2.9e+02;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GSTSNIGNNYVS 13
DB 580 GSTNIGNNNIS 591

RESULT 30
ID Q95SG4 PRELIMINARY; PRT; 1272 AA.
AC Q95SG4;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE GH27809P
GN Name=CG3189; ORFNames=CG30421;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champagne M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacled J., Paragas V., Park S., Pounenavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Ceiniker S.;
RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY060809; AAL28357.1; -.
DR HSSP; Q93009; INBF.
DR FLYBase; FBgn0050421; CG30421.
DR GO; GO:0004157; F:cysteine-type endopeptidase activity; IEA.
DR GO; GO:0004221; F:ubiquitin thiolesterase activity; IEA.
DR GO; GO:0006511; P:ubiquitin-dependent protein catabolism; IEA.
DR InterPro; IPR001394; Peptidase_C19.
DR Pfam; PF00443; UCH; 1.
DR PROSITE; PS00972; UCH_2_1; 1.
DR PROSITE; PS00973; UCH_2_2; UNKNOWN_1.
DR PROSITE; PS50935; UCH_2_3; 1.
SQ SEQUENCE 1272 AA; 138909 MW; E9BBD8A3125CAD4 CRC64;

Query Match 62.1%; Score 41; DB 2; Length 1272;
Best Local Similarity 61.5%; Pred. No. 3.9e+02;
Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGSTNIGNNYVS 13

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DB 928 SGSSNSGDRHWS 940

|||||
RESULT 31
ID Q9W117 PRELIMINARY; PRT; 1272 AA.
AC Q9W117;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE CG30421-Pa.
GN ORFNames=CG30421;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gockayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazer R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abriil J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burks K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriere W., Fleischmann W.,
RA Folsler G., Gabrielian A.E., Garcia N.S., Gelbart W.M., Glasser K.,
RA Glodde A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibbegam C.,
RA Jaitai M., Kalush F., Karpen G.H., Ke Z., Kemison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacled J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svrtkac R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wasserman D.A., Weinszock G.M., Weissenbach J.,
RA Williams S.M., Woodage, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng X.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Ceiniker S.E., Wheeler D.A., Kromoller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Pacled J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svrtkac R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinszock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT melanogaster euchromatic genome sequence."
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN
RP SEQUENCE FROM N.A.

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RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskaas R.,
RA Patel S., Friese E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Mirra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu U., Berman B.P.,
RA Bettecourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Hartle N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN
RN [5]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN
RN [6]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003465; AAF47260.2; -.
DR HSSP; Q93009; INBF.
DR FlyBase; FBgn0050421; CG30421.
DR GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.
DR GO; GO:0004221; F:ubiquitin thiolesterase activity; IEA.
DR InterPro; IPR001394; Peptidase_C19.
DR Pfam; PF00443; UCH; 1.
DR PROSITE; PS00972; UCH_2_1; 1.
DR PROSITE; PS00973; UCH_2_2; UNKNOWN_1.
DR PROSITE; PS50235; UCH_2_3; 1.
SQ SEQUENCE 1272 AA; 138810 MW; 70783F26B8AC2306 CRC64;

Query Match 62.1%; Score 41; DB 2; Length 1272;
Best Local Similarity 61.5%; Pred. No. 3.9e+02;
Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGSTNIGNNVYS 13
DB 928 SGSSNSGDMHVS 940

RESULT 32
ID 0811E2 PRELIMINARY; PRT; 1298 AA.
AC 0811E2;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE CG30421-PA.
GN ORFNames=CG30421;
OS Drosophila pseudoobscura (Fruit Fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7237;
RN
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Tucson 14011-0121.4;
RA Bergman C.M., Pfeiffer B.D., Rincon-Limas D.E., Hoskins R.A.,
RA Gaitre A., Mungall C.J., Wang A.M., Krommiller B., Pacleb J., Park S.,
RA Stapleton M., Wan K., George R.A., de Jong P.J., Botas J., Rubin G.M.,
RA Celniker S.E.;
RT "Assessing the impact of comparative genomic sequence data on the
RT functional annotation of the Drosophila genome.";

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RL Genome Biol. 3:research0086-research0086(2002).
DR EMBL; AY190942; AAC01028.1; -.
DR HSSP; Q93009; INBF.
DR FlyBase; FBgn0064435; Dpse\CG30421.
DR GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.
DR GO; GO:0004221; F:ubiquitin thiolesterase activity; IEA.
DR GO; GO:0006511; F:ubiquitin-dependent protein catabolism; IEA.
DR InterPro; IPR001394; Peptidase_C19.
DR Pfam; PF00443; UCH; 1.
DR PROSITE; PS00972; UCH_2_1; 1.
DR PROSITE; PS00973; UCH_2_2; UNKNOWN_1.
DR PROSITE; PS50235; UCH_2_3; 1.
SQ SEQUENCE 1298 AA; 141590 MW; 44D4C7CB21B05257 CRC64;

Query Match 62.1%; Score 41; DB 2; Length 1298;
Best Local Similarity 61.5%; Pred. No. 4e+02;
Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGSTNIGNNVYS 13
DB 924 SGSSNSGDMHVS 936

RESULT 33
ID 0811A0 PRELIMINARY; PRT; 1336 AA.
AC 0811A0;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE CG30421-PA.
GN ORFNames=CG30421;
OS Drosophila virilis (Fruit Fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7244;
RN
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Tucson 15010-1001.10;
RA Bergman C.M., Pfeiffer B.D., Rincon-Limas D.E., Hoskins R.A.,
RA Gaitre A., Mungall C.J., Wang A.M., Krommiller B., Pacleb J., Park S.,
RA Stapleton M., Wan K., George R.A., de Jong P.J., Botas J., Rubin G.M.,
RA Celniker S.E.;
RT "Assessing the impact of comparative genomic sequence data on the
RT functional annotation of the Drosophila genome.";
RL Genome Biol. 3:research0086-research0086(2002).
DR EMBL; AY190953; AAC01072.1; -.
DR HSSP; Q93009; INBF.
DR FlyBase; FBgn0064534; Dlit\CG30421.
DR GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.
DR GO; GO:0004221; F:ubiquitin thiolesterase activity; IEA.
DR GO; GO:0006511; F:ubiquitin-dependent protein catabolism; IEA.
DR InterPro; IPR001394; Peptidase_C19.
DR Pfam; PF00443; UCH; 1.
DR PROSITE; PS00972; UCH_2_1; 1.
DR PROSITE; PS00973; UCH_2_2; UNKNOWN_1.
DR PROSITE; PS50235; UCH_2_3; 1.
SQ SEQUENCE 1336 AA; 144636 MW; ABBB15BAE6F4CA66 CRC64;

Query Match 62.1%; Score 41; DB 2; Length 1336;
Best Local Similarity 61.5%; Pred. No. 4.1e+02;
Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGSTNIGNNVYS 13
DB 965 SGSSNSGDMHVS 977

RESULT 34
ID 081150 PRELIMINARY; PRT; 1701 AA.
AC 081150;

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DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical protein.
GN ORFNames=PF11_0324;
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Paul N., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.S., Nene V., Shalimov S.J., Sub B., Peterson J., Anguoli S.,
RA Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
RA Martin D.M., Fairhead A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McEvedy G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrell B.;
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum."
RL Nature 419:498-511(2002).
RW EMBL; AE014840; AAN35908.1; -
KW Hypothetical protein.
SQ SEQUENCE 1701 AA; 206848 MW; B7823F1A5CEC9B7 CRC64;

Query Match 62.1%; Score 41; DB 2; Length 1701;
Best Local Similarity 63.6%; Pred. No. 5.2e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 STSNIGNNYVS 13
Db 1306 SNNNISNNYIS 1316

RESULT 35
LV1F HUMAN STANDARD; PRT; 109 AA.
ID LV1F_HUMAN
AC P04208;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig lambda chain V-I region WAH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=83221661; PubMed=6407018;
RA Takahashi Y., Takahashi N., Tetaert D., Putnam F.W.;
RT "Complete covalent structure of a human immunoglobulin D: sequence of
RT the lambda light chain."
RL Proc. Natl. Acad. Sci. U.S.A. 80:3686-3690(1983).
DR PIR; A01967; LIHUMA.
DR HSSP; P01703; 7PAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; Igv_1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 97
FT DOMAIN 98 109 V segment.
FT DISULFID 22 89 J segment.
FT NON TER 109 109 By similarity.
SQ SEQUENCE 109 AA; 11725 MW; B17785F6A8DF9BAC CRC64;

Query Match 60.6%; Score 40; DB 1; Length 109;

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Best Local Similarity 72.7%; Pred. No. 48;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GSTSNIGNNYV 12
Db 24 GSSSNIGNRYV 34

RESULT 36
LV1B HUMAN STANDARD; PRT; 112 AA.
ID LV1B_HUMAN
AC P01700;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig lambda chain V-I region HA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=71103824; PubMed=5532227;
RA Shinoda T., Titani K., Putnam F.W.;
RT "Amino acid sequence of human lambda chains. II. Chymotryptic peptides
RT and sequence of protein Ha."
RL J. Biol. Chem. 245:4475-4487(1970).
CC -I- MISCELLANEOUS: This is a Bence-Jones protein.
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A01963; LIHUMA.
DR HSSP; P01703; 7PAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; Igv_1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region; Pyrolydione carboxylic acid.
FT DOMAIN 1 106
FT MOD RES 1 90 Pyrolydione carboxylic acid.
FT DISULFID 22 90 By similarity.
FT NON TER 112 112
SQ SEQUENCE 112 AA; 11896 MW; 8D73378F5CD039 CRC64;

Query Match 60.6%; Score 40; DB 1; Length 112;
Best Local Similarity 63.6%; Pred. No. 50;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GSTSNIGNNYV 12
Db 25 GSSNGTGNVYV 35

RESULT 37
O8GFB2 PRELIMINARY; PRT; 159 AA.
ID O8GFB2
AC O8GFB2;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Orf23.
GN Name=orf23;
OS Photorhabdus luminescens (Xenorhabdus luminescens).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photorhabdus.
OX NCBI_TaxID=23486;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=W14;
RX MEDLINE=21185117; PubMed=11286884; DOI=10.1016/S0966-842X(01)01978-3;

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RA Waterfield N.R., Bowen D.J., Fetherston J.D., Perry R.D.,
 RA ffrench-Constant R.H.;
 RT "The *tc* genes of *Photobacterium*: a growing family.";
 RL *Trends Microbiol.* 9:185-191(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NA4;
 RX MEDLINE=22454990; PubMed=12564983; DOI=10.1016/S0966-842X(02)02463-0;
 RA Waterfield N.R., Daborn P.J., ffrench-Constant R.H.;
 RT "Genomic islands in *Photobacterium*.";
 RL *Trends Microbiol.* 10:541-545(2002).
 DR EMBL: AF346500; AAC07189.1; -
 DR InterPro: IPR006514; DUF796.
 DR Pfam: PF05638; DUF796; 1.
 SQ SEQUENCE 159 AA; 18032 MW; FF35A023A8913ADC CRC64;
 Query Match 60.6%; Score 40; DB 2; Length 159;
 Best Local Similarity 70.0%; Pred. No. 71;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 2 GSTSNIGNNY 11
 DB 22 GSTSNIGNNY 31
 RESULT 38
 ID 076611 PRELIMINARY; PRT; 314 AA.
 AC 076611;
 DT 01-NOV-1998 (TRENDBL. 08, Created)
 DT 01-MAR-2003 (TRENDBL. 23, Last sequence update)
 DT 01-OCT-2003 (TRENDBL. 25, Last annotation update)
 DE Hypothetical protein T07H3.6.
 GN Name=T07H3.6; ORFNames=T07H3.6;
 OS *Caenorhabditis elegans*.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
 OC Rhabditidae; Peloderinae; *Caenorhabditis*.
 NC NCBI_TaxID=6239;
 RX MEDLINE=9069613; PubMed=9851916;
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX WormBase Consortium;
 RG "Genome sequence of the nematode *C. elegans*: a platform for
 RT investigating biology. The *C. elegans* Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Beck C., O'Brien D., Kramer J.;
 RT "The sequence of *C. elegans* cosmid T07H3.";
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Wilson R.;
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RG WormBase Consortium;
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF077540; AAC26307.2; -
 DR PIR: T33378; T33378.
 DR WormBase: WBGene00020329; T07H3.6.
 DR WormPep: T07H3.6; CE32065.
 DR InterPro: IPR002083; MATH.
 DR InterPro: IPR008974; Traf_like;
 RP

DR Pfam: PF00917; MATH; 1.
 DR SMART: SM00061; MATH; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 314 AA; 35980 MW; 47496DB8B1B09C11C CRC64;
 Query Match 60.6%; Score 40; DB 2; Length 314;
 Best Local Similarity 72.7%; Pred. No. 1.4e+02;
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 3 STSNIGNNYVS 13
 DB 34 STSNIGNNYVS 44
 RESULT 39
 ID 08W1R8 PRELIMINARY; PRT; 315 AA.
 AC 08W1R8;
 DT 01-MAR-2002 (TRENDBL. 20, Created)
 DT 01-MAR-2002 (TRENDBL. 20, Last sequence update)
 DT 01-MAR-2004 (TRENDBL. 26, Last annotation update)
 DE Blind.
 OS *Lycopersicon esculentum* (Tomato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Solanales; Solanaceae; Solanum.
 NC NCBI_TaxID=4081;
 RX PubMed=11805344; DOI=10.1073/pnas.022516199;
 RA Schmitz G., Tillmann B., Carriero F., Fiore C., Cellini F., Theres K.;
 RT "The tomato *Blind* gene encodes a MYB transcription factor that
 RT controls the formation of lateral meristems.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:1064-1069(2002).
 CC 1-1 SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC 1-1 SIMILARITY: Contains 2 Myb-like domains.
 DR EMBL: AF426174; AAL6934.1; -
 DR HSSP: P06876; IMBX.
 DR TRANSFAC: T05529; -
 DR GO: GO:0005634; C:nucleus; IEA.
 DR GO: GO:0003677; F:DNA binding; IEA.
 DR Pfam: PF00249; Myb DNA-binding; 2.
 DR SMART: SM00717; SANT; 2.
 DR PROSITE: PS00037; MYB_1; UNKNOWN_1.
 DR PROSITE: PS00334; MYB_2; 1.
 DR PROSITE: PS50090; MYB_3; 2.
 KW Nuclear protein.
 SQ SEQUENCE 315 AA; 35518 MW; 8FD393A69BBD97B6 CRC64;
 Query Match 60.6%; Score 40; DB 2; Length 315;
 Best Local Similarity 58.3%; Pred. No. 1.4e+02;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 1 SGSTSNIGNNYV 12
 DB 285 SGSTSNIGNNYV 296
 RESULT 40
 ID 08F1Z5 PRELIMINARY; PRT; 410 AA.
 AC 08F1Z5;
 DT 01-MAR-2003 (TRENDBL. 23, Created)
 DT 01-MAR-2003 (TRENDBL. 23, Last sequence update)
 DT 01-MAR-2003 (TRENDBL. 23, Last annotation update)
 DE Hypothetical protein ci206.
 GN OrderedLocNames=ci206;
 OS *Escherichia coli* O6.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; *Escherichia*.
 NC NCBI_TaxID=217992;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=06:H1 / CFT073 / ATCC 700928 / UPEC;
 RX MEDLINE=22388234; PubMed=12471157; DOI=10.1073/pnas.252529799;
 RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
 RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackert J., Stroud D.,
 RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
 RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
 RT "Extensive mosaic structure revealed by the complete genome sequence
 of uropathogenic Escherichia coli.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
 DR EMBL; AE016758; AAN79668.1; -.
 KM Complete proteome.
 SQ SEQUENCE 410 AA; 41613 MM; 958A652E860819DD CRC64;

Query Match 60.6%; Score 40; DB 2; Length 410;
 Best Local Similarity 80.0%; Pred. No. 1.8e+02;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SGGSTNIGNN 10
 |||||
 Db 212 SGGSTLNAGNN 221

Search completed: March 31, 2005, 12:09:43
 Job time : 88.4948 secs

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OM protein - protein search, using sw model

Run on: March 31, 2005, 11:42:18 ; Search time 54.25 Seconds
(without alignments)
49.905 Million cell updates/sec

Title: US-10-614-959-14
Perfect score: 35
Sequence: 1 DVSKRPS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues
Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	7	3	AA79072 Anti-fact
2	35	100.0	99	7	ADJ80338 Vlamda g
3	35	100.0	109	4	AAU02544 Anti-adip
4	35	100.0	110	3	AA796060 Human ant
5	35	100.0	110	4	AAU02558 Anti-adip
6	35	100.0	110	4	AAU02612 Anti-adip
7	35	100.0	110	4	AAU02627 Anti-adip
8	35	100.0	110	4	AAU02629 Anti-adip
9	35	100.0	111	2	AAU19883 CEA-speci
10	35	100.0	111	4	AAU02542 Anti-adip
11	35	100.0	111	4	AAU02551 Anti-adip
12	35	100.0	111	4	AAU02585 Anti-adip
13	35	100.0	111	7	ADK17416 Anti-huma
14	35	100.0	111	8	ADG42838 scry Ab12
15	35	100.0	214	8	ABM85072 Human dia
16	35	100.0	236	8	ABM85084 Human dia
17	35	100.0	240	5	ABP45887 Human Bly
18	35	100.0	240	7	ADG96714 Single ch
19	35	100.0	241	5	ADG96871 Human Bly
20	35	100.0	241	8	ADG34307 Single ch
21	35	100.0	242	8	ADG34317 Neurokini
22	35	100.0	242	8	ADG34317 Neurokini
23	35	100.0	243	5	ADG96743 Human Bly
24	35	100.0	243	7	ADG96743 Single ch
25	35	100.0	243	8	ADG34310 Neurokini

26	35	100.0	243	8	ADG34306 Neurokini
27	35	100.0	244	8	ADG34303 Neurokini
28	35	100.0	245	5	ABP45915 Human Bly
29	35	100.0	245	7	ADG96742 Single ch
30	35	100.0	245	7	ADG98057 TNF proli
31	35	100.0	245	8	ADG83862 Chemokine
32	35	100.0	245	8	ADG34308 Neurokini
33	35	100.0	245	8	ADG34313 Neurokini
34	35	100.0	246	5	ABP45902 Human Bly
35	35	100.0	246	5	ABP45906 Human Bly
36	35	100.0	246	7	ADG96733 Single ch
37	35	100.0	246	7	ADG96729 Single ch
38	35	100.0	246	8	ADG83872 Chemokine
39	35	100.0	247	5	ABP45671 Human Bly
40	35	100.0	247	5	ABP45674 Human Bly
41	35	100.0	247	5	ABP45432 Human Bly
42	35	100.0	247	5	ABP45923 Human Bly
43	35	100.0	247	5	ABP45917 Human Bly
44	35	100.0	247	5	ABP45696 Human Bly
45	35	100.0	247	5	ABP45888 Human Bly

ALIGNMENTS

RESULT 1	AA79072	standard; peptide; 7 AA.
ID	AA79072	
XX	AA79072;	
AC	12-JUN-2000	(first entry)
DT		
XX		
DE	Anti-factor IX/IXa antibody L chain V domain CDR2 amino acid sequence.	
XX		
KW	Complementarity determining region 2; CDR2; antibody; Gla domain;	
KW	factor IX/IXa; blood coagulation; deep venous thrombosis; light chain;	
KW	arterial thrombosis; unstable angina; post myocardial infarction;	
KW	coronary artery bypass graft; CABG; stroke; tumour growth; metastasis;	
KW	percutaneous transluminal coronary angioplasty; PTCA; inflammation;	
KW	septic shock; hypotension; adult respiratory distress syndrome; ARDS;	
KW	arterial fibrillation; disseminated intravascular coagulopathy; DIC.	
XX		
OS	Homo sapiens.	
XX		
PN	W0200012562-A1.	
PD	09-MAR-2000.	
XX		
PF	26-AUG-1999; 99WO-US019453.	
XX		
PR	28-AUG-1998; 98US-0098233P.	
XX	03-MAR-1999; 99US-0122767P.	
PA	(GETH) GENENTECH INC.	
XX		
PI	Adams CW, Devaux B, Eaton DL, Haas PE, Judice JK, Kirchhofer D;	
PT	Suggest S;	
XX		
DR	WPI: 2000-256595/22.	
XX		
PT	Novel human anti-Factor IX/IXa antibodies against IX/IXa gamma-	
PT	carboxyglutamic acid domains useful as anti-coagulant in thrombosis,	
PT	stroke, and post myocardial infarction.	
XX		
PS	Claim 8; Fig 2; 84pp; English.	
XX		
CC	This sequence represents a complementarity determining region 2 (CDR2) of	
CC	the light chain variable domain of a human anti-factor IX/IXa Gla domain	
CC	antibody. Factor IXa is a vitamin K dependent plasma serine protease that	
CC	participates in the blood coagulation pathways. The Gla domain of factor	
CC	IXa and its zymogen factor IX contains important structural determinants	
CC	for interaction with high affinity binding sites on vascular endothelial	

CC cells and platelets. Compositions comprising the antibodies are used for
CC the treatment or prophylaxis of thrombotic or coagulopathic diseases or
CC disorders in a mammal for which inhibiting a FIX/IXa mediated event is
CC indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable
CC angina, post myocardial infarction, post surgical thrombosis, coronary
CC artery bypass graft (CABG), percutaneous transluminal coronary
CC angioplasty (PTCA), stroke, tumour growth, invasion or metastasis,
CC inflammation, septic shock, hypotension, adult respiratory distress
CC syndrome (ARDS), arterial fibrillation and disseminated intravascular
CC coagulopathy (DIC)

XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 35; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
DB 1 DVSKRPS 7

RESULT 2
ADJ80338
ID ADJ80338 standard; protein; 99 AA.
XX
AC ADJ80338;
XX
DT 06-MAY-2004 (first entry)
XX
DE Vlamda gene locus antibody amino acid sequence #7.
XX
KM hybrid antibody; antibody; framework region; homology; immunogenicity.
XX
OS Homo sapiens.
XX
PN WO2003048321-A2.
XX
PD 12-JUN-2003.
XX
PF 03-DEC-2002; 2002MO-US038450.
XX
PR 03-DEC-2001; 2001US-0336591P.
XX
PA (ALEX-) ALEXION PHARM INC.
XX
PI Rother R, Wu D;
XX
DR WPI; 2003-513753/48.
XX
PT Producing a hybrid antibody or hybrid antibody fragment by operatively
XX linking the selected framework sequences to one or more complementarity
XX determining regions of the initial antibody.
XX
PS Disclosure; SEQ ID NO 98; 77pp; English.

CC The invention relates to a method of producing a hybrid antibody or
CC hybrid antibody fragment by: (i) providing an initial antibody having
CC specificity for a target; (ii) determining the sequence of a variable
CC region of the initial antibody; (iii) selecting a first component of the
CC variable region consisting of FR1, FR2, FR3 and FR4; (iv) comparing the
CC sequence of the first component to sequences contained in a reference
CC database of antibody sequences or antibody fragment sequences from a
CC target species; (v) selecting a sequence from an antibody in the database
CC which demonstrates a high degree of homology to the first component; (vi)
CC selecting a second component of the variable region which is different
CC than the first component; the second component selected from the group
CC consisting of FR1, FR2, FR3 and FR4; (vii) comparing the sequence of the
CC second component to sequences contained in a reference database of
CC antibody sequences or antibody fragment sequences from the target species
CC; (viii) selecting a sequence from the database which demonstrates a high
CC degree of homology to the second component and which is from a different
CC antibody than the selected antibody; and (ix) operatively linking the

CC selected framework sequences to one or more complementarity determining
CC regions (CDRs) of the initial antibody to produce a hybrid antibody or
CC hybrid antibody fragment. The method is useful for producing a hybrid
CC antibody or hybrid antibody fragment (clonated). The antibody and
CC fragments are useful for therapeutic and diagnostic purposes. The method
CC uses entire framework regions from a single antibody variable heavy or
CC variable light chain to receive the CDRs. This produces antibodies that
CC are highly homologous and exhibit reduced immunogenicity while
CC maintaining an optimum binding profile. This sequence represents the
CC amino acid sequence of an antibody from the Vlamda gene locus.

XX
SQ Sequence 99 AA;

Query Match 100.0%; Score 35; DB 7; Length 99;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
DB 52 DVSKRPS 58

RESULT 3
AAU02544
ID AAU02544 standard; protein; 109 AA.
XX
AC AAU02544;
XX
DT 29-AUG-2001 (first entry)
XX
DE Anti-adipocyte monoclonal antibody light chain, FAT 31.
XX
KM Antibody; adipocyte; heavy chain; light chain; obesity; fat;
XX heart disease; complementarity determining region; CDR.
XX
OS Homo sapiens.
XX
PN WO200127279-A1.
XX
PD 19-APR-2001.
XX
PF 11-OCT-2000; 2000MO-GB003900.
XX
PR 12-OCT-1999; 99US-0158812P.
XX
PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Edwards BM, Main SH, Vaughan TJ;
XX
DR WPI; 2001-282031/29.
XX
DR N-PSDB; AAS03444.
XX
PT Panel of specific binding members of antibody molecules which bind to
XX whole adipocytes is used in the treatment of obesity and obesity related
XX diseases.
XX
PS Claim 1; Page 120; 182pp; English.

CC AAU02501-AA102635, and AAU02641-AAU02748 represent the amino acid
CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
CC and heavy chain complementarity determining regions (CDR) of the
CC invention. The antibodies can be used in the treatment of obesity and
CC obesity related diseases. The antibodies can be used to deliver drugs or
CC pro-drugs directly to the fat mass of an obese patient or the antibody
CC can be used as a therapeutic itself. Antibodies binding specifically to
CC adipocytes can be used to activate the immune system to destroy the cells
CC by complement mediated lysis. The antibodies may be labeled with a
CC detectable label such as radiolabel, fluorescent or chemical group and
CC used in methods of diagnosis in human subjects e.g. to determine the
CC presence of adipocyte antigen on the surface of an adipocyte to detect or
CC determine the presence or level of adipocytes in a cell or tissue sample.
CC The antibodies can be used as an alternative means of treatment for obese
CC patients other than undergoing surgery to remove excess fat. Antibodies

CC for different types of fat deposits can also be produced e.g. intra-
CC abdominal fat associated with heart disease
XX
SQ Sequence 109 AA;

Query Match 100.0%; Score 35; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
Db 51 DVSKRPS 57

RESULT 4

AAV96060
ID AAV96060 standard; protein; 110 AA.

XX AAV96060;

DT 05-DEC-2000 (first entry)

XX Human anti-DAF antibody LU30 light chain variable region.

XX LU30; human; antibody; VL domain; decay accelerating factor; DAF;

KM phage display; subtractive panning; lung cancer; lung carcinoma;

XX lung adenocarcinoma; therapy; diagnosis.

OS Homo sapiens.

XX Key Location/Qualifiers

FT 23..36 /label=CDRI

FT /note="complementarity determining region I"

FT 25..35 /note="hypervariable loop region"

FT 52..58 /label=CDRII

FT /note="complementarity determining region II"

FT 52..54 /note="hypervariable loop residues"

FT 91..100 /label=CDRIII

FT /note="complementarity determining region III"

FT 93..99 /note="hypervariable loop residues"

XX WO200052054-A2.

XX 08-SEP-2000.

XX 29-FEB-2000; 2000WO-US005352.

XX 01-MAR-1999; 99US-0122262P.

XX (GETH) GENENTECH INC.

XX Carter PJ, Ridgway JB;

XX WPI; 2000-594169/56.

XX Making antibodies (e.g. anti-decay accelerating factor antibody) for

XX diagnosing or treating e.g. lung cancer comprises identifying an antigen

XX that is differentially expressed on the surface of two or more distinct

XX cell populations.
XX Disclosure; Fig 5A; 52pp; English.
XX The present sequence is that of the light chain variable region (VL) of
XX the anti-decay accelerating factor (DAF) human antibody LU30. The VH of
XX region is given in AAV96063. LU30 has a binding affinity (Kd) for DAF of
XX about 13 nM. It was produced using a novel method for making antibodies
XX which can be used for cancer diagnosis or therapy. The method comprises:

CC (a) binding an antibody phage from a naive antibody phage library to a
CC live cancer cell; (b) selecting an antibody phage or antibody which binds
CC selectively to the live cancer cell; and (c) identifying an antigen to
CC which the antibody phage or antibody binds. To obtain LU30, a human scFv
CC library was used to search for tumour-associated antigens by panning the
CC lung adenocarcinoma cell line 1264, and counter-selecting with a non-
CC tumour bronchial epithelial cell line, BEAS-2B. The invention also
CC describes a method for identifying an antigen which is differentially
CC expressed on the surface of 2 or more distinct cell populations. The anti-
CC -DAF human antibody, or a composition comprising the antibody, is useful
CC for in vivo cancer diagnosis or therapy. In particular, the antibody is
CC useful for diagnosing or treating lung cancer; e.g. small-cell lung
CC cancer, non-small cell lung cancer, large cell lung carcinoma, lung
CC adenocarcinoma, or squamous cell lung carcinoma (all claimed)

XX SQ Sequence 110 AA;

Query Match 100.0%; Score 35; DB 3; Length 110;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
Db 52 DVSKRPS 58

RESULT 5

AAU02558
ID AAU02558 standard; protein; 110 AA.

XX AAU02558;

DT 29-AUG-2001 (first entry)

XX Anti-adipocyte monoclonal antibody light chain, PAT 44.

KM Antibody; adipocyte; heavy chain; light chain; obesity; fat;

XX heart disease; complementarity determining region; CDR.

XX Homo sapiens.

XX WO200127279-A1.

XX 19-APR-2001.

XX 11-OCT-2000; 2000WO-GB003900.

XX 12-OCT-1999; 99US-0158812P.

XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Edwards BM, Main SH, Vaughan TJ;

XX WPI; 2001-282031/29.

XX N-PSDB; AAS03458.

XX Panel of specific binding members of antibody molecules which bind to

XX whole adipocytes is used in the treatment of obesity and obesity related

XX diseases.
XX Claim 1; Page 128-129; 182pp; English.

XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid

XX sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,

XX and heavy chain complementarity determining regions (CDR) of the

XX invention. The antibodies can be used in the treatment of obesity and

XX obesity related diseases. The antibodies can be used to deliver drugs or

XX pro-drugs directly to the fat mass of an obese patient or the antibody

XX can be used as a therapeutic itself. Antibodies binding specifically to

XX adipocytes can be used to activate the immune system to destroy the cells

XX by complement mediated lysis. The antibodies may be labeled with a

XX detectable label such as radiolabel, fluorescent or chemical group and

XX used in methods of diagnosis in human subjects e.g. to determine the

CC presence of adipocyte antigen on the surface of an adipocyte to detect or
CC determine the presence or level of adipocytes in a cell or tissue sample.
CC The antibodies can be used as an alternative means of treatment for obese
CC patients other than undergoing surgery to remove excess fat. Antibodies
CC for different types of fat deposits can also be produced e.g. intra-
CC abdominal fat associated with heart disease
CC
XX Sequence 110 AA;
SQ

Query Match 100.0%; Score 35; DB 4; Length 110;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DVSKRPS 7
| | | | |
DB 51 DVSKRPS 57

RESULT 6

AAU02612 ID AAU02612 standard; protein: 110 AA.

XX AC AAU02612;

XX DT 29-AUG-2001 (first entry)

XX DE Anti-adipocyte monoclonal antibody light chain, FAT 99.

XX KW Antibody; adipocyte; heavy chain; light chain; obesity; fat;
XX heart disease; complementarity determining region; CDR.

XX OS Homo sapiens.

XX PN W0200127279-A1.

XX PD 19-APR-2001.

XX PF 11-OCT-2000; 2000WO-GB003900.

XX PR 12-OCT-1999; 99US-0158812P.

XX PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX PI Edwards BM, Main SH, Vaughan TJ;

XX DR WPI, 2001-282031/29.

XX DR N-PSDB; AAS03512.

PT Panel of specific binding members of antibody molecules which bind to
PT whole adipocytes is used in the treatment of obesity and obesity related
PT diseases.

XX Claim 1; Page 163; 182pp; English.

XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
XX sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
XX and heavy chain complementarity determining regions (CDR) of the
XX invention. The antibodies can be used in the treatment of obesity and
XX obesity related diseases. The antibodies can be used to deliver drugs or
XX pro-drugs directly to the fat mass of an obese patient or the antibody
XX can be used as a therapeutic itself. Antibodies binding specifically to
XX adipocytes can be used to activate the immune system to destroy the cells
XX by complement mediated lysis. The antibodies may be labeled with a
XX detectable label such as radiolabel, fluorescent or chemical group and
XX used in methods of diagnosis in human subjects e.g. to determine the
XX presence of adipocyte antigen on the surface of an adipocyte to detect or
XX determine the presence or level of adipocytes in a cell or tissue sample.
XX The antibodies can be used as an alternative means of treatment for obese
XX patients other than undergoing surgery to remove excess fat. Antibodies
XX for different types of fat deposits can also be produced e.g. intra-
XX abdominal fat associated with heart disease
XX
XX Sequence 110 AA;
SQ

Query Match 100.0%; Score 35; DB 4; Length 110;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DVSKRPS 7
| | | | |
DB 51 DVSKRPS 57

RESULT 7

AAU02627 ID AAU02627 standard; protein: 110 AA.

XX AC AAU02627;

XX DT 29-AUG-2001 (first entry)

XX DE Anti-adipocyte monoclonal antibody light chain, FAT 112.

XX KW Antibody; adipocyte; heavy chain; light chain; obesity; fat;
XX heart disease; complementarity determining region; CDR.

XX OS Homo sapiens.

XX PN W0200127279-A1.

XX PD 19-APR-2001.

XX PF 11-OCT-2000; 2000WO-GB003900.

XX PR 12-OCT-1999; 99US-0158812P.

XX PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX PI Edwards BM, Main SH, Vaughan TJ;

XX DR WPI, 2001-282031/29.

XX DR N-PSDB; AAS03527.

PT Panel of specific binding members of antibody molecules which bind to
PT whole adipocytes is used in the treatment of obesity and obesity related
PT diseases.

XX Claim 1; Page 172; 182pp; English.

XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
XX sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
XX and heavy chain complementarity determining regions (CDR) of the
XX invention. The antibodies can be used in the treatment of obesity and
XX obesity related diseases. The antibodies can be used to deliver drugs or
XX pro-drugs directly to the fat mass of an obese patient or the antibody
XX can be used as a therapeutic itself. Antibodies binding specifically to
XX adipocytes can be used to activate the immune system to destroy the cells
XX by complement mediated lysis. The antibodies may be labeled with a
XX detectable label such as radiolabel, fluorescent or chemical group and
XX used in methods of diagnosis in human subjects e.g. to determine the
XX presence of adipocyte antigen on the surface of an adipocyte to detect or
XX determine the presence or level of adipocytes in a cell or tissue sample.
XX The antibodies can be used as an alternative means of treatment for obese
XX patients other than undergoing surgery to remove excess fat. Antibodies
XX for different types of fat deposits can also be produced e.g. intra-
XX abdominal fat associated with heart disease
XX
XX Sequence 110 AA;
SQ

Query Match 100.0%; Score 35; DB 4; Length 110;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DVSKRPS 7
| | | | |
DB 51 DVSKRPS 57

```

XX RESULT 8
XX AAU02629 ID AAU02629 standard; protein, 110 AA.
XX AC AAU02629;
XX DT 29-AUG-2001 (first entry)
XX DE Anti-adipocyte monoclonal antibody light chain, FAT 113.
XX KM Antibody; adipocyte; heavy chain; light chain; obesity; fat;
XX KW heart disease; complementarity determining region; CDR.
XX OS Homo sapiens.
XX WO200127279-A1.
XX PN 19-APR-2001.
XX PD 11-OCT-2000; 2000WO-GB003900.
XX PF 12-OCT-1999; 99US-0158812P.
XX PR (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX PA Edwards BW, Main SH, Vaughan TJ;
XX PI WPI; 2001-282031/29.
XX DR N-PSDB; AAS03529.
XX PT Panel of specific binding members of antibody molecules which bind to
XX PR whole adipocytes is used in the treatment of obesity and obesity related
XX PS diseases.
XX PS Claim 1; Page 173; 182pp; English.
CC AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
CC and heavy chain complementarity determining regions (CDR) of the
CC invention. The antibodies can be used in the treatment of obesity and
CC obesity related diseases. The antibodies can be used to deliver drugs or
CC pro-drugs directly to the fat mass of an obese patient or the antibody
CC can be used as a therapeutic itself. Antibodies binding specifically to
CC adipocytes can be used to activate the immune system to destroy the cells
CC by complement mediated lysis. The antibodies may be labeled with a
CC detectable label such as radiolabel, fluorescent or chemical group and
CC used in methods of diagnosis in human subjects e.g. to determine the
CC presence of adipocyte antigen on the surface of an adipocyte to detect or
CC determine the presence or level of adipocytes in a cell or tissue sample.
CC The antibodies can be used as an alternative means of treatment for obese
CC patients other than undergoing surgery to remove excess fat. Antibodies
CC for different types of fat deposits can also be produced e.g. intra-
CC abdominal fat associated with heart disease
XX SQ Sequence 110 AA;
XX
XX Query Match 100.0%; Score 35; DB 4; Length 110;
XX Best Local Similarity 100.0%; Pred. No. 6.1;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0,
XX QY 1 DVSKRPS 7
XX Db |||||
XX 51 DVSKRPS 57
XX
XX RESULT 9
XX AAM19883 ID AAM19883 standard; protein, 111 AA.
XX AC AAM19883;
XX NC AAM19883;
XX
```

DT	07-DEC-1997	(first entry)
DE	CEA-specific antibody CEA1, CEA2, CEA3 VL sequence.	
XX		
XX	Carcinoembryonic antigen; CEA; human; antibody; scFv; tumour marker;	
KW	Lung cancer; breast cancer; colon cancer; adenocarcinoma; diagnosis.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	
FT	Region	
FT	/label= CDR1	
FT	/note= "complementarity determining region 1"	
FT	Region	
FT	/label= CDR2	
FT	/note= "complementarity determining region 2"	
FT	/label= CDR3	
FT	/note= "complementarity determining region 3"	
PN	WO9720932-A1.	
PD	12-JUN-1997.	
XX		
PF	09-DEC-1996; 96WO-GB003043.	
PR	07-DEC-1995; 95GB-00025004.	
PR	23-MAY-1996; 96GB-00010824.	
PR	11-OCT-1996; 96GB-00021295.	
XX		
PA	(CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.	
XX		
PI	Osbourn JK, Allen DJ, McCafferty JG;	
XX		
DR	WPI; 1997-319779/29.	
XX	N-PsDB; AAT72133.	
PT	Specific binding members for human carcinoembryonic antigen - bind to the	
PT	A3-B3 extracellular domain of hCEA and are substantially non-cross-	
PT	reactive with human liver cells; used for diagnosing cancer.	
XX		
PS	Claim 14; Fig 1b; 128pp; English.	
XX		
CC	This polypeptide sequence comprises the light chain variable region (VL)	
CC	of human carcinoembryonic antigen (hCEA)-specific antibodies CEA1, CEA2	
CC	and CEA3. VH (AAT72126-32) and VL (AAT72133-35) gene sequences were	
CC	obtained for anti-hCEA antibodies CEA1-CEA7 (see AAU19876-85). A claimed	
CC	specific binding member (A) comprises an hCEA specific antibody antigen	
CC	binding domain that has a dissociation constant for hCEA of less than 1 x	
CC	10 ⁻⁸ M, is non-cross-reactive with human liver cells, and	
CC	preferentially binds to the A3-B3 extracellular domain of hCEA and/or to	
CC	cell-associated hCEA over hCEA over soluble hCEA. Preferred (A) include	
CC	painings of VH and VL sequences from CEA1-7, or their CDR sequences, as	
CC	well as CEA6 VH and VL variants. (A) is used to detect cells expressing	
CC	hCEA, in vivo or in vitro, especially tumour cells for diagnosing cancer,	
CC	e.g. adenocarcinoma of the colon, lung or breast	
XX		
SQ	Sequence 111 AA;	
Query Match	100.0%; Score 35; DB 2; Length 111;	
Best Local Similarity	100.0%; Pred. No. 6.1;	
Matches 7; Conservative	0; Mismatches 0; Indels 0; Gaps 0.	
OY	1 DVSKRPS 7 	
Db	51 DVSKRPS 57	
RESULT 10		
ID	AAU02542 standard; protein; 111 AA.	
XX		
AC	AAU02542;	

XX 29-AUG-2001 (first entry)
 DT Anti-adipocyte monoclonal antibody light chain, FAT 30.
 XX
 DE Antibody; adipocyte; heavy chain; light chain; obesity; fat;
 XX heart disease; complementarity determining region; CDR.
 XX
 OS Homo sapiens.
 XX WO200127279-A1.
 XX
 PN 19-APR-2001.
 XX
 PD 11-OCT-2000; 2000WO-GB003900.
 XX
 PF 12-OCT-1999; 99US-0158812P.
 XX
 PR (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX
 PA Edwards BM, Main SH, Vaughan TJ;
 XX WPI; 2001-282031/29.
 XX N-PSDB; AAS03442.
 DR
 DR Panel of specific binding members of antibody molecules which bind to
 PT whole adipocytes is used in the treatment of obesity and obesity related
 PT diseases.
 XX
 XX Claim 1; Page 118-119; 182pp; English.
 PS
 XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
 CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
 CC and heavy chain complementarity determining regions (CDR) of the
 CC invention. The antibodies can be used in the treatment of obesity and
 CC obesity related diseases. The antibodies can be used to deliver drugs or
 CC pro-drugs directly to the fat mass of an obese patient or the antibody
 CC can be used as a therapeutic itself. Antibodies binding specifically to
 CC adipocytes can be used to activate the immune system to destroy the cells
 CC by complement mediated lysis. The antibodies may be labeled with a
 CC detectable label such as radiolabel, fluorescent or chemical group and
 CC used in methods of diagnosis in human subjects e.g. to determine the
 CC presence of adipocyte antigen on the surface of an adipocyte to detect or
 CC determine the presence or level of adipocytes in a cell or tissue sample.
 CC The antibodies can be used as an alternative means of treatment for obese
 CC patients other than undergoing surgery to remove excess fat. Antibodies
 CC for different types of fat deposits can also be produced e.g. intra-
 CC abdominal fat associated with heart disease
 CC
 CC Sequence 111 AA;
 SQ
 Query Match 100.0%; Score 35; DB 4; Length 111;
 Best Local Similarity 100.0%; Pred. No. 6.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DVSKRPS 7
 DB 51 DVSKRPS 57
 DB
 RESULT 11
 AAU02551
 ID AAU02551 standard; protein; 111 AA.
 XX
 XX AAU02551;
 XX
 DT 29-AUG-2001 (first entry)
 XX
 DE Anti-adipocyte monoclonal antibody light chain, FAT 37.
 XX
 DE Antibody; adipocyte; heavy chain; light chain; obesity; fat;
 KM heart disease; complementarity determining region; CDR.
 XX

OS Homo sapiens.
 XX
 XX WO200127279-A1.
 XX
 PN 19-APR-2001.
 XX
 PD 11-OCT-2000; 2000WO-GB003900.
 XX
 PF 12-OCT-1999; 99US-0158812P.
 XX
 PR (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX
 PA Edwards BM, Main SH, Vaughan TJ;
 XX WPI; 2001-282031/29.
 XX N-PSDB; AAS03451.
 DR
 DR Panel of specific binding members of antibody molecules which bind to
 PT whole adipocytes is used in the treatment of obesity and obesity related
 PT diseases.
 XX
 XX Claim 1; Page 124; 182pp; English.
 PS
 XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
 CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
 CC and heavy chain complementarity determining regions (CDR) of the
 CC invention. The antibodies can be used in the treatment of obesity and
 CC obesity related diseases. The antibodies can be used to deliver drugs or
 CC pro-drugs directly to the fat mass of an obese patient or the antibody
 CC can be used as a therapeutic itself. Antibodies binding specifically to
 CC adipocytes can be used to activate the immune system to destroy the cells
 CC by complement mediated lysis. The antibodies may be labeled with a
 CC detectable label such as radiolabel, fluorescent or chemical group and
 CC used in methods of diagnosis in human subjects e.g. to determine the
 CC presence of adipocyte antigen on the surface of an adipocyte to detect or
 CC determine the presence or level of adipocytes in a cell or tissue sample.
 CC The antibodies can be used as an alternative means of treatment for obese
 CC patients other than undergoing surgery to remove excess fat. Antibodies
 CC for different types of fat deposits can also be produced e.g. intra-
 CC abdominal fat associated with heart disease
 CC
 CC Sequence 111 AA;
 SQ
 Query Match 100.0%; Score 35; DB 4; Length 111;
 Best Local Similarity 100.0%; Pred. No. 6.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DVSKRPS 7
 DB 52 DVSKRPS 58
 DB
 RESULT 12
 AAU02585
 ID AAU02585 standard; protein; 111 AA.
 XX
 XX AAU02585;
 XX
 DT 29-AUG-2001 (first entry)
 XX
 DE Anti-adipocyte monoclonal antibody light chain, FAT 72.
 XX
 DE Antibody; adipocyte; heavy chain; light chain; obesity; fat;
 KM heart disease; complementarity determining region; CDR.
 XX
 XX Homo sapiens.
 XX
 XX WO200127279-A1.
 XX
 PN 19-APR-2001.
 XX
 PD 11-OCT-2000; 2000WO-GB003900.
 XX

PR 12-OCT-1999; 99US-0158812P.
XX
XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX Edwards BM, Main SH, Vaughan TV;
XX WPI; 2001-282031/29.
DR N-PSDB; AAS03485.
XX
XX Panel of specific binding members of antibody molecules which bind to
PT whole adipocytes is used in the treatment of obesity and obesity related
PT diseases.
XX
XX Claim 1; Page 146; 182pp; English.
XX
CC AAU02501-AAU02655, and AAU02641-AAU02748 represent the amino acid
CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
CC and heavy chain complementarity determining regions (CDR) of the
CC invention. The antibodies can be used in the treatment of obesity and
CC obesity related diseases. The antibodies can be used to deliver drugs or
CC pro-drugs directly to the fat mass of an obese patient or the antibody
CC can be used as a therapeutic itself. Antibodies binding specifically to
CC adipocytes can be used to activate the immune system to destroy the cells
CC by complement mediated lysis. The antibodies may be labeled with a
CC detectable label such as radiolabel, fluorescent or chemical group and
CC used in methods of diagnosis in human subjects e.g. to determine the
CC presence of adipocyte antigen on the surface of an adipocyte to detect or
CC determine the presence or level of adipocytes in a cell or tissue sample.
CC The antibodies can be used as an alternative means of treatment for obese
CC patients other than undergoing surgery to remove excess fat. Antibodies
CC for different types of fat deposits can also be produced e.g. intra-
CC abdominal fat associated with heart disease
XX
SQ Sequence 111 AA;

Query Match 100.0%; Score 35; DB 4; Length 111;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 51 DVSKRPS 57

RESULT 13
ADK17416
ID ADK17416 standard; protein; 111 AA.
XX
XX ADK17416;
XX
XX 06-MAY-2004 (first entry)
DT
XX Anti-human CXCR4 loop 6 ScFv antibody VI region.
DE
XX anti-HIV; cytosstatic; virucide; single chain antibody; yeast;
KM HIV; cancer; CCR5.
XX
XX Synthetic.
OS
XX WO2003066830-A2.
XX
XX 14-AUG-2003.
PD
XX 07-FEB-2003; 2003WO-US003763.
PF
XX 08-FEB-2002; 2002US-00071866.
PR 08-FEB-2002; 2002US-00072031.
PR 25-APR-2002; 2002US-00133978.
XX
XX (GENE-) GENETASTIX CORP.
PA
XX Hua S, Pauling MH, Zhu L;
PI
XX

DR WPI; 2003-731501/69.
XX
XX Selecting an scFv against a peptide target by expressing a target fusion
PT protein having a DNA binding domain or activation domain of a
PT transcription activator, useful for diagnosing, preventing and/or
PT treating HIV infection and cancer.
XX
XX Claim 123; SEQ ID NO 61; 150pp; English.
PS

XX The invention relates to a method of selecting a single chain antibody
CC (scFv) against a peptide target in a yeast by expressing a library of
CC scFv fusion proteins in yeast cells, expressing a target fusion protein
CC in the yeast cells expressing the scFv fusion proteins having either the
CC DNA binding domain or the activation domain of the transcription
CC activator which is not comprised in the scFv fusion proteins, and a
CC target peptide, and selecting those yeast cells in which a reporter gene
CC is expressed. Each scFv fusion protein comprises either an activation
CC domain or a DNA binding domain of a transcription activator and a scFv
CC having a heavy chain of a variable region (VH) of antibody whose sequence
CC varies within the library, a light chain of a variable region (VL) of
CC antibody whose sequence varies within the library independently of the VH
CC and a linker peptide which links the VH and VL. The expression of the
CC reporter gene is activated by a reconstituted transcriptional activator
CC formed by binding of the scFv fusion protein to the target fusion
CC protein. The methods and compositions of the present invention are useful
CC for preventing and/or treating HIV infection and cancer. This sequence
CC corresponds to the VI region of an anti-human CXCR4 loop 6 antibody gene
CC and used to generate the scFv antibody of the invention.
XX
SQ Sequence 111 AA;

Query Match 100.0%; Score 35; DB 7; Length 111;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 52 DVSKRPS 58

RESULT 14
ADG42838
ID ADG42838 standard; protein; 111 AA.
XX
XX ADG42838;
XX
XX 26-FEB-2004 (first entry)
DT
XX scFv Ab124 light chain variable region.
DE
XX
XX HIV infection; HIV type 1; HIV type 2; cancer; breast; prostate; liver;
KM renal; lung; skin; ovarian; cervical; brain; thyroid; stomach; colon;
KM lymphoma; leukaemia; pancreas; chemokine receptor; antibody.
XX
XX Synthetic.
OS
XX US2003206909-A1.
XX
XX 06-NOV-2003.
PD
XX 07-FEB-2003; 2003US-00360828.
PF
XX 08-FEB-2002; 2002US-00071866.
PR 08-FEB-2002; 2002US-00072201.
PR 25-APR-2002; 2002US-00133978.
XX
XX (HUA S.) HUA S.
PA (PAUL L.) PAULING M H.
PA (ZHU L.) ZHU L.
XX
XX Hua S, Pauling MH, Zhu L;
PI
XX WPI; 2004-051479/05.
DR

DR N-PSDB, ADD42836.
PT Antibody binding loop of human chemokine receptor useful for the
PT treatment of HIV infection and cancer.
XX
XX
PS Claim 6; SEQ ID NO 61; 74pp; English.
XX

The invention relates to an antibody that binds to loop 6 of human
CC chemokine receptor (CXCR4). The antibody is useful in the treatment or
CC prevention of HIV infection (e.g. HIV type 1 and HIV type 2) and cancer
CC of (e.g. breast, prostate, liver, renal, lung, skin, ovarian, cervical,
CC brain, thyroid, stomach, colon, lymphoma, leukaemia and pancreas cancer
CC cells), for screening drugs, for diagnosing disease or condition
CC associated with interaction with chemokine receptor. The present sequence
CC is used in the exemplification of the present invention.

SO Sequence 111 AA;
XX

Query Match 100.0%; Score 35; DB 8; Length 111;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0

CY 1 DVSKRPS 7
|||
52 DVSKRPS 58

Db

RESULT 15
ID ABM85072
ABM85072 standard; protein; 214 AA.
AC AEM85072;
XX
XX 18-NOV-2004 (first entry)
DT
XX
DE Human diagnostic and therapeutic pprotein SEQ ID NO:5321.
XX
XX gene therapy; human diagnostic and therapeutic polynucleotide; dltnp.
KM
XX Homo sapiens.
OS
PN MO2004023973-A2.
XX
PD 25-MAR-2004.
XX
PE 12-SEP-2003; 2003WO-US028227.
PF
PR 12-SEP-2002; 2002US-0410259P.
PR 12-SEP-2002; 2002US-0410260P.
XX
PA (INCY-) INCYTE CORP.
XX
XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harshorne TA, Suchorolski MT, Altus CM, Plets SJ, Elder LV;
PI Mooney EM, Delegeane AM, Panesar IS, Barville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
PI Perella CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LT;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Velt UA, Klinton BS;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patuary S, Shi X, Suarez CJ;
XX
XX WPI: 2004-329368/30.
DR N-PSDB; ACN43724.
XX

New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
XX in gene mapping.
XX
PS Claim 27; Page; 190pp; English.
XX

The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A

CC	polynucleotide of the invention may have a use in gene therapy. The human
CC	diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC	used to diagnose a particular condition, disease or disorder associated
CC	with human molecules, e.g. cell proliferative disorders,
CC	autoimmune/inflammatory disorder, developmental disorder, endocrine
CC	disorder, neurological disorders, gastrointestinal disorders, or
CC	infections caused by virus, bacteria, fungi or parasite. The dithp
CC	molecules may also be used in genetic mapping, in identifying individuals
CC	from minute biological samples, in detecting single nucleotide
CC	polymorphisms, as molecular weight markers, and for somatic or germline
CC	gene therapy. The present sequence represents a dithp protein of the
CC	invention. Note: The sequence data for this patent is not represented in
CC	the printed specification, but was obtained in electronic format directly
CC	from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX	
SQ	Sequence 214 AA;
Query Match	100.0%; Score 35; DB 8; Length 214;
Best Local Similarity	100.0%; Pred. No. 12;
Matches	7; Conservative 0; Mismatches 0; Indels 0; Gaps 0
OY	1 DVSKRPS 7
DB	71 DVSRRPS 77
RESULT 16	
ABM85084	
ABM85084	standard; protein; 236 AA.
AC	ABM85084;
XX	
DT	18-NOV-2004 (first entry)
XX	
DE	Human diagnostic and therapeutic protein SEQ ID NO:5333.
XX	
KM	gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX	
OS	Homo sapiens.
XX	
PN	WO2004023973-A2.
PD	
25-MAR-2004.	
PF	12-SEP-2003; 2003WO-US028227.
PR	12-SEP-2002; 2002US-0410259P.
PR	12-SEP-2002; 2002US-0410260P.
XX	
PA	(INCY-) INCYTE CORP.
XX	
PI	Schmidt JF, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI	Hathidorne TA, Suchorolski MT, Altus CM, Pitts SJ, Rider LV,
PI	Mooney EM, Delegeane AM, Panesar JS, Barville SC, Reddy TP;
PI	Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
PI	Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LJ;
PI	Lacease RE, Spiro PA, Stewart EA, Wingrove J, Vait UA, Kirton BS;
PI	Xu Y, Kwong M, Policky JT, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI	Pacury S, Shi X, Suarez CJ;
XX	
DR	WPI; 2004-329368/30.
DR	N-PDSB; ACN43736.
XX	
PT	New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT	in diagnosing a condition, disease or disorder associated with human
PT	molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT	in gene mapping.
XX	
PS	Claim 27; Page; 190pp; English.
XX	
CC	The invention relates to novel diagnostic and therapeutic polynucleotides
CC	selected from one of the 2722 sequences defined in the specification. A
CC	polynucleotide of the invention may have a use in gene therapy. The human

CC diagnostic and therapeutic polynucleotides (dthp) or polypeptides may be
 CC used to diagnose a particular condition, disease or disorder associated
 CC with human molecules, e.g. cell proliferative disorders,
 CC autoimmune/inflammatory disorder, developmental disorder, endocrine
 CC disorder, neurological disorders, gastrointestinal disorders, or
 CC infections caused by virus, bacteria, fungi or parasite. The dthp
 CC molecules may also be used in genetic mapping, in identifying individuals
 CC from minute biological samples, in detecting single nucleotide
 CC polymorphisms, as molecular weight markers, and for somatic or germ-line
 CC gene therapy. The present sequence represents a dthp protein of the
 CC invention. Note: The sequence data for this patent is not represented in
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm

XX SQ Sequence 236 AA;

Query Match 100.0%; Score 35; DB 8; Length 236;
 Best Local Similarity 100.0%; Pred. NO. 14;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
 |||||
 Db 71 DVSKRPS 77

RESULT 17

ABP45887 ID ABP45887 standard; protein; 240 AA.

XX AC ABP45887;

XX DT 19-AUG-2002 (first entry)

XX DE Human Blys binding scFv SEQ ID 1898.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 XX tumour necrosis factor; B cell proliferation; B cell differentiation;
 XX immunosuppressive; immunostimulant; antirheumatic;
 XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 XX common variable immunodeficiency; acquired immunodeficiency syndrome.

XX OS Homo sapiens.

XX PN WO200202641-A1.

XX PD 10-JAN-2002.

XX PF 15-JUN-2001; 2001WO-US019110.

XX PR 16-JUN-2000; 2000US-0212210P.

XX PR 17-OCT-2000; 2000US-0240816P.

XX PR 16-MAR-2001; 2001US-0276248P.

XX PR 21-MAR-2001; 2001US-0277379P.

XX PR 25-MAY-2001; 2001US-0293499P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI (CMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX PT Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX WPI; 2002-114799/15.

XX DR WPI; 2002-114799/15.

XX PT Antibodies against B lymphocyte Stimulating polypeptides, useful for the

XX diagnosis and treatment of cancers and immune disorders.

XX PS Claim 1; Page 2666-2667; 3148pp; English.

XX CC This invention describes novel antibodies that immunospecifically bind to

CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the

CC tumour necrosis factor (TNF) super family and induces B cell

CC proliferation and differentiation. The antibodies of the invention have

CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,

CC antirheumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys
 CC and so may be used to detect and quantitate the presence of Blys in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of Blys. They may also be
 CC administered to treat diseases associated with aberrant Blys expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method of
 CC the invention

XX SQ Sequence 240 AA;

Query Match 100.0%; Score 35; DB 5; Length 240;
 Best Local Similarity 100.0%; Pred. NO. 14;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
 |||||
 Db 181 DVSKRPS 187

RESULT 18

ADG96714 ID ADG96714 standard; protein; 240 AA.

XX AC ADG96714;

XX DT 11-MAR-2004 (first entry)

XX DE Single chain antibody that immunospecifically binds Blys SeqID 1898.

XX antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
 XX B cell proliferation; differentiation; scFv; myasthenia gravis;
 XX multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
 XX carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;
 XX antiinflammatory; antistimatic; antiallergic; cytostatic.

XX OS Unidentified.

XX PN WO2003055979-A2.

XX PD 10-JUL-2003.

XX PF 14-NOV-2002; 2002WO-US036496.

XX PR 16-NOV-2001; 2001US-0311469P.

XX PR 19-DEC-2001; 2001US-0340817P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Ruben SM, Barash SC, Choi GH, Vaughan TV, Hilbert D;

XX WPI; 2003-505530/47.

XX DR WPI; 2003-505530/47.

XX PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator

XX rheumatoid arthritis, asthma and leukemia.

XX PS Example 1; SEQ ID NO 1898; 394pp; English.

XX CC This invention relates to novel antibodies that immunospecifically bind

XX to B lymphocyte stimulator (Blys). The Blys gene has been mapped to

XX chromosome 13q34 and encodes a protein that is a member of the tumour

XX necrosis factor superfamily and induces both in vivo and in vitro B cell

XX proliferation and differentiation. Specifically, it refers to single

XX heavy chain antibody molecules (scFvs) derived, preferably, from the variable

XX fragment thereof, of either human, murine, rat or monkey Blys. The

XX present invention refers to the use of such antibodies in various methods

XX for the detection, diagnosis and prognosis of diseases related to the

CC aberrant expression or inappropriate function of BLyS or its receptor. As
CC such, these compositions are useful for identifying immune disorders
CC including myasthenia gravis and multiple sclerosis, inflammatory
CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
CC as AIDS and proliferative disorders including leukaemia, carcinoma and
CC lymphoma. Accordingly, they can be described as exhibiting various
CC activities such as antirheumatic, antiarthritic, neuroprotective,
CC antiinflammatory, antisthmatic, antiallergic and cytostatic. This
CC polypeptide sequence is a single chain antibody that binds BLyS of the
CC invention. NOTE: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 240 AA;
Query Match 100.0%; Score 35; DB 7; Length 240;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DVSKRPS 7
DB 181 DVSKRPS 187
RESULT 19
ABP46044
ID ABP46044 standard; protein; 241 AA.
XX
AC ABP46044;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human BLyS binding scFv SEQ ID 2055.
XX
Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KM tumour necrosis factor; B cell proliferation; B cell differentiation;
KM immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KM common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US019110.
XX
PR 16-JUN-2000; 2000US-0212210P.
PR 17-OCT-2000; 2000US-0240816P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
XX WPI; 2002-114799/15.
XX
DR Anticodons against B lymphocyte stimulating polypeptides, useful for the
XX
XX diagnosis and treatment of cancers and immune disorders.
XX
PS Claim 1; Page 2849-2850; 3148pp; English.
XX
XX This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to

CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP4728 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
SQ Sequence 241 AA;
Query Match 100.0%; Score 35; DB 5; Length 241;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DVSKRPS 7
DB 182 DVSKRPS 188
RESULT 20
ADG96871
ID ADG96871 standard; protein; 241 AA.
XX
AC ADG96871;
XX
DT 11-MAR-2004 (first entry)
XX
DE Single chain antibody that immunospecifically binds Blys SeqID 2055.
XX
Blys; B lymphocyte stimulator; BLyS; tumour necrosis factor;
KM cell proliferation; differentiation; scFv; myasthenia gravis;
KM multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
KM carcinoma; lymphoma; antirheumatic; antiallergic; neuroprotective;
KM antiinflammatory; antisthmatic; antiallergic; cytostatic.
XX
OS Unidentified.
XX
PN WO2003055979-A2.
XX
PD 10-JUL-2003.
XX
PF 14-NOV-2002; 2002WO-US036496.
XX
PR 16-NOV-2001; 2001US-0331469P.
PR 19-DEC-2001; 2001US-0340817P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PI Ruben SM, Barash SC, Choi GH, Vaughan TV, Hilbert D;
XX
XX WPI; 2003-505530/47.
XX
XX Novel antibody that immunospecifically binds to a B lymphocyte stimulator
PT (Blys), useful for detecting and treating diseases or disorders e.g.
PT rheumatoid arthritis, asthma and leukemia.
XX
PS Example 1; SEQ ID NO 2055; 394pp; English.
XX
XX This invention relates to novel antibodies that immunospecifically bind
CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
CC chromosome 13q34 and encodes a protein that is a member of the tumour
CC necrosis factor superfamily and induces both in vivo and in vitro B cell
CC proliferation and differentiation. Specifically, it refers to single
CC chain antibody molecules (scFvs) derived, preferably, from the variable
CC heavy CDR3 region that immunospecifically bind to a polypeptide, or
CC fragment thereof, of either human, murine, rat or monkey Blys. The
CC present invention refers to the use of such antibodies in various methods
CC for the detection, diagnosis and prognosis of diseases related to the
CC aberrant expression or inappropriate function of Blys or its receptor. As

CC such, these compositions are useful for identifying immune disorders
CC including myasthenia gravis and multiple sclerosis, inflammatory
CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
CC as AIDS and proliferative disorders including leukaemia, carcinoma and
CC lymphoma. Accordingly, they can be described as exhibiting various
CC activities such as antirheumatic, antiarthritic, neuroprotective,
CC antiinflammatory, antiallergic, antiallergic and cytostatic. This
CC polypeptide sequence is a single chain antibody that binds Blys of the
CC invention. NOTE: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

CC Sequence 241 AA;

Query Match 100.0%; Score 35; DB 7; Length 241;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
Db 182 DVSKRPS 188

RESULT 21

ADG34301
ID ADG34301 standard; protein; 242 AA.

AC ADG34301;

XX 26-FEB-2004 (first entry)

DE Neurokinin B antibody SEQ ID NO:24.

KW antibody; neurokinin B; hypotensive; gynaecological; gene therapy;
KM hypertension; pre-eclampsia; NKB.

XX Synthetic.

XX WO2003102136-A2.

XX 11-DEC-2003.

XX 29-MAY-2003; 2003WO-US016802.

XX 30-MAY-2002; 2002US-0383802P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM;

XX WPI; 2004-053456/05.

XX N-PSDB; ADG34282.

XX New antibody that specifically binds neurokinin B, useful for preparing a
XX composition for treating or preventing hypertension or preeclampsia.

XX Claim 2; SEQ ID NO 24; 127bp; English.

XX The invention relates to a novel antibody specifically binding neurokinin
XX B. An antibody of the invention has hypotensive, and gynaecological
XX activity, and may have a use in gene therapy. The antibody is useful for
XX preparing a composition for treating or preventing hypertension or pre-
XX eclampsia. The present sequence is used in the exemplification of the
XX invention.

XX Sequence 242 AA;

Query Match 100.0%; Score 35; DB 8; Length 242;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
XX

Db 182 DVSKRPS 188

RESULT 22

ADG34317
ID ADG34317 standard; protein; 242 AA.

AC ADG34317;

XX 26-FEB-2004 (first entry)

DE Neurokinin B antibody SEQ ID NO:40.

KW antibody; neurokinin B; hypotensive; gynaecological; gene therapy;
KM hypertension; pre-eclampsia; NKB.

XX Synthetic.

XX WO2003102136-A2.

XX 11-DEC-2003.

XX 29-MAY-2003; 2003WO-US016802.

XX 30-MAY-2002; 2002US-0383802P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM;

XX WPI; 2004-053456/05.

XX N-PSDB; ADG34296.

XX New antibody that specifically binds neurokinin B, useful for preparing a
XX composition for treating or preventing hypertension or preeclampsia.

XX Claim 2; SEQ ID NO 40; 127bp; English.

XX The invention relates to a novel antibody specifically binding neurokinin
XX B. An antibody of the invention has hypotensive, and gynaecological
XX activity, and may have a use in gene therapy. The antibody is useful for
XX preparing a composition for treating or preventing hypertension or pre-
XX eclampsia. The present sequence is used in the exemplification of the
XX invention.

XX Sequence 242 AA;

Query Match 100.0%; Score 35; DB 8; Length 242;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
Db 182 DVSKRPS 188

RESULT 23

ABP45916
ID ABP45916 standard; protein; 243 AA.

AC ABP45916;

XX 19-AUG-2002 (first entry)

XX Human Blys binding scFv SEQ ID 1927.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
XX tumour necrosis factor; B cell proliferation; B cell differentiation;
XX immunosuppressive; immunostimulant; immunomodulatory; antineumatic;
XX antitumor; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
XX systemic lupus erythematosus; rheumatoid arthritis; CYID; AIDS;
XX common variable immunodeficiency; acquired immunodeficiency syndrome.

XX 29-MAY-2003; 2003WO-US016802.
PF 30-MAY-2002; 2002US-0383802P.
PR (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Ruben SM;
XX WPI; 2004-053456/05.
DR N-PSDB; ADG34291.
XX New antibody that specifically binds neurokinin B, useful for preparing a
PT composition for treating or preventing hypertension or preclampsia.
XX Claim 2; SEQ ID NO 33; 127bp; English.
PS The invention relates to a novel antibody specifically binding neurokinin
CC B. An antibody of the invention has hypotensive, and gynaecological
CC activity, and may have a use in gene therapy. The antibody is useful for
CC preparing a composition for treating or preventing hypertension or pre-
CC eclampsia. The present sequence is used in the exemplification of the
CC invention.
XX Sequence 243 AA;
SQ
Qy 1 DVSKRPS 7
Db 183 DVSKRPS 189
Query Match 100.0%; Score 35; DB 8; Length 243;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULT 26
ADG34306
ID ADG34306 standard; protein; 243 AA.
XX ADG34306;
AC 26-FEB-2004 (first entry)
XX Neurokinin B antibody SEQ ID NO:29.
DE
XX antibody; neurokinin B; hypotensive; gynaecological; gene therapy;
KW hypertension; pre-eclampsia; NKB.
XX Synthetic.
XX WO2003102136-A2.
PN 11-DEC-2003.
PD 29-MAY-2003; 2003WO-US016802.
PF 30-MAY-2002; 2002US-0383802P.
PR (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Ruben SM;
XX WPI; 2004-053456/05.
DR N-PSDB; ADG34287.
XX New antibody that specifically binds neurokinin B, useful for preparing a
PT composition for treating or preventing hypertension or preclampsia.
XX Claim 2; SEQ ID NO 29; 127bp; English.
PS The invention relates to a novel antibody specifically binding neurokinin
CC B. An antibody of the invention has hypotensive, and gynaecological
CC activity, and may have a use in gene therapy. The antibody is useful for
CC activity, and may have a use in gene therapy. The antibody is useful for

CC preparing a composition for treating or preventing hypertension or pre-
CC eclampsia. The present sequence is used in the exemplification of the
CC invention.
XX Sequence 243 AA;
SQ
Qy 1 DVSKRPS 7
Db 183 DVSKRPS 189
Query Match 100.0%; Score 35; DB 8; Length 243;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULT 27
ADG34303
ID ADG34303 standard; protein; 244 AA.
XX ADG34303;
AC 26-FEB-2004 (first entry)
XX Neurokinin B antibody SEQ ID NO:26.
DE
XX antibody; neurokinin B; hypotensive; gynaecological; gene therapy;
KW hypertension; pre-eclampsia; NKB.
XX Synthetic.
XX WO2003102136-A2.
PN 11-DEC-2003.
PD 29-MAY-2003; 2003WO-US016802.
PF 30-MAY-2002; 2002US-0383802P.
PR (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Ruben SM;
XX WPI; 2004-053456/05.
DR N-PSDB; ADG34284.
XX New antibody that specifically binds neurokinin B, useful for preparing a
PT composition for treating or preventing hypertension or preclampsia.
XX Claim 2; SEQ ID NO 26; 127bp; English.
PS The invention relates to a novel antibody specifically binding neurokinin
CC B. An antibody of the invention has hypotensive, and gynaecological
CC activity, and may have a use in gene therapy. The antibody is useful for
CC preparing a composition for treating or preventing hypertension or pre-
CC eclampsia. The present sequence is used in the exemplification of the
CC invention.
XX Sequence 244 AA;
SQ
Qy 1 DVSKRPS 7
Db 184 DVSKRPS 190
Query Match 100.0%; Score 35; DB 8; Length 244;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULT 28
ABP45915
ID ABP45915 standard; protein; 245 AA.
XX ABP45915;
AC

XX DT 19-AUG-2002 (first entry)
XX DE Human BlyS binding scFv SEQ ID 1926.
XX KW BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
XX KW tumour necrosis factor; B cell proliferation; B cell differentiation;
XX KW immunosuppressive; immunostimulant; immunomodulatory; antineumatic;
XX KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
XX KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
XX KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX OS Homo sapiens.
XX PN WO200202641-A1.
XX PD 10-JAN-2002.
XX PF 15-JUN-2001; 2001WO-US019110.
XX PR 16-JUN-2000; 2000US-0212210P.
XX PR 17-OCT-2000; 2000US-0240816P.
XX PR 16-MAR-2001; 2001US-0276248P.
XX PR 21-MAR-2001; 2001US-027379P.
XX PR 25-MAY-2001; 2001US-0293499P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PA (CMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX DR WPI; 2002-114799/15.
XX PT Antibodies against B lymphocyte Stimulating polypeptides, useful for the
XX PT diagnosis and treatment of cancers and immune disorders.
XX PS Claim 1; Page 2699-2700; 3148pp; English.
XX SS This invention describes novel antibodies that immunospecifically bind to
XX CC B lymphocyte Stimulator (BlyS) polypeptides. BlyS is a member of the
XX CC tumour necrosis factor (TNF) super family and induces B cell
XX CC proliferation and differentiation. The antibodies of the invention have
XX CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
XX CC antineumatic and antiAIDS activity and can be used in vaccines to
XX CC inhibit the expression and activity of BlyS. The antibodies bind to BlyS
XX CC and so may be used to detect and quantitate the presence of BlyS in
XX CC biological samples and may be used in this way to diagnose disease
XX CC associated with aberrant expression of BlyS. They may also be
XX CC administered to treat diseases associated with aberrant BlyS expression
XX CC and activity such as cancer, immune, and autoimmune disorders and
XX CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
XX CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
XX CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
XX CC the antibodies and fragments of the antibodies described in the method of
XX CC the invention
XX SQ Sequence 245 AA;
XX
XX Query Match 100.0%; Score 35; DB 5; Length 245;
XX Best Local Similarity 100.0%; Pred. No. 14;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DVSKRPS 7
Db 185 DVSKRPS 191
RESULT 29
ID ADG96742 standard; protein; 245 AA.
XX ADG96742;
XX AC
XX

DT 11-MAR-2004 (first entry)
XX DE Single chain antibody that immunospecifically binds BlyS Segid 1926.
XX KW antibody; B lymphocyte stimulator; BlyS; tumour necrosis factor;
XX KW B cell proliferation; differentiation; scFv; myasthenia gravis;
XX KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
XX KW carcinoma; lymphoma; antineumatic; antirheumatic; neuroprotective;
XX KW antineumatic; antirheumatic; antiallergic; cytostatic.
XX OS Undefined.
XX PN WO2003055979-A2.
XX PD 10-JUL-2003.
XX PF 14-NOV-2002; 2002WO-US036496.
XX PR 16-NOV-2001; 2001US-0331469P.
XX PR 19-DEC-2001; 2001US-0340817P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Ruben SM, Barash SC, Choi GH, Vaughan TV, Hilbert D;
XX DR WPI; 2003-505530/47.
XX DE Novel antibody that immunospecifically binds to a B lymphocyte stimulator
XX PT (BlyS), useful for detecting and treating diseases or disorders e.g.
XX PT rheumatoid arthritis, asthma and leukemia.
XX PS Example 1; SEQ ID NO 1926; 394pp; English.
XX SS This invention relates to novel antibodies that immunospecifically bind
XX CC to B lymphocyte stimulator (BlyS). The BlyS gene has been mapped to
XX CC chromosome 13q34 and encodes a protein that is a member of the tumour
XX CC necrosis factor superfamily and induces both in vivo and in vitro B cell
XX CC proliferation and differentiation. Specifically, it refers to single
XX CC chain antibody molecules (scFvs) derived, preferably, from the variable
XX CC heavy CDR3 region that immunospecifically bind to a polypeptide, or
XX CC fragment thereof, of either human, murine, rat or monkey BlyS. The
XX CC present invention refers to the use of such antibodies in various methods
XX CC for the detection, diagnosis and prognosis of diseases related to the
XX CC aberrant expression or inappropriate function of BlyS or its receptor. As
XX CC such, these compositions are useful for identifying immune disorders
XX CC including myasthenia gravis and multiple sclerosis, inflammatory
XX CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
XX CC as AIDS and proliferative disorders including leukaemia, carcinoma and
XX CC lymphoma. Accordingly, they can be described as exhibiting various
XX CC activities such as antineumatic, antirheumatic, neuroprotective,
XX CC antiinflammatory, antiallergic, antineumatic and cytostatic. This
XX CC polypeptide sequence is a single chain antibody that binds BlyS of the
XX CC invention. NOTE: The sequence data for this patent did not form part of
XX CC the printed specification, but was obtained in electronic format
XX CC directly from WIPO at fcp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 245 AA;
XX
XX Query Match 100.0%; Score 35; DB 7; Length 245;
XX Best Local Similarity 100.0%; Pred. No. 14;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DVSKRPS 7
Db 185 DVSKRPS 191
RESULT 30
ID ADG98057
XX ADG98057 standard; protein; 245 AA.
XX AC
XX ADG98057;
XX

Qy 1 DVSKRPS 7
Db 185 DVSKRPS 191

RESULT 32

ADG34308 standard; protein; 245 AA.
ADG34308;
26-FEB-2004 (first entry)

Neurokinin B antibody SEQ ID NO:31.
antibody; neurokinin B; hypotensive; gynaecological; gene therapy;
hypertension; pre-eclampsia; NKB.

Synthetic.
WO2003102136-A2.
11-DEC-2003.
29-MAY-2003; 2003WO-US016802.
30-MAY-2002; 2002US-0383802P.
(HUMA-) HUMAN GENOME SCI INC.
Rosen CA, Ruben SM;
WPI: 2004-053456/05.
N-PSDB; ADG34289.

New antibody that specifically binds neurokinin B, useful for preparing a composition for treating or preventing hypertension or preeclampsia.
Claim 2; SEQ ID NO 31; 127bp; English.

The invention relates to a novel antibody specifically binding neurokinin B. An antibody of the invention has hypotensive, and gynaecological activity, and may have a use in gene therapy. The antibody is useful for preparing a composition for treating or preventing hypertension or pre-eclampsia. The present sequence is used in the exemplification of the invention.

Sequence 245 AA;
Query Match 100.0%; Score 35; DB 8; Length 245;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
Db 185 DVSKRPS 191

RESULT 33

ADG34313 standard; protein; 245 AA.
ADG34313;
26-FEB-2004 (first entry)

Neurokinin B antibody SEQ ID NO:36.
antibody; neurokinin B; hypotensive; gynaecological; gene therapy;
hypertension; pre-eclampsia; NKB.
Synthetic.

Sequence 245 AA;
Query Match 100.0%; Score 35; DB 8; Length 245;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
Db 185 DVSKRPS 191

RESULT 34

ADG34302 standard; protein; 246 AA.
ADG34302;
19-AUG-2002 (first entry)

Human Blys binding scFv SEQ ID 1913.
Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
tumour necrosis factor; B cell proliferation; B cell differentiation;
immunomodulatory; immunostimulant; antitumour; antineoplastic;
antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
common variable immunodeficiency; acquired immunodeficiency syndrome.

Homo sapiens.
WO200202641-A1.
10-JAN-2002.
15-JUN-2001; 2001WO-US019110.
16-JUN-2000; 2000US-0212210P.
17-OCT-2000; 2000US-0240816P.
16-MAR-2001; 2001US-0276248P.
21-MAR-2001; 2001US-0277379P.
25-MAY-2001; 2001US-0293499P.
(HUMA-) HUMAN GENOME SCI INC.
(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

PN WO2003102136-A2.
XX 11-DEC-2003.
XX 29-MAY-2003; 2003WO-US016802.
XX 30-MAY-2002; 2002US-0383802P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Ruben SM;
XX WPI: 2004-053456/05.
XX N-PSDB; ADG34294.
XX New antibody that specifically binds neurokinin B, useful for preparing a composition for treating or preventing hypertension or preeclampsia.
XX Claim 2; SEQ ID NO 36; 127bp; English.

The invention relates to a novel antibody specifically binding neurokinin B. An antibody of the invention has hypotensive, and gynaecological activity, and may have a use in gene therapy. The antibody is useful for preparing a composition for treating or preventing hypertension or pre-eclampsia. The present sequence is used in the exemplification of the invention.

Sequence 245 AA;
Query Match 100.0%; Score 35; DB 8; Length 245;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
Db 185 DVSKRPS 191

RESULT 34

ADG34302 standard; protein; 246 AA.
ADG34302;
19-AUG-2002 (first entry)

Human Blys binding scFv SEQ ID 1913.
Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
tumour necrosis factor; B cell proliferation; B cell differentiation;
immunomodulatory; immunostimulant; antitumour; antineoplastic;
antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
common variable immunodeficiency; acquired immunodeficiency syndrome.

Homo sapiens.
WO200202641-A1.
10-JAN-2002.
15-JUN-2001; 2001WO-US019110.
16-JUN-2000; 2000US-0212210P.
17-OCT-2000; 2000US-0240816P.
16-MAR-2001; 2001US-0276248P.
21-MAR-2001; 2001US-0277379P.
25-MAY-2001; 2001US-0293499P.
(HUMA-) HUMAN GENOME SCI INC.
(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX WPI; 2002-114799/15.
XX
XX Antibodies against B lymphocyte Stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.
XX
XX
PS Claim 1; Page 2683-2684; 3148pp; English.
XX
XX This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antineoplastic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
SQ Sequence 246 AA;
XX
Query Match 100.0%; Score 35; DB 5; Length 246;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DVSKRPS 7
|||
186 DVSKRPS 192
DB
RESULT 35
ABP45906
ID ABP45906 standard; protein; 246 AA.
XX
AC ABP45906;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human Blys binding scFv SEQ ID 1917.
XX
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antineoplastic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
PN WO200202641-A1.
XX
PD 10-JAN-2002.
XX
PF 15-JUN-2001; 2001WO-US019110.
XX
PR 16-JUN-2000; 2000US-0212210P.
PR 17-OCT-2000; 2000US-0240816P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTI-BODY TECHNOLOGY.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX

DR WPI; 2002-114799/15.
XX
XX Antibodies against B lymphocyte Stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.
XX
XX
PS Claim 1; Page 2688-2689; 3148pp; English.
XX
XX This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antineoplastic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
SQ Sequence 246 AA;
XX
Query Match 100.0%; Score 35; DB 5; Length 246;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DVSKRPS 7
|||
186 DVSKRPS 192
DB
RESULT 36
ADG96733
ID ADG96733 standard; protein; 246 AA.
XX
AC ADG96733;
XX
DT 11-MAR-2004 (first entry)
XX
DE Single chain antibody that immunospecifically binds Blys SegID 1917.
XX
XX antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
KW B cell proliferation; differentiation; scFv; myasthenia gravis;
KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
KW carcinoma; lymphoma; antineoplastic; antiarthritic; neuroprotective;
KW antiinflammatory; antiasthmatic; antiallergic; cytostatic.
XX
OS Unidentified.
XX
PN WO2003055979-A2.
XX
PD 10-JUL-2003.
XX
PF 14-NOV-2002; 2002WO-US036496.
XX
PR 16-NOV-2001; 2001US-0331469P.
PR 19-DEC-2001; 2001US-0340817P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
XX WPI; 2003-505530/47.
XX
PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator
PT (Blys), useful for detecting and treating diseases or disorders e.g.
PT rheumatoid arthritis, asthma and leukemia.
XX

PS Example 1, SEQ ID NO 1917, 394pp; English.
XX
CC This invention relates to novel antibodies that immunospecifically bind
CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
CC chromosome 13q34 and encodes a protein that is a member of the tumour
CC necrosis factor superfamily and induces both in vivo and in vitro B cell
CC proliferation and differentiation. Specifically, it refers to single
CC chain antibody molecules (scFvs) derived, preferably, from the variable
CC heavy CDR3 region that immunospecifically bind to a polypeptide, or
CC fragment thereof, of either human, murine, rat or monkey Blys. The
CC present invention refers to the use of such antibodies in various methods
CC for the detection, diagnosis and prognosis of diseases related to the
CC aberrant expression or inappropriate function of Blys or its receptor. As
CC such, these compositions are useful for identifying immune disorders
CC including myasthenia gravis and multiple sclerosis, inflammatory
CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
CC as AIDS and proliferative disorders including leukaemia, carcinoma and
CC lymphoma. Accordingly, they can be described as exhibiting various
CC activities such as antirheumatic, antiarthritic, neuroprotective,
CC antiinflammatory, antiallergic and cytostatic. This
CC polypeptide sequence is a single chain antibody that binds Blys of the
CC invention. NOTE: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 246 AA;

Query Match 100.0%; Score 35; DB 7; Length 246;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 186 DVSKRPS 192

RESULT 37
ADG96729 standard; protein; 246 AA.

ADG96729;
11-MAR-2004 (first entry)

Single chain antibody that immunospecifically binds Blys SegID 1913.

antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
B cell proliferation; differentiation; scFv; myasthenia gravis;
multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;
antiinflammatory; antiallergic; cytostatic.

Unidentified.

WO2003055979-A2.

10-JUL-2003.

14-NOV-2002; 2002WO-US036496.

16-NOV-2001; 2001US-031469P.

19-DEC-2001; 2001US-0340817P.

(HUMA-) HUMAN GENOME SCI INC.

Ruben SM, Barash SC, Choi GH, Vaughan TV, Hilbert D;

WPI; 2003-505530/47.

Novel antibody that immunospecifically binds to a B lymphocyte stimulator
(Blys), useful for detecting and treating diseases or disorders e.g.
rheumatoid arthritis, asthma and leukemia.

PS Example 1, SEQ ID NO 1913, 394pp; English.
XX
CC This invention relates to novel antibodies that immunospecifically bind
CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
CC chromosome 13q34 and encodes a protein that is a member of the tumour
CC necrosis factor superfamily and induces both in vivo and in vitro B cell
CC proliferation and differentiation. Specifically, it refers to single
CC chain antibody molecules (scFvs) derived, preferably, from the variable
CC heavy CDR3 region that immunospecifically bind to a polypeptide, or
CC fragment thereof, of either human, murine, rat or monkey Blys. The
CC present invention refers to the use of such antibodies in various methods
CC for the detection, diagnosis and prognosis of diseases related to the
CC aberrant expression or inappropriate function of Blys or its receptor. As
CC such, these compositions are useful for identifying immune disorders
CC including myasthenia gravis and multiple sclerosis, inflammatory
CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
CC as AIDS and proliferative disorders including leukaemia, carcinoma and
CC lymphoma. Accordingly, they can be described as exhibiting various
CC activities such as antirheumatic, antiarthritic, neuroprotective,
CC antiinflammatory, antiallergic and cytostatic. This
CC polypeptide sequence is a single chain antibody that binds Blys of the
CC invention. NOTE: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 246 AA;

Query Match 100.0%; Score 35; DB 7; Length 246;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 186 DVSKRPS 192

RESULT 38
ADE83872 standard; protein; 246 AA.

ADE83872;

29-JAN-2004 (first entry)

Chemokine beta-4 binding antibody F002C08 protein SEQ ID NO:31.

antibody; chemokine beta-4; CK-B4; single chain Fvs; scFvs;
antiapoptotic; dermatological; antiinflammatory; immunosuppressive;
antirheumatic; antiallergic; cerebroprotective; cytostatic; anti-HIV;
vulnery; dermatitis; autoimmune disease; rheumatoid arthritis;
systemic lupus erythematosus; autoimmune encephalitis; cancer;
HIV infection; wound; inflammatory disorder; human; psoriasis.

Synthetic.

Homo sapiens.

WO2003092597-A2.

13-NOV-2003.

30-APR-2003; 2003WO-US013414.

01-MAY-2002; 2002US-0376561P.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Ruben SM;

WPI; 2004-022614/02.

N-PSDB; ADE83855.

New antibody that specifically binds to a chemokine beta-4 polypeptide,
useful for diagnosing, treating, preventing or ameliorating psoriasis.

PT rheumatoid arthritis, systemic lupus erythematosus, cancer, HIV infection
PT and wounds.
XX
PS Claim 1; SEQ ID NO 31; 181bp; English.

XX The present invention describes an antibody (I) that specifically binds
CC to a chemokine beta-4 (CK-B4) polypeptide. Where (I) comprises a first
CC amino acid sequence at least 95% identical to a second amino acid
CC sequence comprising a VH complementarity determining region (CDR) or VL
CC CDR of any of the single chain Fvs (scFvs) from any of 17 fully defined
CC sequences of 245-253 amino acids (ADB83861 to ADB83877). Also described:
CC (1) a kit comprising (1); (2) an isolated nucleic acid molecule encoding
CC (1); (3) a vector comprising the isolated nucleic acid of (2); (4) a host
CC cell comprising the vector of (3); (5) a cell line engineered to express
CC (1); (6) an antibody that binds the same epitope as (1); (7) an antibody
CC that competitively inhibits the binding (1) to a CK-B4 polypeptide; (8) a
CC method for detecting aberrant expression of CK-B4 polypeptide, comprising
CC assaying the level of CK-B4 polypeptide expression in a first biological
CC sample of an individual using at least one of (1), and comparing the
CC level of CK-B4 polypeptide assayed in the biological sample with a
CC standard level of CK-B4 polypeptide expression or level of CK-B4
CC polypeptide in a second, normal biological sample, where an increase or
CC decrease in the assayed level of CK-B4 polypeptide in the first
CC biological sample compared to the standard level is indicative of
CC aberrant expression; and (9) a method of treating, preventing or
CC ameliorating psoriasis, dermatitis or an autoimmune disease, comprising
CC administering (1) to the animal. (I) has antipsoriatic, dermatological,
CC antiinflammatory, immunosuppressive, antirheumatic, antineuritic,
CC cerebroprotective, cytostatic, anti-HIV and vulnerary activities. The
CC methods and compositions of the present invention are useful for
CC diagnosing, treating, preventing or ameliorating psoriasis, dermatitis or
CC an autoimmune disease such as rheumatoid arthritis, systemic lupus
CC erythematosus and autoimmune encephalitis. They can also be used in
CC cancer, HIV infection, wounds and inflammatory disorders. The present
CC sequence is used in the exemplification of the present invention.
XX
SQ Sequence 246 AA;

Query Match 100.0%; Score 35; DB 8; Length 246;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
|||
Db 186 DVSKRPS 192

RESULT 39
ABP45671
ID ABP45671 standard; protein; 247 AA.

XX AC ABP45671;

XX DT 19-AUG-2002 (first entry)

XX DE Human Blys binding scFv SEQ ID 1682.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
XX tumour necrosis factor; B cell proliferation; B cell differentiation;
XX immunosuppressive; immunostimulant; immunomodulatory; antineuritic;
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
XX common variable immunodeficiency; acquired immunodeficiency syndrome.

XX OS Homo sapiens.

XX PN WO200202641-A1.

XX PD 10-JAN-2002.

XX PF 15-JUN-2001; 2001WO-US019110.

XX PR 16-JUN-2000; 2000US-0212210P.

PR 17-OCT-2000; 2000US-0240816P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.

XX (HUMA-) HUMAN GENOME SCI INC.
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX WPI; 2002-114799/15.

XX Antibodies against B lymphocyte Stimulating polypeptides, useful for the
XX diagnosis and treatment of cancers and immune disorders.

XX PS Claim 1; Page 2409-2410; 3148pp; English.

XX This invention describes novel antibodies that immunospecifically bind to
XX B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
XX tumour necrosis factor (TNF) super family and induces B cell
XX proliferation and differentiation. The antibodies of the invention have
XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
XX antineuritic and antiAIDS activity and can be used in vaccines to
XX inhibit the expression and activity of Blys. The antibodies bind to Blys
XX and so may be used to detect and quantitate the presence of Blys in
XX biological samples and may be used in this way to diagnose disease
XX associated with aberrant expression of Blys. They may also be
XX administered to treat diseases associated with aberrant Blys expression
XX and activity such as cancer, immune, and autoimmune disorders and
XX diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
XX immunodeficiency (e.g. common variable immunodeficiency (CVID) and
XX acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
XX the antibodies and fragments of the antibodies described in the method of
XX the invention
XX
SQ Sequence 247 AA;

Query Match 100.0%; Score 35; DB 5; Length 247;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
|||
Db 187 DVSKRPS 193

RESULT 40
ABP45674
ID ABP45674 standard; protein; 247 AA.

XX AC ABP45674;

XX DT 19-AUG-2002 (first entry)

XX DE Human Blys binding scFv SEQ ID 1685.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
XX tumour necrosis factor; B cell proliferation; B cell differentiation;
XX immunosuppressive; immunostimulant; immunomodulatory; antineuritic;
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
XX common variable immunodeficiency; acquired immunodeficiency syndrome.

XX OS Homo sapiens.

XX PN WO200202641-A1.

XX PD 10-JAN-2002.

XX PF 15-JUN-2001; 2001WO-US019110.

XX PR 16-JUN-2000; 2000US-0212210P.

XX PR 17-OCT-2000; 2000US-0240816P.

PR 16-MAR-2001; 2001US-0276248P.
PR 23-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.

XX (HUMA-) HUMAN GENOME SCI INC.
XX (CMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

PI Ruben SM, Baraah SC, Choi GH, Vaughan T, Hilbert D;

DR WPI; 2002-114799/15.

XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.

XX Claim 1; Page 2413-2414; 3148pp; English.

CC This invention describes novel antibodies that immunospecifically bind to
CC B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of BLyS. The antibodies bind to BLyS
CC and so may be used to detect and quantitate the presence of BLyS in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of BLyS. They may also be
CC administered to treat diseases associated with aberrant BLyS expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention

XX SQ Sequence 247 AA;

Query Match 100.0%; Score 35; DB 5; Length 247;

Best Local Similarity 100.0%; Pred. NO. 14;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7

Db 188 DVSKRPS 194

Search completed: March 31, 2005, 12:02:31
Job time : 55.25 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: March 31, 2005, 11:51:44 ; Search time 13.6719 Seconds
(without alignments)
38.220 Million cell updates/sec

Title: US-10-614-959-14

Perfect score: 35

Sequence: 1 DVSKRPS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

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3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCITUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	100.0	7	4	US-09-383-667-14
2	35	100.0	111	2	US-08-652-816A-15
3	35	100.0	112	3	US-09-025-769B-19
4	35	100.0	112	4	US-09-070A-19
5	35	100.0	112	4	US-09-490-153-19
6	35	100.0	112	4	US-09-490-324-19
7	31	88.6	7	4	US-09-383-667-25
8	31	88.6	7	4	US-09-424-840B-125
9	31	88.6	235	2	US-08-378-939-12
10	31	88.6	236	3	US-08-487-550-10
11	31	88.6	236	4	US-09-526-098-10
12	31	88.6	236	4	US-09-526-098-10
13	31	88.6	1039	4	US-09-383-916-10
14	31	88.6	1882	3	US-09-369-364A-13
15	30	85.7	110	3	US-09-025-769B-33
16	30	85.7	110	3	US-09-025-769B-33
17	30	85.7	110	3	US-09-490-070A-33
18	30	85.7	110	4	US-09-490-070A-33
19	30	85.7	110	4	US-09-490-153-33
20	30	85.7	110	4	US-09-490-153-33
21	30	85.7	110	4	US-09-490-324-33
22	29	82.9	215	3	US-09-247-373B-42
23	29	82.9	215	3	US-09-232-290-17
24	28	80.0	111	4	US-09-252-991A-23989
25	28	80.0	140	4	US-09-134-000C-5577
26	28	80.0	217	4	US-09-134-000C-5577
27	28	80.0	294	4	US-09-134-000C-4555

28	28	80.0	366	4	US-09-270-767-43922	Sequence 43922, A
29	28	80.0	514	4	US-09-252-991A-18161	Sequence 18161, A
30	28	80.0	692	4	US-09-540-236-2750	Sequence 2750, A
31	28	80.0	894	2	US-08-867-941-15	Sequence 15, App1
32	28	80.0	898	2	US-08-867-941-11	Sequence 11, App1
33	28	80.0	1118	4	US-09-538-092-423	Sequence 423, App
34	28	80.0	2150	4	US-09-321-987B-2	Sequence 2, App1
35	28	80.0	2165	4	US-09-800-729-155	Sequence 155, App
36	28	80.0	2432	3	US-09-074-658-15	Sequence 15, App1
37	28	80.0	2439	3	US-09-074-658-11	Sequence 11, App1
38	27	77.1	70	4	US-09-107-532A-7296	Sequence 7296, Ap
39	27	77.1	77	4	US-09-246-796A-17949	Sequence 17949, A
40	27	77.1	78	4	US-09-270-767-38080	Sequence 38080, A
41	27	77.1	78	4	US-09-270-767-53297	Sequence 53297, A
42	27	77.1	81	3	US-08-858-207A-476	Sequence 476, App
43	27	77.1	108	4	US-09-248-796A-22912	Sequence 22912, A
44	27	77.1	116	4	US-09-583-110-4891	Sequence 4891, Ap
45	27	77.1	124	4	US-09-107-433-3333	Sequence 3333, Ap

ALIGNMENTS

RESULT 1
US-09-383-667-14
; Sequence 14, Application US/09383667
; Patent No. 6624295
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia W.
; APPLICANT: Devaux, Brigitte
; APPLICANT: Eaton, Dan L.
; APPLICANT: Hase, Philip E.
; APPLICANT: Judice, J. Kevin
; APPLICANT: Kirchofer, Daniel
; APPLICANT: Suggest, Shelley
; TITLE OF INVENTION: Human Anti-Factor IX/Xa Antibodies
; FILE REFERENCE: P1661R2
; CURRENT APPLICATION NUMBER: US/09/383,667
; EARLIER FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098,233
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: US 60/122,767
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 14
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-383-667-14
Query Match 100.0%; Score 35; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. NO. 4.1e+05; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DVSKRPS 7
DB 1 DVSKRPS 7
RESULT 2
US-08-652-816A-15
; Sequence 15, Application US/08652816A
; Patent No. 5672215
; GENERAL INFORMATION:
; APPLICANT: Osbourn, JK
; APPLICANT: Allen, DJ
; APPLICANT: McCafferty, JG
; TITLE OF INVENTION: Specific binding members, materials and
; TITLE OF INVENTION: methods.
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,816A
FILING DATE: 23-MAY-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.4
FILING DATE: 02-DEC-1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.8
FILING DATE: 02-DEC-1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 23-SEP-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 9525004.9
FILING DATE: 07-DEC-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 9610824.6
FILING DATE: 23-MAY-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/02240
FILING DATE: 02-DEC-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/244,597
FILING DATE: 01-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/33308
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-652-816A-15

Query Match 100.0%; Score 35; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 51 DVSKRPS 57

RESULT 3
US-09-025-769B-19
Sequence 19, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas

CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-19

Query Match 100.0%; Score 35; DB 3; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 52 DVSKRPS 58

RESULT 4
US-09-490-070A-19
Sequence 19, Application US/0949070A
Patent No. 6696248
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
White & McCaulliffe
STREET: 1666 K Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:

NAME: Colin G. Sandercock, Esq.
 REGISTRATION NUMBER: 31,298
 REFERENCE/DOCKET NUMBER: 37629-0005
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 912-2000
 TELEFAX: (202) 912-2020
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 112 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 19:
 US-09-490-070A-19

Query Match 100.0%; Score 35; DB 4; Length 112;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
 DB 52 DVSKRPS 58

RESULT 5
 US-09-490-153-19
 Sequence 19, Application US/09490153
 Patent No. 6706484
 GENERAL INFORMATION:
 APPLICANT: Knappik, Achim
 Pack, Peter
 Ilag, Vic
 Ge, Liming
 Moroney, Simon
 Plueckthun, Andreas
 TITLE OF INVENTION: Protein/(Poly)peptide libraries
 NUMBER OF SEQUENCES: 373
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
 STREET: 1251 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10021
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/490,153
 FILING DATE: 24-Jan-2000
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/025,769B
 FILING DATE: 18-FEB-1998
 APPLICATION NUMBER: EP 95 11 3021.0
 FILING DATE: 18-AUG-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: James F. Haley, Jr., Esq.
 REGISTRATION NUMBER: 27,794
 REFERENCE/DOCKET NUMBER: MORPHO/5
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212)596-9000
 TELEFAX: (212)596-9090
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 112 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 19:

US-09-490-153-19

Query Match 100.0%; Score 35; DB 4; Length 112;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
 DB 52 DVSKRPS 58

RESULT 6
 US-09-490-324-19
 Sequence 19, Application US/09490324
 Patent No. 6828422
 GENERAL INFORMATION:
 APPLICANT: Knappik, Achim
 Pack, Peter
 Ilag, Vic
 Ge, Liming
 Moroney, Simon
 Plueckthun, Andreas
 TITLE OF INVENTION: Protein/(Poly)peptide libraries
 NUMBER OF SEQUENCES: 373
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
 STREET: 1251 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10021
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/490,324
 FILING DATE: 24-Jan-2000
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/025,769
 FILING DATE: 18-FEB-1998
 APPLICATION NUMBER: EP 95 11 3021.0
 FILING DATE: 18-AUG-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: James F. Haley, Jr., Esq.
 REGISTRATION NUMBER: 27,794
 REFERENCE/DOCKET NUMBER: MORPHO/5
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212)596-9000
 TELEFAX: (212)596-9090
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 112 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 19:
 US-09-490-324-19

Query Match 100.0%; Score 35; DB 4; Length 112;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
 DB 52 DVSKRPS 58

RESULT 7
 US-09-383-667-25
 Sequence 25, Application US/09383667

Patent No. 6624295
GENERAL INFORMATION:
APPLICANT: Adams, Camelia W.
APPLICANT: Devaux, Brigitte
APPLICANT: Baton, Dan L.
APPLICANT: Haas, Philip E.
APPLICANT: Judice, J. Kevin
APPLICANT: Kirchofer, Daniel
APPLICANT: Suggett, Shelley
TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
FILE REFERENCE: P1661R2
CURRENT APPLICATION NUMBER: US/09/383,667
CURRENT FILING DATE: 1999-08-26
EARLIER APPLICATION NUMBER: US 60/098,233
EARLIER FILING DATE: 1998-08-28
EARLIER APPLICATION NUMBER: US 60/122,767
EARLIER FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 32
SEQ ID NO 25
LENGTH: 7
TYPE: PRT
ORGANISM: Homo sapiens
US-09-383-667-25

Query Match 88.6%; Score 31; DB 4; Length 7;
Best Local Similarity 85.7%; Pred. No. 4.1e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSRRPS 7
Db 1 EVSKRPS 7

RESULT 8
US-09-424-840B-125
Sequence 125, Application US/09424840B
Patent No. 6790938
GENERAL INFORMATION:
APPLICANT: Berchtold, Peter
APPLICANT: Escher, Robert F. A.
TITLE OF INVENTION: ANTI-GPIIb/IIIa RECOMBINANT ANTIBODIES
FILE REFERENCE: 100564-09049
CURRENT APPLICATION NUMBER: US/09/424,840B
CURRENT FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: DE 19820663.1
PRIOR FILING DATE: 1998-05-08
PRIOR APPLICATION NUMBER: DE 19755227.7
PRIOR FILING DATE: 1997-12-12
PRIOR APPLICATION NUMBER: DE 19723904.8
PRIOR FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 128
SOFTWARE: PatentIn version 3.1
SEQ ID NO 125
LENGTH: 7
TYPE: PRT
ORGANISM: Homo sapiens
US-09-424-840B-125

Query Match 88.6%; Score 31; DB 4; Length 7;
Best Local Similarity 85.7%; Pred. No. 4.1e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSRRPS 7
Db 1 EVSKRPS 7

RESULT 9
US-08-378-939-12
Sequence 12, Application US/08378939
Patent No. 5876961
GENERAL INFORMATION:
APPLICANT: CROME, JAMES SCOTT

APPLICANT: LEWIS, ALAN PETER
TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
STREET: 555 THIRTEENTH ST. N.W.
CITY: WASHINGTON
STATE: D. C.
COUNTRY: U.S.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,939
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/952640
FILING DATE: 01-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: ERNST, BARBARA G
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1808-118
TELEPHONE: (202) 783-6040
TELEFAX: (202) 783-6031
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-378-939-12

Query Match 88.6%; Score 31; DB 2; Length 235;
Best Local Similarity 85.7%; Pred. No. 33;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSRRPS 7
Db 71 EVSKRPS 77

RESULT 10
US-08-487-550-10
Sequence 10, Application US/08487550
Patent No. 6113898
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF.
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DONALD, SWECKER & MATHIAS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,550
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435


```

: ATTORNEY/AGENT INFORMATION:
: NAME: Teekin, Robin L.
: REGISTRATION NUMBER: 35,030
: REFERENCE/DOCKET NUMBER: 012712-131
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 703-836-6620
: TELEFAX: 703-836-2021
: INFORMATION FOR SEQ ID NO: 10:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 236 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-487-550-10

Query Match      88.6%; Score 31; DB 3; Length 236;
Best Local Similarity 71.4%; Pred. No. 33;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DVSKRPS 7
       |:|||||
Db      71 DINKRPS 77

RESULT 11
US-09-526-098-10
: Sequence 10, Application US/09526098
: Patent No. 6492134
: GENERAL INFORMATION:
: APPLICANT: Anderson, Darrell R.
: TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
: TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
: TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
: NUMBER OF SEQUENCES: 12
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
: STREET: 699 Prince Street
: CITY: Alexandria
: STATE: VA
: COUNTRY: USA
: ZIP: 22314
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/526,098
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 09/383,916
: FILING DATE:
: APPLICATION NUMBER: US 08/487,550
: FILING DATE: 07-JUN-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Teekin, Robin L.
: REGISTRATION NUMBER: 35,030
: REFERENCE/DOCKET NUMBER: 012712-131
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 703-836-6620
: TELEFAX: 703-836-2021
: INFORMATION FOR SEQ ID NO: 10:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 236 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-09-526-098-10

Query Match      88.6%; Score 31; DB 4; Length 236;
Best Local Similarity 71.4%; Pred. No. 33;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DVSKRPS 7
       |:|||||
Db      71 DINKRPS 77

RESULT 12
US-09-383-916-10
: Sequence 10, Application US/09383916
: Patent No. 6709654
: GENERAL INFORMATION:
: APPLICANT: Anderson, Darrell R.
: TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
: TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
: TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
: NUMBER OF SEQUENCES: 12
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
: STREET: 699 Prince Street
: CITY: Alexandria
: STATE: VA
: COUNTRY: USA
: ZIP: 22314
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/383,916
: FILING DATE: 26-AUG-1999
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/487,550
: FILING DATE: 07-JUN-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Teekin, Robin L.
: REGISTRATION NUMBER: 35,030
: REFERENCE/DOCKET NUMBER: 012712-131
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 703-836-6620
: TELEFAX: 703-836-2021
: INFORMATION FOR SEQ ID NO: 10:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 236 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-09-383-916-10

Query Match      88.6%; Score 31; DB 4; Length 236;
Best Local Similarity 71.4%; Pred. No. 33;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DVSKRPS 7
       |:|||||
Db      71 DINKRPS 77

RESULT 13
US-09-949-016-7859
: Sequence 7859, Application US/09949016
: Patent No. 6812339
: GENERAL INFORMATION:
: APPLICANT: VENTER, J. Craig et al.
: TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
: TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: C0001307
: CURRENT APPLICATION NUMBER: US/09/949,016
: CURRENT FILING DATE: 2000-04-14
: PRIOR APPLICATION NUMBER: 60/241,755
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 7859
LENGTH: 1039
TYPE: PRT
ORGANISM: Human
US-09-949-016-7859

Query Match
Best Local Similarity 100.0%; Score 31; DB 4; Length 1039;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRP 6
Db 915 DVSKRP 920

RESULT 14
US-09-369-364A-13
Sequence 13, Application US/09369364A
Patent No. 6391610
GENERAL INFORMATION:
APPLICANT: Apce, Suneel
APPLICANT: Hurskainen, Tiina L.
APPLICANT: Hirohata, Satoshi
TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
FILE REFERENCE: 26473/4007/10-30-00
CURRENT APPLICATION NUMBER: US/09/369,364A
CURRENT FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 1882
TYPE: PRT
ORGANISM: Homo sapiens ADAMTS-9
FEATURE:
NAME/KEY: MOD RES
LOCATION: (468)
OTHER INFORMATION: Xaa = C
NAME/KEY: MOD RES
LOCATION: (521)
OTHER INFORMATION: Xaa = Y
US-09-369-364A-13

Query Match
Best Local Similarity 88.6%; Score 31; DB 3; Length 1882;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRP 6
Db 1543 DVSKRP 1548

RESULT 15
US-09-025-769B-33
Sequence 33, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESSES:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave

STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-33

Query Match
Best Local Similarity 85.7%; Score 30; DB 3; Length 110;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DVSKRP 7
Db 52 DVSNRPS 58

RESULT 16
US-09-025-769B-53
Sequence 53, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESSES:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULAR TYPE: protein
US-09-025-7698-53

Query Match 85.7%; Score 30; DB 3; Length 110;
Best Local Similarity 85.7%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
Db 52 DVSNRPS 58

RESULT 17
US-09-490-070A-33
Sequence 33, Application US/09490070A
Patent No. 6696248

GENERAL INFORMATION:
APPLICANT: Knappik, Achim

Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckhann, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESSES:
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman

STREET: 1666 K Street, N.W., Suite 300
CITY: Washington

STATE: D.C.
COUNTRY: USA
ZIP: 20006

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A

FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.

REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005

TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020

INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids

TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear

MOLECULAR TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-490-070A-33

Query Match 85.7%; Score 30; DB 4; Length 110;

Best Local Similarity 85.7%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
Db 52 DVSNRPS 58

RESULT 18
US-09-490-070A-53
Sequence 53, Application US/09490070A
Patent No. 6696248

GENERAL INFORMATION:
APPLICANT: Knappik, Achim

Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckhann, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESSES:
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman

STREET: 1666 K Street, N.W., Suite 300
CITY: Washington

STATE: D.C.
COUNTRY: USA
ZIP: 20006

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A

FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.

REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005

TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000

INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids

TYPE: amino acid
TOPOLOGY: linear

MOLECULAR TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 53:
US-09-490-070A-53

Query Match 85.7%; Score 30; DB 4; Length 110;
Best Local Similarity 85.7%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
Db 52 DVSNRPS 58

RESULT 19
US-09-490-153-33
Sequence 33, Application US/09490153
Patent No. 6706484

GENERAL INFORMATION:
APPLICANT: Knappik, Achim

Ilag, Vic

Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-490-153-33
Query Match 85.7%; Score 30; DB 4; Length 110;
Best Local Similarity 85.7%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 DVSRRPS 7
Db 52 DVSRRPS 58
RESULT 20
US-09-490-153-53
Sequence 53, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,153
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 53:
US-09-490-153-53
Query Match 85.7%; Score 30; DB 4; Length 110;
Best Local Similarity 85.7%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 DVSRRPS 7
Db 52 DVSRRPS 58
RESULT 21
US-09-490-324-33
Sequence 33, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-490-324-33

Query Match 85.7%; Score 30; DB 4; Length 110;
Best Local Similarity 85.7%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 52 EVNKRPS 58

RESULT 22
US-09-490-324-53
Sequence 53, Application US/09490324
Patent No. 6828422
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,324
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769
FILING DATE: 18-FEB-1998
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 53:
US-09-490-324-53

Query Match 85.7%; Score 30; DB 4; Length 110;
Best Local Similarity 85.7%; Pred. No. 25;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 52 EVNKRPS 58

RESULT 23
US-09-247-373B-42
Sequence 42, Application US/09247373B
Patent No. 6168854
GENERAL INFORMATION:
APPLICANT: MCGONIGLE, BRIAN
APPLICANT: O'KEEFE, DANIEL
TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE ENZYMES
FILE REFERENCE: CL-1108-A
CURRENT APPLICATION NUMBER: US/09/247,373B
CURRENT FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 08/924,747
PRIOR FILING DATE: 1997-09-05
NUMBER OF SEQ ID NOS: 56
SOFTWARE: Microsoft Office 97
SEQ ID NO 42
LENGTH: 215
TYPE: PRT
ORGANISM: SOYBEAN
US-09-247-373B-42

Query Match 82.9%; Score 29; DB 3; Length 215;
Best Local Similarity 71.4%; Pred. No. 85;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 197 DISSRPS 203

RESULT 24
US-09-232-290-17
Sequence 17, Application US/09232290A
Patent No. 6815540
GENERAL INFORMATION:
APPLICANT: PLUECKHUHN, ANDREAS
APPLICANT: NIEBA, LARS
APPLICANT: HONGEGGER, ANNEMARIE
TITLE OF INVENTION: IMMUNOGLOBULIN SUPER FAMILY DOMAINS AND FRAGMENTS WITH
FILE REFERENCE: MORPHO/7
CURRENT APPLICATION NUMBER: US/09/232,290A
CURRENT FILING DATE: 1999-01-15
EARLIER APPLICATION NUMBER: PCT/EP96/02230
EARLIER FILING DATE: 1996-05-23
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 17
LENGTH: 111
TYPE: PRT
ORGANISM: Homo sapiens
US-09-232-290-17

Query Match 80.0%; Score 28; DB 4; Length 111;
Best Local Similarity 71.4%; Pred. No. 70;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 52 EVNKRPS 58

RESULT 25
US-09-252-991A-23989
Sequence 23989, Application US/09252991A
Patent No. 6551795

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; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23989
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23989

Query Match      80.0%; Score 28; DB 4; Length 140;
Best Local Similarity 71.4%; Pred. No. 90;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 DVSKRPS 7
Db      73 DASKKPS 79

RESULT 26
US-09-134-000C-5577
; Sequence 5577, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5577
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (25)-(37)
; OTHER INFORMATION: Amino acids 25 & 37 are Xaa wherein Xaa = any amino acid.
US-09-134-000C-5577

Query Match      80.0%; Score 28; DB 4; Length 217;
Best Local Similarity 71.4%; Pred. No. 1.4e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 DVSKRPS 7
Db      160 DLSKQPS 166

RESULT 27
US-09-134-000C-4555
; Sequence 4555, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
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; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4555
; LENGTH: 294
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-4555

Query Match      80.0%; Score 28; DB 4; Length 294;
Best Local Similarity 71.4%; Pred. No. 2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 DVSKRPS 7
Db      27 DASKKPS 33

RESULT 28
US-09-270-767-43922
; Sequence 43922, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Hornburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43922
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-43922

Query Match      80.0%; Score 28; DB 4; Length 366;
Best Local Similarity 71.4%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 DVSKRPS 7
Db      297 DVERKPS 303

RESULT 29
US-09-252-991A-18161
; Sequence 18161, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18161
; LENGTH: 514
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18161

Query Match      80.0%; Score 28; DB 4; Length 514;
Best Local Similarity 85.7%; Pred. No. 3.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 DVSKRPS 7
Db      1111111111
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Db 44 DVSKRPS 50

RESULT 30

US-09-540-236-2750
; Sequence 2750, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breston et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540.236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2750
; LENGTH: 692
; TYPE: PRT
; ORGANISM: M.catarhalis
US-09-540-236-2750

Query Match 80.0%; Score 28; DB 4; Length 692;
Best Local Similarity 71.4%; Pred. No. 4.9e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 300 DVKRRPA 306

RESULT 31

US-08-867-941-15
; Sequence 15, Application US/08867941
; Patent No. 5977337
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M
; APPLICANT: Du, Run-Pan
; APPLICANT: Wang, Quijun
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/867.941
; FILING DATE: 03-JUN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-681 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 894 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-867-941-15

Query Match 80.0%; Score 28; DB 2; Length 894;
Best Local Similarity 71.4%; Pred. No. 6.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 287 DVKRRPA 293

RESULT 32

US-08-867-941-11
; Sequence 11, Application US/08867941
; Patent No. 5977337
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M
; APPLICANT: Du, Run-Pan
; APPLICANT: Wang, Quijun
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/867.941
; FILING DATE: 03-JUN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-681 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 898 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-867-941-11

Query Match 80.0%; Score 28; DB 2; Length 898;
Best Local Similarity 71.4%; Pred. No. 6.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 287 DVKRRPA 293

RESULT 33

US-09-538-092-423
; Sequence 423, Application US/09538092
; Patent No. 675314
; GENERAL INFORMATION:
; APPLICANT: Gloc, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538.092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352

;; PRIOR FILING DATE: 1999-04-01
;; PRIOR APPLICATION NUMBER: 60/178,965
;; PRIOR FILING DATE: 2000-02-01
;; NUMBER OF SEQ ID NOS: 1387
;; SOFTWARE: CuratSeqFormatter Version 0.9
;; SEQ ID NO: 423
;; LENGTH: 1118
;; TYPE: PRT
;; ORGANISM: Saccharomyces cerevisiae
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: (0)...(0)
;; OTHER INFORMATION: Polypeptide Accession Number YII151C
US-09-538-092-423

Query Match 80.0%; Score 28; DB 4; Length 1118;
Best Local Similarity 71.4%; Pred. No. 8.2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 94 DASKRPS 100

RESULT 34
US-09-321-987B-2
;; Sequence 2, Application US/09321987B
;; Patent No. 6730820
;; GENERAL INFORMATION:
;; APPLICANT: Kimble, Judith E
;; APPLICANT: Bielloch, Robert H
;; TITLE OF INVENTION: Agent and Method for Modulating Cell Migration
;; FILE REFERENCE: 960236.95386
;; CURRENT APPLICATION NUMBER: US/09/321,987B
;; CURRENT FILING DATE: 1999-05-28
;; PRIOR APPLICATION NUMBER: 60/087,170
;; PRIOR FILING DATE: 1998-05-29
;; PRIOR APPLICATION NUMBER: 60/129,023
;; PRIOR FILING DATE: 1999-04-13
;; NUMBER OF SEQ ID NOS: 5
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO: 2
;; LENGTH: 2150
;; TYPE: PRT
;; ORGANISM: Caenorhabditis elegans
US-09-321-987B-2

Query Match 80.0%; Score 28; DB 4; Length 2150;
Best Local Similarity 71.4%; Pred. No. 1.7e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 1452 DVQKRPT 1458

RESULT 35
US-09-800-729-155
;; Sequence 155, Application US/09800729
;; Patent No. 6605592
;; GENERAL INFORMATION:
;; APPLICANT: Nt et al.
;; TITLE OF INVENTION: 32 Human secreted proteins
;; FILE REFERENCE: P2044P1
;; CURRENT APPLICATION NUMBER: US/09/800,729
;; CURRENT FILING DATE: 2001-03-08
;; PRIOR APPLICATION NUMBER: PCT/US00/26013
;; PRIOR FILING DATE: 2000-09-22
;; PRIOR APPLICATION NUMBER: 60/155,709
;; PRIOR FILING DATE: 1999-09-24
;; NUMBER OF SEQ ID NOS: 217
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO: 155

;; LENGTH: 2165
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-800-729-155

Query Match 80.0%; Score 28; DB 4; Length 2165;
Best Local Similarity 71.4%; Pred. No. 1.7e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 1467 DVQKRPT 1473

RESULT 36
US-09-074-658-15
;; Sequence 15, Application US/09074658
;; Patent No. 6184371
;; GENERAL INFORMATION:
;; APPLICANT: Loomore, Sheena M
;; APPLICANT: Run-Pan Du
;; APPLICANT: Qijun Wang
;; APPLICANT: Yang, Yan-Ping
;; APPLICANT: Klein, Michel H
;; TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
;; NUMBER OF SEQUENCES: 78
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Sim & McBurney
;; STREET: 6th Floor, 330 University Avenue
;; CITY: Toronto
;; STATE: Ontario
;; COUNTRY: Canada
;; ZIP: M5G 1R7
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/074,658
;; FILING DATE: 08-MAY-1998
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Stewart, Michael I
;; REGISTRATION NUMBER: 24,973
;; REFERENCE/DOCKET NUMBER: 1038-795
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (416) 595-1155
;; TELEFAX: (416) 595-1163
;; INFORMATION FOR SEQ ID NO: 15:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 2432 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-09-074-658-15

Query Match 80.0%; Score 28; DB 3; Length 2432;
Best Local Similarity 71.4%; Pred. No. 1.9e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 287 DVKKRPA 293

RESULT 37
US-09-074-658-11
;; Sequence 11, Application US/09074658
;; Patent No. 6184371
;; GENERAL INFORMATION:
;; APPLICANT: Loomore, Sheena M
;; APPLICANT: Run-Pan Du


```

; APPLICANT: Quijun Wang
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESSES:
; ADDRESS: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/074,658
; FILING DATE: 08-MAY-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-795
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2439 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; US-09-074-658-11
;
Query Match      80.0%; Score 28; DB 3; Length 2439;
Best Local Similarity 71.4%; Pred. No. 1.9e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 DVSKRPS 7
Db      287 DVKRRPA 293

RESULT 38
US-09-107-532A-7296
; Sequence 7296, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESSES:
; ADDRESS: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER READABLE FORM:
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
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; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Arinello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: 489
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 7296:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 70 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
;
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...70
; SEQUENCE DESCRIPTION: SEQ ID NO: 7296:
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; US-09-107-532A-7296
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Query Match      77.1%; Score 27; DB 4; Length 70;
Best Local Similarity 71.4%; Pred. No. 72;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 DVSKRPS 7
Db      15 DCSRRPS 21

RESULT 39
US-09-248-796A-17949
; Sequence 17949, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCES: 107196,132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 17949
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Candida albicans
;
; US-09-248-796A-17949
;
Query Match      77.1%; Score 27; DB 4; Length 77;
Best Local Similarity 71.4%; Pred. No. 80;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 DVSKRPS 7
Db      6 NLSKRPS 12

RESULT 40
US-09-270-767-38080
; Sequence 38080, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
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; NUMBER OF SEQ ID NOS: 62517
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 38080
 ; LENGTH: 78
 ; TYPE: PRT
 ; ORGANISM: Drosophila melanogaster
 ; FEATURE:
 ; OTHER INFORMATION: Xaa means any amino acid
 US-09-270-767-38080

Query Match 77.1%; Score 27; DB 4; Length 78;
 Best Local Similarity 71.4%; Pred. No. 81;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 DVSKRPS 7
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 Db 47 DAXKRPS 53

Search completed: March 31, 2005, 12:13:27
 Job time : 13.6719 secs

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OM protein - protein search, using sw model

Run on: March 31, 2005, 12:10:00 ; Search time 39.1562 Seconds
(without alignments)
59.279 Million cell updates/sec

Title: US-10-614-959-14
Perfect score: 35
Sequence: 1 DVSKRPS 7

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Gapop 10.0 , Gapext 0.5

Searched: 1413372 seqs, 331592847 residues

Total number of hits satisfying chosen parameters: 1413372

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	100.0	99	US-10-308-817-98	Sequence 98, Appl
2	35	100.0	99	US-10-453-698-98	Sequence 98, Appl
3	35	100.0	110	US-10-447-331-1	Sequence 1, Appl
4	35	100.0	111	US-10-360-828-61	Sequence 61, Appl
5	35	100.0	240	US-09-880-748-1898	Sequence 1898, Ap
6	35	100.0	240	US-10-293-418-1898	Sequence 1898, Ap
7	35	100.0	241	US-09-880-748-2055	Sequence 2055, Ap
8	35	100.0	241	US-10-293-418-2055	Sequence 2055, Ap
9	35	100.0	243	US-09-880-748-1927	Sequence 1927, Ap
10	35	100.0	243	US-10-293-418-1927	Sequence 1927, Ap
11	35	100.0	245	US-09-880-748-1926	Sequence 1926, Ap
12	35	100.0	245	US-10-293-418-1926	Sequence 1926, Ap
13	35	100.0	245	US-10-293-418-3241	Sequence 3241, Ap

14	35	100.0	246	10	US-09-880-748-1913	Sequence 1913, Ap
15	35	100.0	246	10	US-09-880-748-1917	Sequence 1917, Ap
16	35	100.0	246	15	US-10-293-418-1913	Sequence 1913, Ap
17	35	100.0	246	15	US-10-293-418-1917	Sequence 1917, Ap
18	35	100.0	247	10	US-09-880-748-1443	Sequence 1443, Ap
19	35	100.0	247	10	US-09-880-748-1682	Sequence 1682, Ap
20	35	100.0	247	10	US-09-880-748-1685	Sequence 1685, Ap
21	35	100.0	247	10	US-09-880-748-1707	Sequence 1707, Ap
22	35	100.0	247	10	US-09-880-748-1899	Sequence 1899, Ap
23	35	100.0	247	10	US-09-880-748-1928	Sequence 1928, Ap
24	35	100.0	247	10	US-09-880-748-1934	Sequence 1934, Ap
25	35	100.0	247	15	US-10-293-418-1443	Sequence 1443, Ap
26	35	100.0	247	15	US-10-293-418-1682	Sequence 1682, Ap
27	35	100.0	247	15	US-10-293-418-1685	Sequence 1685, Ap
28	35	100.0	247	15	US-10-293-418-1707	Sequence 1707, Ap
29	35	100.0	247	15	US-10-293-418-1899	Sequence 1899, Ap
30	35	100.0	247	15	US-10-293-418-1928	Sequence 1928, Ap
31	35	100.0	247	15	US-10-293-418-1934	Sequence 1934, Ap
32	35	100.0	249	10	US-09-880-748-1419	Sequence 1419, Ap
33	35	100.0	249	10	US-09-880-748-1618	Sequence 1618, Ap
34	35	100.0	249	10	US-09-880-748-2049	Sequence 2049, Ap
35	35	100.0	249	10	US-09-880-748-2065	Sequence 2065, Ap
36	35	100.0	249	15	US-10-293-418-1419	Sequence 1419, Ap
37	35	100.0	249	15	US-10-293-418-1618	Sequence 1618, Ap
38	35	100.0	249	15	US-10-293-418-2049	Sequence 2049, Ap
39	35	100.0	250	10	US-09-880-748-859	Sequence 859, App
40	35	100.0	250	15	US-10-293-418-859	Sequence 859, App
41	35	100.0	251	10	US-09-880-748-917	Sequence 917, App
42	35	100.0	251	10	US-09-880-748-925	Sequence 925, App
43	35	100.0	251	10	US-09-880-748-1309	Sequence 1309, App
44	35	100.0	251	10	US-09-880-748-1671	Sequence 1671, App
45	35	100.0	251	10	US-09-880-748-1671	Sequence 1671, App

ALIGNMENTS

RESULT 1
US-10-308-817-98
Sequence 98, Application US/10308817
Publication No. US20030219861A1
GENERAL INFORMATION:
APPLICANT: Rother, Russel
TITLE OF INVENTION: HYBRID ANTIBODIES
FILE REFERENCE: 1087-37
CURRENT APPLICATION NUMBER: US/10/308,817
CURRENT FILING DATE: 2002-12-03
NUMBER OF SEQ ID NOS: 195
SOFTWARE: PatentIn version 3.1
SEQ ID NO 98
LENGTH: 99
TYPE: PRT
ORGANISM: human
US-10-308-817-98

Query Match 100.0%; Score 35; DB 15; Length 99;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
Db 52 DVSKRPS 58

RESULT 2
US-10-453-698-98
Sequence 98, Application US/10453698
Publication No. US20040038308A1
GENERAL INFORMATION:
APPLICANT: Rother, Russel
TITLE OF INVENTION: HYBRID ANTIBODIES
FILE REFERENCE: 82 CIP (1087-37 CIP)

; CURRENT APPLICATION NUMBER: US/10/453,698
; CURRENT FILING DATE: 2003-06-03
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 98
; LENGTH: 99
; TYPE: PRT
; ORGANISM: human
US-10-453-698-98

Query Match 100.0%; Score 35; DB 15; Length 99;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
|||
Db 52 DVSKRPS 58

RESULT 3
US-10-447-331-1
; Sequence 1, Application US/10447331
; Publication No. US20030219434A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; TITLE OF INVENTION: ANTIBODIES FOR CANCER THERAPY AND
; FILE REFERENCE: GENENT, 122A
; CURRENT APPLICATION NUMBER: US/10/447,331
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: US/09/515,825
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/122262
; PRIOR FILING DATE: 1999-03-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-447-331-1

Query Match 100.0%; Score 35; DB 15; Length 110;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
|||
Db 52 DVSKRPS 58

RESULT 4
US-10-360-828-61
; Sequence 61, Application US/10360828
; Publication No. US20030206909A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shaobing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS
; FILE REFERENCE: 22636-727
; CURRENT APPLICATION NUMBER: US/10/360,828
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 10/071,866
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 10/072,301
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 10/133,978
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61

; LENGTH: 111
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VL of scFv Ab124
US-10-360-828-61

Query Match 100.0%; Score 35; DB 15; Length 111;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
|||
Db 52 DVSKRPS 58

RESULT 5
US-09-880-748-1898
; Sequence 1898, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P5523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1898
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1898

Query Match 100.0%; Score 35; DB 10; Length 240;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
|||
Db 181 DVSKRPS 187

RESULT 6
US-10-293-418-1898
; Sequence 1898, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P5523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21

```

; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1898
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1898

```

```

Query Match          100.0%; Score 35; DB 15; Length 240;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 DVSKRPS 7
        |||||
Db      181 DVSKRPS 187

```

```

RESULT 7
; Sequence 2055, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2055
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2055

```

```

Query Match          100.0%; Score 35; DB 10; Length 241;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY      1 DVSKRPS 7
        |||||
Db      182 DVSKRPS 188

```

```

RESULT 8
US-10-293-418-2055
; Sequence 2055, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19

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; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2055
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-2055

```

```

Query Match          100.0%; Score 35; DB 15; Length 241;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 DVSKRPS 7
        |||||
Db      182 DVSKRPS 188

```

```

RESULT 9
US-09-880-748-1927
; Sequence 1927, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1927
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1927

```

```

Query Match          100.0%; Score 35; DB 10; Length 243;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 DVSKRPS 7
        |||||
Db      183 DVSKRPS 189

```

```

RESULT 10
US-10-293-418-1927
; Sequence 1927, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2

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; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1927
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1927
```

```

Query Match          100.0%; Score 35; DB 15; Length 243;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```

Qy      1 DVSKRPS 7
        |||||
Db      183 DVSKRPS 189
```

```

RESULT 11
US-09-880-748-1926
; Sequence 1926, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1926
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1926
```

```

Query Match          100.0%; Score 35; DB 10; Length 245;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy      1 DVSKRPS 7
        |||||
Db      185 DVSKRPS 191
```

```

RESULT 12
US-10-293-418-1926
```

```

; Sequence 1926, Application US/10293418
; Publication No. US2003022396A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1926
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1926
```

```

Query Match          100.0%; Score 35; DB 15; Length 245;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```

Qy      1 DVSKRPS 7
        |||||
Db      185 DVSKRPS 191
```

```

RESULT 13
US-10-293-418-3241
; Sequence 3241, Application US/10293418
; Publication No. US2003022396A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 3241
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-3241
```

Query Match 100.0%; Score 35; DB 15; Length 245;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
|||
Db 185 DVSKRPS 191

RESULT 14

US-09-880-748-1913
; Sequence 1913, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1913
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1913

Query Match 100.0%; Score 35; DB 10; Length 246;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
|||
Db 186 DVSKRPS 192

RESULT 15
US-09-880-748-1917
; Sequence 1917, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1917
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1917

Query Match 100.0%; Score 35; DB 10; Length 246;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
|||
Db 186 DVSKRPS 192

RESULT 16

US-10-293-418-1913
; Sequence 1913, Application US/10293418
; Publication No. US2003022396A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1913
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1913

Query Match 100.0%; Score 35; DB 15; Length 246;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
|||
Db 186 DVSKRPS 192

RESULT 17
US-10-293-418-1917
; Sequence 1917, Application US/10293418
; Publication No. US2003022396A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248

; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17,210
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1917
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1917

Query Match 100.0%; Score 35; DB 15; Length 246;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 186 DVSKRPS 192

RESULT 18
US-09-880-748-1443
; Sequence 1443, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1443
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1443

Query Match 100.0%; Score 35; DB 10; Length 247;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 187 DVSKRPS 193

RESULT 19
US-09-880-748-1682
; Sequence 1682, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248

; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1682
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1682

Query Match 100.0%; Score 35; DB 10; Length 247;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 187 DVSKRPS 193

RESULT 20
US-09-880-748-1685
; Sequence 1685, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1685
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1685

Query Match 100.0%; Score 35; DB 10; Length 247;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 188 DVSKRPS 194

RESULT 21
US-09-880-748-1707
; Sequence 1707, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17


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; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1707
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1707

```

```

Query Match      100.0%; Score 35; DB 10; Length 247;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy      1 DVSKRPS 7
      |||||
Db      187 DVSKRPS 193

```

```

RESULT 22
US-09-880-748-1899
; Sequence 1899, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1899
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1899

```

```

Query Match      100.0%; Score 35; DB 10; Length 247;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 DVSKRPS 7
      |||||
Db      187 DVSKRPS 193

```

```

RESULT 23
US-09-880-748-1928
; Sequence 1928, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816

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```

; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1928
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1928

```

```

Query Match      100.0%; Score 35; DB 10; Length 247;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 DVSKRPS 7
      |||||
Db      187 DVSKRPS 193

```

```

RESULT 24
US-09-880-748-1934
; Sequence 1934, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1934
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1934

```

```

Query Match      100.0%; Score 35; DB 10; Length 247;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 DVSKRPS 7
      |||||
Db      187 DVSKRPS 193

```

```

RESULT 25
US-10-293-418-1443
; Sequence 1443, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523p2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16

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PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1443
LENGTH: 247
TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-418-1443

Query Match 100.0%; Score 35; DB 15; Length 247;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DVSKRPS 7
DB 187 DVSKRPS 193

RESULT 26
US-10-293-418-1682
Sequence 1682, Application US/10293418
Publication No. US20030223996A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OR INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PFS23P2
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1682
LENGTH: 247
TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-418-1682

Query Match 100.0%; Score 35; DB 15; Length 247;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DVSKRPS 7
DB 187 DVSKRPS 193

RESULT 27

US-10-293-418-1685
Sequence 1685, Application US/10293418
Publication No. US20030223996A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OR INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PFS23P2
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1685
LENGTH: 247
TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-418-1685

Query Match 100.0%; Score 35; DB 15; Length 247;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DVSKRPS 7
DB 188 DVSKRPS 194

RESULT 28
US-10-293-418-1707
Sequence 1707, Application US/10293418
Publication No. US20030223996A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OR INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PFS23P2
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1707
LENGTH: 247
TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-418-1707

Query Match 100.0%; Score 35; DB 15; Length 247;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
|||
Db 187 DVSKRPS 193

RESULT 29

US-10-293-418-1899
; Sequence 1899, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:

; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1899
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1899

Query Match 100.0%; Score 35; DB 15; Length 247;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
|||
Db 187 DVSKRPS 193

RESULT 30

US-10-293-418-1928
; Sequence 1928, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:

; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248

; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1928
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1928

QY 1 DVSKRPS 7
|||
Db 187 DVSKRPS 193

Query Match 100.0%; Score 35; DB 15; Length 247;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
|||
Db 187 DVSKRPS 193

RESULT 31

US-10-293-418-1934
; Sequence 1934, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:

; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1934
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1934

Query Match 100.0%; Score 35; DB 15; Length 247;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
|||
Db 187 DVSKRPS 193

RESULT 32

US-09-880-748-1419
; Sequence 1419, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:

; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT FILING DATE: 2001-06-15

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; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1419
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1419

Query Match
Best Local Similarity 100.0%; Score 35; DB 10; Length 249;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 189 DVSKRPS 195

RESULT 33
US-09-880-748-1618
; Sequence 1618, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P5523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1618
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1618

Query Match
Best Local Similarity 100.0%; Score 35; DB 10; Length 249;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 189 DVSKRPS 195

RESULT 34
US-09-880-748-2049
; Sequence 2049, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P5523
; CURRENT APPLICATION NUMBER: US/09/880,748
```

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; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2049
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2049

Query Match
Best Local Similarity 100.0%; Score 35; DB 10; Length 249;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 189 DVSKRPS 195

RESULT 35
US-09-880-748-2065
; Sequence 2065, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P5523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2065
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2065

Query Match
Best Local Similarity 100.0%; Score 35; DB 10; Length 249;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 189 DVSKRPS 195

RESULT 36
US-10-293-418-1419
; Sequence 1419, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P5523P2
```

```

; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1419
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1419
```

```

Query Match      100.0%; Score 35; DB 15; Length 249;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy      1 DVSKRPS 7
        |||||
Db      189 DVSKRPS 195
```

```

RESULT 37
US-10-293-418-1618
; Sequence 1618, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1618
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1618
```

```

Query Match      100.0%; Score 35; DB 15; Length 249;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy      1 DVSKRPS 7
        |||||
```

```

Db      189 DVSKRPS 195
```

```

RESULT 38
US-10-293-418-2049
; Sequence 2049, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2049
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-2049
```

```

Query Match      100.0%; Score 35; DB 15; Length 249;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy      1 DVSKRPS 7
        |||||
Db      189 DVSKRPS 195
```

```

RESULT 39
US-10-293-418-2065
; Sequence 2065, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2065
```

; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-2065

Query Match 100.0%; Score 35; DB 15; Length 249;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
|||
Db 189 DVSKRPS 195

RESULT 40
US-09-880-748-859
; Sequence 859, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 859
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-859

Query Match 100.0%; Score 35; DB 10; Length 250;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
|||
Db 192 DVSKRPS 198

Search completed: March 31, 2005, 12:46:10
Job time : 40.1562 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: March 31, 2005, 11:51:19 ; Search time 9.95312 Seconds
(without alignments)
67.669 Million cell updates/sec

Title: US-10-614-959-14

Perfect score: 35

Sequence: 1 DVSKRPS 7

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_79:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	100.0	99	2 S36057	Ig lambda chain -
2	34	97.1	646	2 G85056	probable receptor-
3	32	91.4	60	2 A24626	Ig lambda chain V-
4	32	91.4	103	2 A38923	AL type amyloid fi
5	32	91.4	111	1 L2HUTR	Ig lambda chain V-
6	32	91.4	423	2 F64690	type IIS restricti
7	31	88.6	110	2 S51149	antibody light cha
8	31	88.6	111	1 L2HUTN	Ig lambda chain V-
9	31	88.6	111	2 S36281	Ig lambda chain V
10	30	85.7	112	2 S31515	Ig lambda chain V
11	30	85.7	112	2 S44105	Ig lambda chain V-
12	30	85.7	416	2 S26836	type II site-speci
13	29	82.9	74	2 AH2642	hypothetical prote
14	29	82.9	88	2 A97425	hypothetical prote
15	29	82.9	337	1 E70191	conserved hypotet
16	29	82.9	377	2 A32548	homeobox protein M
17	29	82.9	404	2 T00750	probable protein P
18	29	82.9	685	2 T21466	hypothetical prote
19	29	82.9	690	2 T21806	hypothetical prote
20	29	82.9	735	2 T00850	probable receptor-
21	29	82.9	972	2 H84903	hypothetical prote
22	29	82.9	1033	2 T37715	actin-interacting
23	29	82.9	1077	2 T21800	hypothetical prote
24	29	82.9	1245	2 G84897	hypothetical prote
25	28	80.0	91	2 T09711	ADP carrier pr
26	28	80.0	111	1 L2HUMC	Ig lambda chain V-
27	28	80.0	189	2 AE1316	GTP cyclonhydrolase
28	28	80.0	189	2 AE1688	GTP cyclonhydrolase
29	28	80.0	235	2 S25759	Ig lambda chain -

30	28	80.0	235	2 S14675	Ig lambda chain -
31	28	80.0	259	2 T40075	60s ribosomal prot
32	28	80.0	292	2 A64624	hypothetical prote
33	28	80.0	296	2 D71891	hypothetical prote
34	28	80.0	300	2 A82017	probable lipoprote
35	28	80.0	301	2 AE0243	hypothetical prote
36	28	80.0	309	2 B83999	mutans block spor
37	28	80.0	310	2 B97777	thioredoxin-disulf
38	28	80.0	310	2 D71703	thioredoxin reduct
39	28	80.0	348	2 G87604	thioredoxin reduct
40	28	80.0	440	2 S65358	familial Alzheimer
41	28	80.0	447	2 S35481	SRPM54 protein - M
42	28	80.0	452	2 T40769	hypothetical prote
43	28	80.0	458	1 Z2BPC2	gene 12 protein -
44	28	80.0	463	2 P04222	4-Hydroxybutyryl-C
45	28	80.0	498	1 HYBSPA	pseudolysin (EC 3.

ALIGNMENTS

RESULT 1

S36057
Ig lambda chain - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000

C:Accession: S36057

R:Williams, S.C.
Submitted to the EMBL Data Library, April 1993

A:Reference number: S36046

A:Accession: S36057

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-99 <MW>

A:Cross-references: EMBL:Z22196, NID:G312319, PIDN:CA80208.1, PID:G312320

C:Superfamily: immunoglobulin V region, immunoglobulin homology.

C:Keywords: heterotrimer, immunoglobulin

F:15-92/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 35; DB 2; Length 99;

Best Local Similarity 100.0%; Pred. No. 1.1; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
DB 52 DVSKRPS 58

RESULT 2

G85056
probable receptor-like protein kinase [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Aug-2004

C:Accession: G85056

R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring

Nature 402, 769-777, 1999

A>Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.

A:Reference number: A85001; MUID:20083488; PMID:10617158

A:Accession: G85056

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-646 <STO>

A:Cross-references: UNIPROT:Q9XEC7; GB:NC_001268; NID:G7267207; PIDN:CA877918.1; GSPDB:G

C:Geneid:8

A:Gene: AT4G04500

A:Map position: 4

C:Superfamily: protein kinase homology

Query Match 97.1%; Score 34; DB 2; Length 646;
Best Local Similarity 85.7%; Pred. No. 12; Indels 0; Gaps 0;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7

Db 606 DISKRPS 612

RESULT 3

IG lambda chain V-II region (Har) - human (fragment)

C/Species: Homo sapiens (man)
C/Date: 25-Oct-1987 #sequence_revision 25-Oct-1987 #text_change 16-Aug-1996
C/Accession: A24626

R/Eulitz, M.; Linke, R.

Biol. Chem. Hoppe-Seyler 366, 907-915, 1985

A/Title: Amyloid fibrils derived from V-region together with C-region fragments from a 1

A/Reference number: A24626; MUID:86077295; PMID:3935132

A/Accession: A24626

A/Molecule type: protein

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

Query Match 91.4%; Score 32; DB 2; Length 60;

Best Local Similarity 85.7%; Pred. No. 3.1;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7

Db 45 DVNRKPS 51

RESULT 4

AL type amyloid fibril protein precursor - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 21-Jan-2000

C/Accession: A38923

R/Eulitz, M.; Linke, R.P.

Biochem. Biophys. Res. Commun. 194, 1427-1434, 1993

A/Title: The precursor molecule of a V-lambda II-immunoglobulin light chain-derived amy1

A/Reference number: A38923; MUID:93356823; PMID:8352801

A/Accession: A38923

A/Molecule type: protein

A/Residues: 1-95/96-103 <EUL>

C/Comment: This protein is derived from an immunoglobulin light chain of lambda type.

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: amyloid; immunoglobulin

F/1-58/Product: AL type amyloid fibril protein #status predicted <MAT>

F/7-83/Domain: immunoglobulin homology <IMM>

Query Match 91.4%; Score 32; DB 2; Length 103;

Best Local Similarity 85.7%; Pred. No. 5.4;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7

Db 43 DVNRKPS 49

RESULT 5

IG lambda chain V-II region (Tro) - human (tentative sequence)

C/Species: Homo sapiens (man)

C/Date: 29-Jul-1981 #sequence_revision 29-Jul-1981 #text_change 09-Jul-2004

C/Accession: A01973

R/Scholz, R.; Yang, C.; Hilschmann, N.

Hope-Seyler's Z. Physiol. Chem. 360, 1903-1918, 1979

A/Title: Zur Struktur der Antikörper. Die Primärstruktur eines monoklonalen IGA 1

A/Reference number: A01973; MUID:80114123; PMID:118915

A/Accession: A01973

A/Molecule type: protein

A/Residues: 1-111 <SCH>

A/Cross-references: UNIPROT:P01707

C/Comment: This chain was isolated from a myeloma protein.

C/Genetics:

A/Gene: GDB:IGLV@
A/Cross-references: GDB:119342; OMIM:147240

A/Map position: 22q11.2-22q11.2

C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (Kap-

tain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: blocked amino end; heterotetramer; immunoglobulin

F/15-92/Domain: immunoglobulin homology <IMM>

F/1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #statu

F/22-90/Disulfide bonds: #status predicted

Query Match 91.4%; Score 32; DB 1; Length 111;

Best Local Similarity 85.7%; Pred. No. 5.9;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7

Db 52 DVNRKPS 58

RESULT 6

type IIS restriction enzyme R protein - Helicobacter pylori (strain 26695)

C/Species: Helicobacter pylori

C/Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004

C/Accession: F64690

R/Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.

Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKen-

son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Wathey, L.

Nature 388, 539-547, 1997

A/Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.;

A/Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A/Reference number: A64520; MUID:97394467; PMID:9252185

A/Accession: F64690

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-423 <TOM>

A/Cross-references: UNIPROT:O25919; GB:AE000637; GB:AE000511; NID:G2314536; PIDN:AD08411

Query Match 91.4%; Score 32; DB 2; Length 423;

Best Local Similarity 85.7%; Pred. No. 23;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7

Db 71 DVNRKPS 77

RESULT 7

antibody light chain V region - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000

C/Accession: S51149

R/de Kruit, V.; Boel, E.; Logtenberg, T.

submitted to the EMBL Data Library, January 1995

A/Description: Selection and application of human SCFV antibody fragments from a semi-sy-

A/Reference number: S51147

A/Accession: S51149

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-110 <DEK>

A/Cross-references: EMBL:X83712

C/Superfamily: immunoglobulin V region; immunoglobulin homology

F/13-90/Domain: immunoglobulin homology <IMM>

Query Match 88.6%; Score 31; DB 2; Length 110;

Best Local Similarity 85.7%; Pred. No. 9.8;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7

Db 50 EVSKRPS 56

RESULT 8

L2HWMN

Ig Lambda chain V-II region (Win) - human (tentative sequence)

C/Species: Homo sapiens (man)

C/Date: 30-Nov-1979 #sequence_revision 30-Nov-1979 #text_change 09-Jul-2004

C/Accession: A01978

R/Chen, B.L.; Chiu, Y.Y.H.; Humphrey, R.L.; Poljak, R.J.

Biochim. Biophys. Acta 537, 9-21, 1978

A/Title: Amino acid sequence of the human myeloma lambda chain Win.

A/Reference number: A01978; PMID:79062503; PMID:102365

A/Accession: A01978

A/Molecule type: protein

A/Residues: 1-111 <CHE>

A/Cross-references: UNIPROT:P01712

C/Comment: This is a Bence Jones protein.

C/Genetics:

A/Gene: GDB:IGLV@

A/Cross-references: GDB:119342; OMIM:147240

A/Map position: 22q11.2-22q11.2

C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: blocked amino end; heterotetramer

F/15-92/Domain: immunoglobulin homology <IMM>

F/22-90/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 88.6%; Score 31; DB 1; Length 111;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSKRPS 7

Db 52 DVSKRPS 58

RESULT 9

S36281

Ig Lambda chain V region (clone alpha-FOG1-A3) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000

C/Accession: S36281

R/Griffiths, A.D.; Malmqvist, M.; Marke, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.

EMBO J. 12, 725-734, 1993

A/Title: Human anti-self antibodies with high specificity from phage display libraries.

A/Reference number: S36256; PMID:93178448; PMID:7679990

A/Accession: S36281

A/Status: preliminary; nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-111 <GR1>

A/Cross-references: EMBL:Z18823; NID:G33414; PIDN:CAA79275.1; PID:G939907

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-92/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 88.6%; Score 31; DB 2; Length 111;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7

Db 52 EVSKRPS 58

RESULT 10

S31515

Ig Lambda chain V region - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000

C/Accession: S31515

R/van der Heijden, R.W.J.; Uytendaele, F.G.C.M.; Osterhaus, A.D.M.E.

submitted to the EMBL Data Library, January 1993

A/Description: V-Lambda-2 gene sequence of a high affinity anti-idiotypic IgM antibody

A/Reference number: S31515

A/Accession: S31515

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-112 <VAN>

A/Cross-references: EMBL:Z19546; NID:G33754; PIDN:CAA79606.1; PID:G33755

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-92/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 85.7%; Score 30; DB 2; Length 112;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSKRPS 7

Db 52 DVSKRPS 58

RESULT 11

S44105

Ig Lambda chain V-J region - human

C/Species: Homo sapiens (man)

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001

C/Accession: S44105

R/Hawkins, R.E.; Zhu, D.; Orecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.

Submitted to the EMBL Data Library, March 1994

A/Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable r

A/Reference number: S44105

A/Accession: S44105

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-112 <HAN>

A/Cross-references: EMBL:Z31388; NID:G472959; PIDN:CAA83263.1; PID:G940517

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-92/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 85.7%; Score 30; DB 2; Length 112;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSKRPS 7

Db 52 DVSKRPS 58

RESULT 12

S26836

Type II site-specific deoxyribonuclease (EC 3.1.21.4) MboII - Moraxella bovis

C/Species: Moraxella bovis

C/Date: 03-Mar-1994 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

C/Accession: S26836

R/Bocklage, H.; Heeger, K.; Mueller-Hill, B.

Nucleic Acids Res. 19, 1007-1013, 1991

A/Title: Cloning and characterization of the MboII restriction-modification system.

A/Reference number: S26835; PMID:91212177; PMID:2020540

A/Accession: S26836

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-416 <BOC>

A/Cross-references: UNIPROT:P23191; EMBL:X56977; NID:G44180; PIDN:CAA40298.1; PID:G44182

C/Keywords: hydrolase

Query Match

Best Local Similarity 85.7%; Score 30; DB 2; Length 416;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRP 6

Db 66 DISKRP 71

RESULT 13
 A:Title: hypothetical protein Atu0540 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
 C:Species: Agrobacterium tumefaciens
 C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
 A:Accession: AH2642
 R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, T.; Karp, P.; Romero, P.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClellan, S.; Science 294, 2317-2323, 2001
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, A.; ster, E.W.
 A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A:Reference number: AB2577; MUID:21608550; PMID:11743193
 A:Accession: AH2642
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-74 <KUR>
 A:Cross-references: UNIPROT:Q8UHW8; GB:AB008688; PIDN:AAL41558.1; PID:g17738891; GSPDB:C
 C:Genetics:
 A:Gene: Atu0540
 A:Map position: circular chromosome

Query Match 82.9%; Score 29; DB 2; Length 74;
 Best Local Similarity 71.4%; Pred. No. 19;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
 |:|:|:|
 Db 2 DISKPS 8

RESULT 14
 A:Title: hypothetical protein AGR_C_956 [imported] - Agrobacterium tumefaciens (strain C58, Cered
 C:Species: Agrobacterium tumefaciens
 C>Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
 A:Accession: A97425
 R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Gurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
 A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
 A:Reference number: A97359; MUID:21608551; PMID:11743194
 A:Accession: A97425
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-88 <KUR>
 A:Cross-references: UNIPROT:Q8UHW8; GB:AB007869; PIDN:AAK86354.1; PID:g15155478; GSPDB:C
 C:Genetics:
 A:Gene: AGR_C_956
 A:Map position: circular chromosome

Query Match 82.9%; Score 29; DB 2; Length 88;
 Best Local Similarity 71.4%; Pred. No. 23;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
 |:|:|:|
 Db 16 DISKPS 22

RESULT 15
 A:Title: conserved hypothetical protein BB0734 - Lyme disease spirochete
 C:Species: Borrelia burgdorferi (Lyme disease spirochete)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 A:Accession: E70191
 R:Fraser, C.M.; Casjens, S.; Hwang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White son, D.; Peterson, J.; Kervatage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.

Nature 390, 580-586, 1997
 A:Authors: Smith, H.O.; Venter, J.C.
 A:Title: Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.
 A:Reference number: A70100; MUID:98065943; PMID:9403685
 A:Accession: E70191
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-337 <KUR>
 A:Cross-references: UNIPROT:O51676; GB:AB001173; GB:AB000783; NID:g2688665; PIDN:AA6708
 A:Experimental source: strain B31
 C:Superfamily: translation factor, SWS type

Query Match 82.9%; Score 29; DB 1; Length 337;
 Best Local Similarity 71.4%; Pred. No. 88;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
 |:|:|:|
 Db 141 DISKPS 147

RESULT 16
 A:Title: homeobox protein Mix.1 - African clawed frog
 C:Species: Xenopus laevis (African clawed frog)
 C>Date: 05-Oct-1989 #sequence_revision 28-Aug-1992 #text_change 09-Jul-2004
 A:Accession: A32548
 R:Roza, F.M.
 Cell 57, 965-974, 1989
 A:Title: Mix.1, a homeobox mRNA inducible by mesoderm inducers, is expressed mostly in t
 A:Reference number: A32548; MUID:89288302; PMID:2567635
 A:Accession: A32548
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-377 <ROS>
 A:Cross-references: UNIPROT:P21711; GB:M27063; NID:g532660; PIDN:AAA49903.1; PID:g532661
 C:Superfamily: unassigned homeobox proteins; homeobox homology
 C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
 F:97-153/Domains: homeobox homology <HOX>

Query Match 82.9%; Score 29; DB 2; Length 377;
 Best Local Similarity 71.4%; Pred. No. 98;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
 |:|:|:|
 Db 280 DISKPS 266

RESULT 17
 A:Title: probable protein phosphatase 2C [imported] - Arabidopsis thaliana
 N:Alternate names: hypothetical protein T2095.6
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
 A:Accession: T00750; G84834
 R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul submitted to the EMBL Data Library, November 1997
 A:Description: Arabidopsis thaliana chromosome II BAC T2095 genomic sequence.
 A:Reference number: Z14159
 A:Accession: T00750
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-404 <ROU>
 A:Cross-references: UNIPROT:Q22200; EMBL:AC002409; NID:g2623294; PID:g2623300
 A:Experimental source: cultivar Columbia
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shee, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: G84834

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-404 <STO>
C;Cross-references: GB:AE002093; NID:G2623300; PIDN:AAH86446.1; GSPDB:GN00139
C;Genetics:
A;Gene: T20B5.6; At2g40860
A;Map position: 2
A;Introns: 178/1; 200/2; 273/3; 308/3; 340/3

Query Match 82.9%; Score 29; DB 2; Length 404;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 43 DVSKRPS 49

RESULT 18

T21466

hypothetical protein F28B1.5 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T21466

R;Matthews, L.

Submitted to the EMBL Data Library, November 1996

A;Reference number: Z19426

A;Accession: T21466

A;Status: preliminary; translated from GB/EMBL/DBDUT

A;Molecule type: DNA

A;Residues: 1-685 <WIL>

A;Cross-references: UNIPROT:O45415; EMBL:Z81517; PIDN:CAB04212.1; GSPDB:GN00023; CESP:F2

A;Experimental source: clone F28B1

C;Genetics:

A;Gene: CESP:F28B1.5

A;Map position: 5

A;Introns: 31/3; 156/3; 258/3; 305/1; 384/3; 500/3; 600/3; 641/3

Query Match 82.9%; Score 29; DB 2; Length 685;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSKRPS 7
Db 347 VSKRPS 352

RESULT 19

T21806

hypothetical protein F35G12.3b - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T21806

R;Chui, C.

Submitted to the EMBL Data Library, October 1994

A;Reference number: Z19473

A;Accession: T21806

A;Status: preliminary; translated from GB/EMBL/DBDUT

A;Molecule type: DNA

A;Residues: 1-690 <WIL>

A;Cross-references: UNIPROT:Q20056; EMBL:Z46242; PIDN:CAA6332.1; GSPDB:GN00021; CESP:F3

A;Experimental source: clone F35G12

C;Genetics:

A;Gene: CESP:F35G12.3b

A;Map position: 3

A;Introns: 37/1; 56/1; 96/3; 132/1; 244/1; 295/1; 332/3; 431/3; 538/2; 612/1

C;Superfamily: yeast hypothetical protein YNL020c; protein kinase homology

Query Match 82.9%; Score 29; DB 2; Length 690;
Best Local Similarity 71.4%; Pred. No. 1.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7

Db 301 DVNRPS 307

RESULT 20

T00850

probable receptor-like protein kinase [imported] - Arabidopsis thaliana

N;Alternate names: hypothetical protein T20F6.8

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 16-Aug-2004

C;Accession: T00850; G84440

R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul

submitted to the EMBL Data Library, March 1998

A;Description: Arabidopsis thaliana chromosome II BAC T20F6 genomic sequence.

A;Reference number: Z14206

A;Accession: T00850

A;Status: translated from GB/EMBL/DBDUT

A;Molecule type: DNA

A;Residues: 1-735 <ROU>

A;Cross-references: UNIPROT:O64505; EMBL:AC002521; NID:G2947056; PID:G2947063

A;Experimental source: cultivar Columbia

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Yankken, S.E.; Unayam, L.; Tallon, L.

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: G84440

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-735 <STO>

A;Cross-references: GB:AE002093; NID:G2947063; PIDN:AA05344.1; GSPDB:GN00139

C;Genetics:

A;Gene: T20F6.8; At2g02780

A;Map position: 2

A;Introns: 421/1; 472/3; 555/1; 619/3; 652/3

C;Superfamily: protein kinase homology

Query Match 82.9%; Score 29; DB 2; Length 735;
Best Local Similarity 85.7%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 695 DVSKRPS 701

RESULT 21

H84903

hypothetical protein At2g46520 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C;Accession: H84903

R;Jian, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Yankken, S.E.; Unayam, L.; Tallon, L.

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: H84903

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-972 <STO>

A;Cross-references: UNIPROT:Q9ZPY7; GB:AE002093; NID:G4415933; PIDN:AA020163.1; GSPDB:GN

C;Genetics:

A;Gene: At2g46520

A;Map position: 2

Query Match 82.9%; Score 29; DB 2; Length 972;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSKRPS 7

Db 311 DVSKRPS 317

RESULT 22

T37715 actin-interacting homolog SPAC15A10.16 [imported] - fission yeast (Schizosaccharomyces f)

C:Species: Schizosaccharomyces pombe
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 15-Sep-2000
C:Accession: T37715

R:Murphy, L.; Harris, D.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, June 1997

A:Reference number: Z21738

A:Accession: T37715

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1033 <MUR>

A:Cross-references: EMBL:Z97208; PIDN:CAB10112.1; GSPDB:GN00066; SPDB:SPAC15A10.16

A:Experimental source: strain 972h; cosmid c15A10

C:Genetics:

A:Gene: SPAC15A1.01; SPDB:SPAC15A10.16

A:Map position: 1

Query Match 82.9%; Score 29; DB 2; Length 1033;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSKRPS 7
Db 298 VSKRPS 303

RESULT 23

T21800 hypothetical protein F35G12.3a - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T21800

R:Chui, C.

submitted to the EMBL Data Library, October 1994

A:Reference number: Z19473

A:Accession: T21800

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1077 <MTL>

A:Cross-references: UNIPROT:Q20050; EMBL:Z46242; PIDN:CAA66326.1; GSPDB:GN00021; CESP:F3

A:Experimental source: clone F35G12

C:Genetics:

A:Gene: CESP:F35G12.3a

A:Map position: 3

Query Match 82.9%; Score 29; DB 2; Length 1077;
Best Local Similarity 71.4%; Pred. No. 2.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 301 DVNRPS 307

RESULT 24

G84897 hypothetical protein At2g46020 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C:Accession: G84897

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.

eues, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: G84897

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1245 <STO>

A:Cross-references: UNIPROT:O82366; GB:AE002093; NID:G3702343; PIDN:AA62900.1; GSPDB:GN

C:Genetics:

A:Gene: At2g46020

A:Map position: 2

Query Match 82.9%; Score 29; DB 2; Length 1245;
Best Local Similarity 71.4%; Pred. No. 3.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 633 DVSKRPS 639

RESULT 25

T09711

ADP,ATP carrier protein CANT2 - upland cotton (fragment)

N:Alternate names: adenine nucleotide translocator 2

C:Species: Gossypium hirsutum (upland cotton)

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004

C:Accession: T09711

R:Shin, H.; Brown, R.M.

submitted to the EMBL Data Library, June 1997

A:Reference number: Z16832

A:Accession: T09711

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-91 <SHI>

A:Cross-references: UNIPROT:O22343; EMBL:AF006490; NID:G2463665; PID:G2463666

A:Experimental source: strain Texas marker1; fiber

C:Genetics:

A:Gene: CANT2

C:Function: catalyzes the exchange of ADP and ATP

C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match 80.0%; Score 28; DB 2; Length 91;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 3 DVSKRPS 9

RESULT 26

L2HDMC Ig lambda chain V-II region (Mcg) - human

C:Species: Homo sapiens (man)

C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004

C:Accession: A90381; A01975

R:Felt, J.W.; Deutsch, H.F.

Biochemistry 13, 4102-4114, 1974

A:Title: Primary structure of the Mcg lambda chain.

A:Reference number: A90381; MUID:75013804; PMID:4415202

A:Accession: A90381

A:Molecule type: Protein

A:Residues: 1-111 <FET>

A:Note: the C region of this chain has the Kern+ and Mcg+ markers

R:Felt, J.W.; Deutsch, H.F.

Immunochimistry 12, 643-652, 1975

A:Title: A new lambda-chain gene.

A:Reference number: A91745; MUID:76093781; PMID:812801

A:Contents: annotation; lambda chain genes

A:Note: the Mcg-type C region appears to be correlated with a very unusual V-region subet

R:Edmundson, A.B.; Ely, K.R.; Abola, E.E.; Schiffer, M.; Panagiotopoulos, N.

Biochemistry 14, 3953-3961, 1975

A:Title: Rotational allomerism and divergent evolution of domains in immunoglobulin light

A:Reference number: A90391
A:Contents: annotation; X-ray crystallography, 2.3 angstroms
A:Comment: This is a Bence Jones protein.
C:Genetics:
A:Gene: GDB:IGLV@
A:Cross-references: GDB:119342; OMIM:147240
A:Map position: 22q11.2-22q11.2
C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (Kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 18 C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: blocked amino end; heterotrimer
F:15-92/Domain: immunoglobulin homology <IMM>
F:1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #status F:22-90/Disulfide bonds: #status predicted

Query Match 80.0%; Score 28; DB 1; Length 111;
Best Local Similarity 71.4%; Pred. No. 48;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
|||:|
Db 52 EVNKRPS 58

RESULT 27
AE1316
GTP cyclohydrolase I homolog lmo1933 [imported] - Listeria monocytogenes (strain EGD-e)
C:Species: Listeria monocytogenes
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AE1316
R:Glaser, P.; Prangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bioecker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Feihl, H.; Jones, L.M.; Karet, U.
Science 294, 849-852, 2001
A:Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurapat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schluecker, T.; Simoes, N.; Tietz, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend, A.; Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AE1316
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-189 <GLA>
A:Cross-references: UNIPROT:Q8Y5X1; GB:NC_003210; PIDN:CAD00011.1; PID:G16411386; GSPDB: C:Genetics:
A:Experimental source: strain EGD-e
A:Gene: lmo1933
C:Superfamily: GTP cyclohydrolase I

Query Match 80.0%; Score 28; DB 2; Length 189;
Best Local Similarity 83.3%; Pred. No. 83;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRP 6
|||:|
Db 112 DVSRRP 117

RESULT 28
AE1688
GTP cyclohydrolase I homolog lin2047 [imported] - Listeria innocua (strain C1p11262)
C:Species: Listeria innocua
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AE1688
R:Glaser, P.; Prangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bioecker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Feihl, H.; Jones, L.M.; Karet, U.
Science 294, 849-852, 2001
A:Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurapat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schluecker, T.; Simoes, N.; Tietz, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend, A.; Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AE1688
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-189 <GLA>
A:Cross-references: UNIPROT:Q92A75; GB:AL592022; PIDN:CAC97277.1; PID:G16414548; GSPDB: C:Genetics:
A:Experimental source: strain C1p11262
A:Gene: lin2047
C:Superfamily: GTP cyclohydrolase I

Query Match 80.0%; Score 28; DB 2; Length 189;
Best Local Similarity 83.3%; Pred. No. 83;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRP 6
|||:|
Db 112 DVSRRP 117

RESULT 29
S25759
Ig lambda chain - human
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S25759
R:Combario, G.; Klobock, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A:Title: V(lambda) and J(lambda) gene segments of the human immunoglobulin lambda
A:Reference number: S16439; MUID:91257162; PMID:1904362
A:Accession: S25759
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-235 <COM>
A:Cross-references: EMBL:X57824; NID:G33747; PIDN:CAA40961.1; PID:G33748
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:150-218/Domain: immunoglobulin homology <IMM>

Query Match 80.0%; Score 28; DB 2; Length 235;
Best Local Similarity 85.7%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
|||:|
Db 71 DVSGRPS 77

RESULT 30
S14675
Ig lambda chain - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 09-Jul-2004
C:Accession: S14675; S12445
R:Vaaiček, T.J.
submitted to the EMBL Data Library, February 1990
A:Reference number: S14675
A:Accession: S14675
A:Molecule type: DNA
A:Residues: 1-235 <VAS1>
A:Cross-references: UNIPROT:Q8WTK4; EMBL:X51754
J. Exp. Med. 172, 609-620, 1990
A:Title: Structure and expression of the human immunoglobulin lambda genes.
A:Reference number: S12440; MUID:90324881; PMID:2115572
A:Accession: S12445
A:Cross-references: EMBL:X51754
C:Genetics:
A:Insertions: 16/1; 130/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:150-218/Domain: immunoglobulin homology <IMM>

Query Match 80.0%; Score 28; DB 2; Length 235;

Best Local Similarity 71.4%; Pred. No. 1e+02; Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 DVSKRPS 7
Db 71 EVTKRPS 77

RESULT 31

T40075

60s ribosomal protein l8 - fission yeast (Schizosaccharomyces pombe)

N/Alternate names: ribosomal protein L7; ribosomal protein L7a, cytosolic

C/Species: Schizosaccharomyces pombe

C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C/Accession: T40075; T45223

R/Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Voiclaert, G.

submitted to the EMBL Data Library, March 1998

A/Reference number: Z21904

A/Accession: T40075

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-259 <L>N>

A/Cross-references: UNIPROT:O13672; EMBL:AL022299; PIDN:CAA18381.1; GSPDB:GN00067; SPDB:

A/Experimental source: strain 972h-1; cosmid C29A3

R/Marchfelder, A.; Clayton, D.A.; Brennicke, A.

Biochim. Biophys. Acta 1397, 146-150, 1998

A/Title: The gene for ribosomal protein L7a in Schizosaccharomyces pombe contains an int

A/Reference number: Z22944; MUID:98234301; PMID:9565672

A/Accession: T45223

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-259 <MAR>

A/Cross-references: EMBL:AJ001133; NID:g3123704; PIDN:CAA04548.1; PID:g3123705

C/Genetics:

A/Gene: rp18-1; SPBC29A3.04; L7A

A/Map position: 2

A/Insertions: 1/3

C/Superfamily: rat ribosomal protein L7a

Query Match 80.0%; Score 28; DB 2; Length 259;

Best Local Similarity 83.3%; Pred. No. 1.1e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DVSKRP 6

Db 124 DVSKRP 129

RESULT 32

A64624

hypothetical protein HP0833 - Helicobacter pylori (strain 26695)

C/Species: Helicobacter pylori

C/Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004

C/Accession: A64624

R/Tomb, J.F.; White, O.; Kelland, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.

Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Knapik, H.G.; Glodek, A.; McKen-

son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Wathey, L.

Nature 388, 539-547, 1997

A/Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karp, P.D.; Smith, H.O.; Fraser, C.

A/Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A/Reference number: A64520; MUID:97394467; PMID:9252185

A/Accession: A64624

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-292 <TOM>

A/Cross-references: UNIPROT:O25504; GB:AE000594; GB:AE000511; NID:g2313957; PIDN:AA00786

C/Genetics:

A/Start codon: TTC

C/Superfamily: Helicobacter pylori hypothetical protein jhp0772

Query Match 80.0%; Score 28; DB 2; Length 292;

Best Local Similarity 85.7%; Pred. No. 1.3e+02;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 DVSKRPS 7
Db 38 DGSKRPS 44

RESULT 33

D71891

hypothetical protein jhp0772 - Helicobacter pylori (strain J99)

C/Species: Helicobacter pylori

A/Variety: strain J99

C/Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004

C/Accession: D71891

R/Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;

Ives, C.; Gibson, R.; Merxer, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;

Nature 397, 176-180, 1999

A/Title: Genomic sequence comparison of two unrelated isolates of the human gastric path

A/Reference number: A71800; MUID:99120557; PMID:9923682

A/Accession: D71891

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-296 <ARN>

A/Cross-references: UNIPROT:Q9ZL10; GB:AE001507; GB:AE001439; NID:g4155326; PIDN:AA006351

A/Experimental source: strain J99

C/Genetics:

A/Gene: jhp0772

C/Superfamily: Helicobacter pylori hypothetical protein jhp0772

Query Match 80.0%; Score 28; DB 2; Length 296;

Best Local Similarity 85.7%; Pred. No. 1.3e+02;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 DVSKRPS 7

Db 38 DGSKRPS 44

RESULT 34

A82017

probable lipoprotein NMA0225 [imported] - Neisseria meningitidis (strain Z2491 serogroup

C/Species: Neisseria meningitidis

C/Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004

C/Accession: A82017

R/Parikh, U.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morell

; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,

Nature 404, 502-506, 2000

A/Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.

A/Reference number: A81775; MUID:20222556; PMID:10761919

A/Accession: A82017

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-300 <PAR>

A/Cross-references: UNIPROT:Q9UWV3; GB:AL167752; GB:AL157959; NID:g7378778; PIDN:CA863536

A/Experimental source: serogroup A, strain Z2491

C/Genetics:

A/Gene: NMA0225

Query Match 80.0%; Score 28; DB 2; Length 300;

Best Local Similarity 71.4%; Pred. No. 1.3e+02;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 DVSKRPS 7

Db 217 DISRPS 223

RESULT 35

AE0243

hypothetical protein YPO1996 [imported] - Yersinia pestis (strain CO92)

C/Species: Yersinia pestis

C/Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004

C/Accession: AE0243

R/Parikh, U.; Wren, B.W.; Thomson, N.R.; Tildall, R.W.; Holden, M.T.G.; Prentice, M.B.;

deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,
Nature 413, 523-527, 2001
A>Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
A/Reference number: AB0001; MUID:21470413; PMID:11586360
A/Accession: AB0243
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-301 <KUR>
A/Cross-references: UNIPROT:Q8ZF00; GB:AL590842; PIDN:CAK90809.1; PID:g15980010; GSPDB:C
C/Genetics:
A/Gene: YPO1996

Query Match 80.0%; Score 28; DB 2; Length 301;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
|:|:|:|
Db 142 DLSQRP 148

RESULT 36
E83999
mutants block sporulation after engulfment spoIIIA [imported] - *Bacillus halodurans* (st
C/Species: *Bacillus halodurans*
C/Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C/Accession: E83999
R/Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Maui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A>Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and
A/Reference number: AB3650; MUID:20512582; PMID:11058132
A/Accession: E83999
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-309 <STO>
A/Cross-references: UNIPROT:Q9K953; GB:AP001516; GB:BA000004; NID:g10175192; PIDN:BAB065
A/Experimental source: strain C-125
C/Genetics:
A/Gene: spoIIIA

Query Match 80.0%; Score 28; DB 2; Length 309;
Best Local Similarity 71.4%; Pred. No. 1.4e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
|:|:|:|
Db 263 EVSKRPA 269

RESULT 37
B97777
thioredoxin-disulfide reductase (EC 1.8.1.9) - *Rickettsia conorii* (strain Malish 7)
C/Species: *Rickettsia conorii*
C/Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C/Accession: B97777
R/Ogata, H.; Andic, S.; Renato-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Ro
Science 293, 2093-2098, 2001
A>Title: Mechanisms of evolution in *Rickettsia conorii* and *Rickettsia prowazekii*.
A/Reference number: A57700; MUID:21442074; PMID:11557893
A/Accession: B97777
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-310 <KUR>
A/Cross-references: UNIPROT:Q92102; GB:AE006914; PIDN:AAJ03156.1; PID:g15619703; GSPDB:C
C/Genetics:
A/Gene: trxB1
C/Superfamily: thioredoxin reductase; thioredoxin reductase homology
C/Keywords: oxidoreductase

Query Match 80.0%; Score 28; DB 2; Length 310;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRP 6
|:|:|:|
Db 87 DLSKRP 92

RESULT 38
D71703
thioredoxin reductase (trxB1) RP445 - *Rickettsia prowazekii*
C/Species: *Rickettsia prowazekii*
C/Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
C/Accession: D71703
R/Anderson, S.G.E.; Zomorodipour, A.; Anderson, J.O.; Scharitz-Ponten, T.; Alsmark, U
Nature 396, 133-140, 1998
A>Title: The genome sequence of *Rickettsia prowazekii* and the origin of mitochondria.
A/Reference number: A71630; MUID:99039499; PMID:9828893
A/Accession: D71703
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-310 <AND>
A/Cross-references: UNIPROT:Q9ZD97; GB:AJ235271; GB:AJ235269; NID:g3868717; PIDN:CAA1490
A/Experimental source: strain Madrid E
C/Genetics:
A/Gene: trxB1; RP445
C/Superfamily: thioredoxin reductase; thioredoxin reductase homology
F.1-308/Domain: thioredoxin reductase homology <TRXB>

Query Match 80.0%; Score 28; DB 2; Length 310;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRP 6
|:|:|:|
Db 87 DLSKRP 92

RESULT 39
G87604
thioredoxin reductase [imported] - *Caulobacter crescentus*
C/Species: *Caulobacter crescentus*
C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C/Accession: G87604
R/Nieman, W.C.; Feldlyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Land, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A>Title: Complete Genome Sequence of the bacterium *Caulobacter crescentus*.
A/Reference number: A87249; MUID:21173698; PMID:11259647
A/Accession: G87604
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-348 <STO>
A/Cross-references: UNIPROT:Q9A4G3; GB:AE005673; NID:g13424487; PIDN:AAK24835.1; GSPDB:C
C/Genetics:
A/Gene: CC2871
C/Superfamily: thioredoxin reductase; thioredoxin reductase homology

Query Match 80.0%; Score 28; DB 2; Length 348;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRP 6
|:|:|:|
Db 104 DLSKRP 109

RESULT 40
S65358
familial Alzheimer's disease protein 1 - human
C/Species: *Homo sapiens* (man)
C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C/Accession: S65358
R/Matsumoto, A.; Matsumoto, R.; Fujiwara, Y.

Eur. J. Biochem. 230, 337-343, 1995
 A;Title: Molecular cloning of human cDNA with a sequence highly similar to that of the d
 A;Reference number: S65358; MUID:95324544; PMID:7601120
 A;Accession: S65358
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-440 <MAT>
 A;Cross-references: UNIPROT:Q7M4L1

Query Match 80.0%; Score 28; DB 2; Length 440;
 Best local Similarity 71.4%; Pred. No. 1.9e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DVSKRPS 7
 ||:||||
 Db 204 DVGRRPS 210

Search completed: March 31, 2005, 12:11:17
 Job time : 11.9531 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 31, 2005, 11:42:54 ; Search time 46.4844 Seconds
(without alignments)
77.113 Million cell updates/sec

Title: US-10-614-959-14
Perfect score: 35
Sequence: 1 DVSKRPS 7

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	97.1	646	2	Q9XEC7 arabidopsis
2	32	91.4	111	1	P01707 homo sapien
3	32	91.4	236	2	Q6PIQ7 homo sapien
4	32	91.4	423	2	O25919 helicobacte
5	31	88.6	111	1	P01712 homo sapien
6	31	88.6	130	2	Q7M0S6 porphyromon
7	31	88.6	233	2	Q7S4H3 neurospora
8	31	88.6	400	2	Q7SZL9 brachydanio
9	31	88.6	402	2	O64WES bacteroides
10	31	88.6	486	2	Q828G3 streptomyce
11	31	88.6	728	2	Q7SFS9 neurospora
12	31	88.6	1292	2	Q6SLD6 cochlilobulu
13	31	88.6	1766	2	Q7SE06 ashbya goss
14	31	88.6	1935	1	AT9S HUMAN
15	30	85.7	164	1	BRL1 MAMGNG
16	30	85.7	212	2	Q9V6F8 drosophila
17	30	85.7	233	2	Q6SUA3 homo sapien
18	30	85.7	236	2	Q6P5S3 homo sapien
19	30	85.7	267	2	Q9BTM2 homo sapien
20	30	85.7	279	1	Y170 BUCBP
21	30	85.7	283	2	Q70914 prunus necr
22	30	85.7	283	2	Q70918 prunus necr
23	30	85.7	285	2	Q71142 prunus necr
24	30	85.7	327	2	Q66V04 homo sapien
25	30	85.7	378	2	Q9XY82 enchytraeus
26	30	85.7	385	2	Q7S098 neurospora
27	30	85.7	401	2	Q6DHL1 moraxella b
28	30	85.7	416	1	T2M2 MORBO
29	30	85.7	508	2	Q80U48 mus musculu
30	30	85.7	530	2	Q6PHCO mus musculu
31	30	85.7	654	2	Q8CA22 mus musculu

32	30	85.7	674	2	Q9DBJ2 mus musculu
33	30	85.7	706	1	TM24_HUMAN
34	30	85.7	706	1	TM24_MOUSE
35	30	85.7	747	2	Q6D0L7 erwinia car
36	30	85.7	833	2	Q6ADP4 leifsonia x
37	30	85.7	1036	2	Q6LMO4 methanococc
38	30	85.7	1059	2	Q64Q01 bacteroides
39	30	85.7	1372	2	Q8SX99 drosophila
40	30	85.7	1372	2	Q9VN46 drosophila
41	29	82.9	59	2	Q6EYX3 vilis vinif
42	29	82.9	74	2	Q8UHW8 agrobacteri
43	29	82.9	80	2	Q6LX05 photobacter
44	29	82.9	88	2	Q7D190 agrobacteri
45	29	82.9	103	2	Q6D0T2 erwinia car

ALIGNMENTS

RESULT 1
Q9XEC7 PRELIMINARY; PRT; 646 AA.
AC Q9XEC7, 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Putative receptor-like protein kinase.
GN Name=Tr26N6.11; Synonyms=AT9404500;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCHI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhong J., Ma P., Parnell L.D., Chen C.-N., Chen E.Y.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Parnell L.D.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Zhong J., Ma P., Parnell L.D., Chen C.-N., Chen E.Y., Mewes H.W.,
RL Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AF076243; AAD29762.1; -;
DR EMBL; AL161500; CAB77918.1; -;
DR PIR; G85056; G85056.
DR HSSP; P06239; 3LCK.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR002902; DUF26.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot Kinase.
DR InterPro; IPR008271; Ser_Thr_Pkin_AS.
DR Pfam; PF01657; DUF26; 2.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_Kinase; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KM ATP-binding; Kinase; Receptor; Serine/threonine-protein kinase;
KW transferase.
SQ SEQUENCE 646 AA; 73439 MW; E1200574D5864207 CRC64;

Query Match 97.1%; Score 34; DB 2; Length 646;
 Best Local Similarity 85.7%; Pred. No. 69;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
 DB 606 DISKPS 612

RESULT 2

LV2D HUMAN STANDARD; PRT; 111 AA.
 AC P01707;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 05-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig lambda chain V-II region TMO.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=80114123; PubMed=118915;
 RA Scholz R., Yang C., Hilschmann N.;
 RT "Rule of antibody structure. Primary structure of a human monoclonal
 RT IgM1-immunoglobulin (myeloma protein Tro). VI. Amino acid sequence of
 RT the L-chain, lambda-type, subgroup II.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 360:1903-1916(1979).
 CC -I- MISCELLANEOUS: This chain was isolated from a myeloma protein.
 CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR HSP; A01973; L2HUTR.
 DR HSP; P01709; 2MCG.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Direct protein sequencing; Immunoglobulin V region;
 KW Pyrolydione carboxylic acid.
 FT MOD_RS 1 106 Ig-like.
 FT DISULFID 22 90 Pyrolydione carboxylic acid.
 FT NON_TER 111 111 By similarity.
 SQ SEQUENCE 111 AA; 11561 MW; 99DC457A12B8F6E1 CRC64;

Query Match 91.4%; Score 32; DB 1; Length 111;
 Best Local Similarity 85.7%; Pred. No. 31;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
 DB 52 DVTMRPS 58

RESULT 3

Q6PI07 PRELIMINARY; PRT; 236 AA.
 DT 05-JUL-2004 (TReMBLrel. 27, Created)
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
 RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedon T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schermer A., Schein J.E.,
 RA Jones S.U., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Strauberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC030983; AA030983.1; -.
 DR HSP; P01709; 1A87.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig-cl.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IgV.
 DR Pfam; PF01654; Cl-set; 1.
 DR SMART; SM00409; Ig; 2.
 DR SMART; SM00407; IGC1; 1.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 KW Hypothetical protein
 SQ SEQUENCE 236 AA; 25021 MW; 4A07BEF60A5FD465 CRC64;

Query Match 91.4%; Score 32; DB 2; Length 236;
 Best Local Similarity 85.7%; Pred. No. 69;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
 DB 71 DVNRKPS 77

RESULT 4

O25919 PRELIMINARY; PRT; 423 AA.
 AC O25919;
 DT 01-JAN-1998 (TReMBLrel. 05, Created)
 DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE Type IIS restriction enzyme R protein (MBOIIR).
 GN OrderedLocustNames=HP1366;
 OS Helicobacter pylori (Campylobacter pylori).
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
 OC Helicobacteraceae; Helicobacter.
 NCBI_TaxID=210;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=26695 / ATCC 700392;
 RX MEDLINE=97394467; PubMed=9252185; DOI=10.1038/41483;
 RA Tomb J.-F., White O., Kestlavage A.R., Clayton R.A., Sutton G.G.,
 RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S.R., Kirkness E.F.,
 RA Dougherty B.A., Nelson K.E., Quackenbush J., Zhou L., Kirkness E.F.,
 RA Peterson S.N., Loftus B.J., Richardson D.L., Dodson R.U., Khalak H.G.,

RA Glodok A., McKenney K., FitzGerald L.M., Lee N., Adams M.D.,
 RA Hickey E.K., Berg D.E., Gocayne J.D., Uterback T.R., Peterson J.D.,
 RA Kelley J.M., Cotton M.D., Weidman J.F., Fujii C., Bowman C.,
 RA Matthey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D.,
 RA Smith H.O., Fraser C.M., Venter J.C.;
 RT "The complete genome sequence of the gastric pathogen *Helicobacter*
 RT *pylori*.";
 RL Nature 388:539-547(1997).
 DR EMBL: AE000637; AAC08410.1; -
 DR PIR: F64690; F64690.
 DR TIGR: HPI366; -
 DR InterPro: IPR003615; HNH_nuc.
 DR SMART: SM00507; HNH; 1.
 DR Complete proteome.
 KW SEQUENCE 423 AA; 50047 MW; 908651C8FE4E58E CRC64;

Query Match 91.4%; Score 32; DB 2; Length 423;
 Best Local Similarity 85.7%; Pred. No. 1.3e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DVSKRPS 7
 |||||
 Db 71 DVSKRPS 77

RESULT 5

LV21_HUMAN STANDARD; PRT; 111 AA.
 AC P01712;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig lambda chain V-II region W1N.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.

RX MEDLINE=7062503; PubMed=102365; DOI=10.1016/0005-2795(78)90598-6;
 RA Chen B.L., Chu Y.-Y.H., Humphrey R.L., Poljak R.U.;
 RT "Amino acid sequence of the human myeloma lambda chain W1N."
 RL Biochim. Biophys. Acta 537:9-21(1978).
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR: A01978; L2HWN.
 DR HSSP: P01709; IDCL.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0003823; F:antigen binding; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS00835; IG_LIKE; 1.
 KW Bence-Jones protein; Direct protein sequencing;
 KW Immunoglobulin V region; Pyrolytic carboxylic acid.
 FT DOMAIN 1 106
 FT MOD_RES 1 1
 FT DISULFID 22 90
 FT NON_TER 111 111
 FT SEQUENCE 111 AA; 11694 MW; 8C9CB95FE721B07C CRC64;

Query Match 88.6%; Score 31; DB 1; Length 111;
 Best Local Similarity 85.7%; Pred. No. 53;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 DVSKRPS 7
 |||||
 Db 52 DVSKRPS 58

RESULT 6

Q7MUS6 PRELIMINARY; PRT; 130 AA.
 AC Q7MUS6;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocusNames=PG1409;
 OS Porphyromonas gingivalis (Bacteroides gingivalis).
 CC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
 CC Porphyromonadaceae; Porphyromonas.
 OC NCBI_TaxID=837;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=W83;
 RX MEDLINE=22829867; PubMed=12949112;
 RX DOI=10.1128/01.185.18.5591-5601.2003.
 RA Nelson K.E., Fleischmann R.D., Desoy R.T., Paulsen I.T., Fouts D.E.,
 RA Eisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M.L.,
 RA Haft D.H., Kolonay J.F., Nelson W.C., Mason T.M., Taiton L., Gray J.,
 RA Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J.,
 RA Dewhirst F.E., Fraser C.M.;
 RT "Complete genome sequence of the oral pathogenic bacterium
 RT *Porphyromonas gingivalis* strain W83."
 RL J. Bacteriol. 185:5591-5601(2003).
 DR EMBL: AE017176; AAC66466.1; -
 DR TIGR: PG1409; -
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 130 AA; 14455 MW; 3F2E1F64F23E5805 CRC64;

Query Match 88.6%; Score 31; DB 2; Length 130;
 Best Local Similarity 71.4%; Pred. No. 63;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DVSKRPS 7
 |||||
 Db 107 DVSKRPS 113

RESULT 7

Q7S4H3 PRELIMINARY; PRT; 233 AA.
 AC Q7S4H3;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein.
 GN Name=NCU0220.1;
 OS Neurospora crassa.
 CC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 CC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
 OC NCBI_TaxID=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OR74A;
 RA Galagan J.E., Galvo S.B., Borkovich K.A., Selker E.U., Read N.D.,
 RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
 RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
 RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
 RA Seltrenmykoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
 RA Kothne G.O., Jedd G., Mewes W., Steben C., Marcotte E., Greenberg D.,
 RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
 RA Kamal M., Kamysellis M., Mauceli E., Bielle C., Rudd S., Frisman D.,
 RA Kravtsova S., Kasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,
 RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.U., Osmani S.A.,
 RA Desouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
 RA Yarden O., Plamann M., Seltzer S., Dunlap J., Radford A., Aramayo R.,
 RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
 RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.,
 RL "The Genome Sequence of the Filamentous Fungus *Neurospora crassa*."
 RL Nature 0:0-0(2003).

-1- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is

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CC      preliminary data.
DR      EMBL; AABX01000366; EAAJ0397.1; -.
DR      GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. .; IEA.
DR      GO; GO:0015035; F:protein disulfide oxidoreductase activity; IEA.
DR      InterPro; IPR001853; DSB_A.
DR      InterPro; IPR010986; DsbA_insertion.
DR      Pfam; PF01323; DSB_A; 1.
KM      Hypothetical protein.
SQ      SEQUENCE 233 AA; 25367 MW; 50B8FA369168929 CRC64;

Query Match      88.6%; Score 31; DB 2; Length 233;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DVSKRPS 7
Db      222 DVSKRPS 228

RESULT 8
Q7SZL9 PRELIMINARY; PRT; 400 AA.
AC      Q7SZL9;
DT      01-OCT-2003 (TREMblrel. 25, Created)
DT      01-OCT-2003 (TREMblrel. 25, Last sequence update)
DT      01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE      ATP-gated Ionotropic P2X receptor subunit 2.
GN      Name=p2rx2; Synonyms=p2rx2;
OS      Brachydanio rerio (Zebrafish) (Danio rerio).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC      Cyprinidae; Danio.
OX      NCBI_TaxID=7955;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=22943235; PubMed=14580944; DOI=10.1016/S0306-4522(03)00566-9;
RA      Kucenas S., Li Z., Cox J.A., Egan T.M., Voigt M.M.;
RT      "Molecular characterization of the zebrafish P2X receptor subunit gene
RT      family.";
RL      Neuroscience 121:935-945(2003).
DR      EMBL; AY292650; AAC21195.1; -.
DR      ZFIN; ZDB-GENE-030319-2; p2rx2.
DR      GO; GO:0009503; C:light-harvesting complex (sensu Viridiplantae); IEA.
DR      GO; GO:0016020; C:membrane; IEA.
DR      GO; GO:0005524; F:ATP binding; IEA.
DR      GO; GO:0005216; F:ion channel activity; IEA.
DR      GO; GO:0016978; F:lipoate-protein ligase B activity; IEA.
DR      GO; GO:0004872; F:receptor activity; IEA.
DR      GO; GO:0006091; P:energy pathway; IEA.
DR      GO; GO:0006811; P:ion transport; IEA.
DR      InterPro; IPR000066; Antenna_a/b.
DR      InterPro; IPR01429; P2X receptor.
DR      Pfam; PF00864; P2X receptor; 1.
DR      TIGRFAMs; TIGR00863; P2X; 1.
KM      Receptor.
SQ      SEQUENCE 400 AA; 45752 MW; EBS71C00171609FS CRC64;

Query Match      88.6%; Score 31; DB 2; Length 400;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DVSKRPS 7
Db      369 DVSKRPS 375

RESULT 9
Q64WES PRELIMINARY; PRT; 402 AA.
AC      Q64WES;
DT      25-OCT-2004 (TREMblrel. 28, Created)
DT      25-OCT-2004 (TREMblrel. 28, Last sequence update)
DT      25-OCT-2004 (TREMblrel. 28, Last annotation update)
DT      25-OCT-2004 (TREMblrel. 28, Last annotation update)

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DE      Predicted nucleoside-diphosphate sugar epimerase.
GN      ORFNames=BP1430;
OS      Bacteroides fragilis.
OC      Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC      Bacteroidaceae; Bacteroides.
OX      NCBI_TaxID=817;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=YCH46;
RA      Kuwahara T., Yamashita A., Hirakawa H., Nakayama H., Toh H., Okada N.,
RA      Kubara S., Hattori M., Hayashi T., Ohnishi Y.;
RT      "Genomic analysis of Bacteroides fragilis reveals extensive DNA
RT      insertions regulating cell surface adaptation.";
RL      Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2004).
DR      EMBL; AP006841; BAD48181.1; -.
SQ      SEQUENCE 402 AA; 45596 MW; 2D56A6DAF87797CC CRC64;

Query Match      88.6%; Score 31; DB 2; Length 402;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DVSKRP 6
Db      348 DVSKRP 353

RESULT 10
Q828G3 PRELIMINARY; PRT; 486 AA.
AC      Q828G3;
DT      01-JUN-2003 (TREMblrel. 24, Created)
DT      01-JUN-2003 (TREMblrel. 24, Last sequence update)
DT      01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE      Putative cytochrome P450.
GN      Name=CYP24; OrderedLocNames=SAV6706;
OS      Streptomyces avermitilis.
OC      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC      Streptomycinae; Streptomycetaceae; Streptomyces.
OX      NCBI_TaxID=33903;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=MA-4680;
RX      MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
RA      Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA      Shinose H., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,
RA      Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RT      "Genome sequence of an industrial microorganism Streptomyces
RT      avermitilis: deducing the ability of producing secondary
RT      metabolites.";
RL      Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=MA-4680;
RX      MEDLINE=22608306; PubMed=12692562;
RA      Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA      Sakaki Y., Hattori M., Omura S.;
RT      "Complete genome sequence and comparative analysis of the industrial
RT      microorganism Streptomyces avermitilis.";
RL      Nat. Biotechnol. 21:526-531(2003).
CC      -1- SIMILARITY: Belongs to the cytochrome P450 family.
DR      EMBL; AP005047; BAC74417.1; -.
DR      HSSP; Q9L142; IGMT.
DR      GO; GO:0004497; F:monooxygenase activity; IEA.
DR      GO; GO:0006118; P:electron transport; IEA.
DR      InterPro; IPR002397; BP450.
DR      InterPro; IPR001128; Cytochrome_P450.
DR      PRINTS; PR00359; BP450.
DR      PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN 1.
KM      Complete proteome: Heme; Monooxygenase; Oxidoreductase.
SQ      SEQUENCE 486 AA; 53354 MW; A728B74F6592E265 CRC64;

Query Match      88.6%; Score 31; DB 2; Length 486;
Best Local Similarity 85.7%; Pred. No. 2.5e+02;

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Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
|||:||||
Db 428 DVSKRPS 434

RESULT 11

Q7SE90 PRELIMINARY; PRT; 728 AA.

AC Q7SE90.01-MAR-2004 (TRENBLrel. 26, Created)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Predicted protein.
GN Name=NCU00559.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
[1]

RP SEQUENCE FROM N.A.

RC STRAIN=OR74A; Galagan J.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA Seitzemikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Koche G.O., Jedd G., Mewes W., Staben C., Barrett R., Gnerre S.,
RA Roy A., Foley K., Naylor J., Thomann N., Rudd S., Fishman D.,
RA Kamal M., Kamysseilis M., Mauceli E., Bielke C., Rudd S., Perkins D., Kroken S.,
RA Krystofova S., Rasmussen C., Metzberg R.L., Perkins D., Kroken S.,
RA Cogoni C., Macino G., Catheides D., Li W., Pratt R.J., Osmari S.A.,
RA Desouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Iander E.S., Nusbaum C., Birren B.,
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa."
RL Nature 0:0-0(2003).

CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.

CC EMBL; AABX0100022; EAA35484.1; -
SQ SEQUENCE 728 AA; 79550 MW; 05A688EBD3850B79 CRC64;

Query Match 88.6%; Score 31; DB 2; Length 728;
Best Local Similarity 85.7%; Pred. No. 3.8e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
|||:||||
Db 336 DVSKRPS 342

RESULT 12

Q6SLD6 PRELIMINARY; PRT; 1292 AA.

AC Q6SLD6.05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Putative histidine kinase HKK1p.
GN Name=HKK1;

OS Cochliobolus heterostrophus (Drechslera maydis).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC Pleosporales; Pleosporaceae; Cochliobolus.
OX NCBI_TaxID=5016;
[1]

RN SEQUENCE FROM N.A.

RC STRAIN=C4; PubMed:14665450; DOI=10.1128/EC.2.6.1151-1161.2003;
RX Catlett N.L., Yoder O.C., Turgeon B.G.;
RT "Whole-genome analysis of two-component signal transduction genes in

RT fungal pathogens.",
RL Eukaryotic Cell 2:1151-1161(2003).
CC -!- SIMILARITY: Contains 1 histidine kinase domain.

DR EMBL; AY456014; AAR29890.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0000156; F:two-component sensor molecule activity; IEA.
DR GO; GO:0000155; F:two-component sensor molecule activity; IEA.
DR GO; GO:0007600; P:sensory perception; IEA.
DR GO; GO:0000160; P:two-component signal transduction system (p. . .); IEA.
DR InterPro; IPR004358; Bact_sens_pr_C.
DR InterPro; IPR011006; Chey_like.
DR InterPro; IPR005467; His_kinase.
DR InterPro; IPR003661; His_kin_N.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF02518; HATPase_C; 1.
DR Pfam; PF00512; HSKA; 1.
DR Pfam; PF00072; Response_reg; 1.
DR PRINTS; PR00344; BCTRLSENSOR.
DR ProDom; PD000039; Response_reg; 1.
DR SMART; SM00387; HATPase_C; 1.
DR SMART; SM00388; HSKA; 1.
DR SMART; SM00448; REC; 1.
DR PROSITE; PS50109; HIS_KIN; 1.
DR PROSITE; PS50110; RESPONSE_REGULATORY; 1.
KM Kinase; Phosphorylation; Sensory transduction.
SQ SEQUENCE 1292 AA; 144730 MW; 57010F00609FF49B CRC64;

Query Match 88.6%; Score 31; DB 2; Length 1292;
Best Local Similarity 85.7%; Pred. No. 6.9e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
|||:||||
Db 45 DVSKRPS 51

RESULT 13

Q7SE06 PRELIMINARY; PRT; 1766 AA.

AC Q7SE06.05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE ABL133Cp.
GN ORFNames=ABL133C;
OS Asbya gossypii (Yeast) (Eremothecium gossypii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Eremothecium.
OX NCBI_TaxID=33169;
[1]

RN SEQUENCE FROM N.A.

RC STRAIN=ATCC 10895;
RA Voegel S.E., Dietrich F.S., Brachat S., Lerch A., Gaffney T.,
RA Phillipsen P.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE016815; AAS50638.1; -
DR AGD; ABL133C; -
SQ SEQUENCE 1766 AA; 179132 MW; BEC73A1CF69F2EA3 CRC64;

Query Match 88.6%; Score 31; DB 2; Length 1766;
Best Local Similarity 85.7%; Pred. No. 9.6e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
|||:||||
Db 1445 DVSKRPS 1451

RESULT 14

DR	PtDrom;PDD02269;	Bacterioferritin; 1.
DR	TIGR8PMs;TIGR80754;	bfr1; 1.
DR	PROSITE; PS00549;	BACTERIOFERRITIN; 1.
DR	PROSITE; PS50905;	FERRITIN_LIKE; 1.
KW	Heme; Iron;	Iron storage; Metal-binding.
FT	DOMAIN	1 147 Ferritin-like diltion.
FT	METAL	18 18 Iron 1 (By similarity).
FT	METAL	49 49 Iron (heme axial ligand) (potential).
FT	METAL	51 51 Iron 1 (By similarity).
FT	METAL	51 51 Iron 2 (By similarity).
FT	METAL	54 54 Iron 1 (By similarity).
FT	METAL	94 94 Iron 2 (By similarity).
FT	METAL	129 129 Iron 1 (By similarity).
FT	METAL	129 129 Iron 2 (By similarity).
FT	METAL	132 132 Iron 2 (By similarity).
SQ	SEQUENCE	164 AA; 18491 MW; 65837DCACFDJ2358 CRC64;
Query Match		85.7%; Score 30; DB 1; Length 164;
Best Local Similarity		83.3%; Pred. No. 1.4e+02;
Matches	5; Conservative	1; Mismatches 0; Indels 0; Gaps 0;
Cy	1 DVSRKP 6	
Dc	:	
	70 DISKRP 75	
RESULT 16		
O9V6F8	PRELIMINARY;	PRT; 212 AA.
ID O9V6F8		
AC O9V6F8:		
DT	01-MAY-2000 (TREMBLrel. 13. Created)	
DT	01-OCT-2002 (TREMBLrel. 22. Last sequence update)	
DT	25-OCT-2004 (TREMBLrel. 28. Last annotation update)	
DE	CG30052-PA (GH25962P).	
GN	Name=Obp49a; ORFNames=CG30052;	
OS	Drosophila melanogaster (fruit fly).	
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Peerygota;	
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	
OC	Ephydroidea; Drosophilidae; Drosophila.	
OX	[1]	
RN	_Taxid=7227;	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=20196006; PubMed=10731132. DOI=10.1126/science.287.5461.2185;	
RA	Adams M.D., Celniker S.B., Holt R.A., Evans C.A., Gocayne J.D.,	
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,	
RA	Gearge R.A., Lewis S.B., Richards S., Ashburner M., Henderson S.N.,	
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,	
RA	Brandon R.C., Rogers Y.H., Blazer R.G., Chapple M., Pfeiffer B.D.,	
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gaber G.L.,	
RA	Abriil J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,	
RA	Ballew R.M., Basu A.A., Baxendale J., Bayraktaroglu I., Beasley E.M.,	
RA	Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,	
RA	Borkovskiy D., Botchan M.R., Bouck J., Brockstein P., Brodtier P.,	
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,	
RA	Cherry J.M., Clawley S., Dahlke C., Dayevport L.B., Davies P.,	
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,	
RA	Dodson K.C., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,	
RA	Dubin K.J., Evangelista C.C., Ferrara C., Ferreira S., Fleischmann W.,	
RA	Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,	
RA	Glodek A., Gong F., Gorrell U.H., Gu Z., Guan P., Harris M.,	
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,	
RA	Hoastin D., Houston K.A., Howland T.J., Wei M.H., Ibegwan C.,	
RA	Jajali M., Kalushen F., Karpen G.H., Ke Z., Kennison J.A., Kerchum K.A.,	
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,	
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang X., Lin X.,	
RA	Liu X., Mettel B., McIntosh T.C., McLeod M.P., McPherson D.,	
RA	Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,	
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,	
RA	Nelson D.R., Nelson K.A., Nixon K., Nusken D.R., Pacle J.M.,	
RA	Palazzolo M., Pittman G.S., Pan S., Pollard J., Puti V., Reese M.G.,	
RA	Reiner K., Remington K., Saunders R.D., Scheefel F., Shen H.,	
RA	Shue B.C., Stiden-Klamos A.I., Stimpson M., Skupsky M.P., Smith T.,	
RA	Spter E., Spalding A.C., Stapleton M., Strong R., Sun E.,	

RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodgett J., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yen R.F., Zaveri J.S., Zhan M., Zhang M., Zhang Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Change M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
 RA Paclele J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskaas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 RT "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*
 RL *melanogaster* euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskaas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
 RL a genomic perspective.";
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426099; PubMed=12537572;
 RA Mirza S., Crosby M.A., Kaminker J.C., Matthews B.B., Campbell K.S.,
 RA Hirdesky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Betencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 RL systematic review.";
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
 [5]
 RP SEQUENCE FROM N.A.
 RX Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RL [6]
 RP SEQUENCE FROM N.A.
 RX Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 RL [7]
 RP SEQUENCE FROM N.A.
 RX STRAIN=Berkeley;
 RA Stapleton M., Brockstein P., Hong L., Aghayani A., Carlson J.,
 RA Change M., Chaver C., Dorsett V., Dresnek D., Farfan D., Frise E.,
 RA George R., Gonzalez W., Gutrin H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nunoo J., Paclele J., Paragas V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celniker S.;
 RT Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AE003821; AA058469.2; -;
 DR EMBL; AY118821; AA050661.1; -;
 DR INAC; Q5V6F8; -;
 DR FLYbase; FBGN0050053; CG30053.
 DR FLYbase; FBGN0050052; ODP49a.
 SO SEQUENCE 212 AA; 23472 MW; 9449E602F390B469 CRC64;

Query Match 85.7%; Score 30; DB 2; Length 212;
 Best Local Similarity 85.7%; Pred. NO. 1.8e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 DVSKRPS 7
 | | | | |

DB 25 DSKRPS 31
 RESULT 17
 ID 06P53 PRELIMINARY; PRT; 233 AA.
 AC 06P53;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Ditchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bonak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Holys S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boulford G.G.,
 RA Blakester R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Kravinsky M.I., Skelton U., Small D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RX Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL; BC018749; AA018749.1; -;
 DR HSSP; P01709; 1A8J.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG-cl.
 DR InterPro; IPR003066; IG-MHC.
 DR InterPro; IPR003596; IG-V.
 DR Pfam; PF07654; C1-set; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00407; IGcl; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 2.
 DR PROSITE; PS00290; IG MHC; UNKNOWN_1.
 KW Hypothetical protein.
 SO SEQUENCE 233 AA; 24509 MW; AA0588B008C9F09 CRC64;

Query Match 85.7%; Score 30; DB 2; Length 233;
 Best Local Similarity 85.7%; Pred. NO. 2e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 DVSKRPS 7
 | | | | |
 Db 71 DVSKRPS 77

RESULT 18
 ID 06P53 PRELIMINARY; PRT; 236 AA.
 AC 06P53;


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DT 05-JUL-2004 (TREMblrel. 27, Created)
DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
RP TISSUE=Glndular pool- thyroid.
RC MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marnett K., Farmer A.A., Rubin G.M., Hong L.,
RA Stopleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Scherch A., Schein J.E.,
RA Jones S.J., Maitra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
SEQUENCE FROM N.A.
RP TISSUE=Glndular pool- thyroid.
RC Strausberg R.;
RA Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC062711; AAH62711.1; -
DR HSSP; P01709; IABJ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003066; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein-
SO SEQUENCE 236 AA; 24928 MW; C036D7FA63468E0D CRC64;

Query Match 85.7%; Score 30; DB 2; Length 236;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
DB 71 DVSNRPS 77

RESULT 19
Q9BTM2 PRELIMINARY; PRT; 267 AA.
ID Q9BTM2
AC Q9BTM2
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-OCT-2003 (TREMblrel. 25, Last sequence update)
DE 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE KIAA0285 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

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OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Lung;
RP MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marnett K., Farmer A.A., Rubin G.M., Hong L.,
RA Stopleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Scherch A., Schein J.E.,
RA Jones S.J., Maitra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
SEQUENCE FROM N.A.
RP TISSUE=Lung;
RC Strausberg R.;
RA Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003598; AAH03598.2; -
SO SEQUENCE 267 AA; 28233 MW; 400C27CCEB01EA107 CRC64;

Query Match 85.7%; Score 30; DB 2; Length 267;
Best Local Similarity 71.4%; Pred. No. 2.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
DB 168 DISERPS 174

RESULT 20
Y170_BUCBP STANDARD; PRT; 279 AA.
ID Y170_BUCBP
AC Q98A52;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Hypothetical protein bnp170 (yba2).
CN OrderedLocustNames=bnp170;
OS Buchnera aphidicola (subsp. Baizongia pistaciae).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
OX NCBI_TaxID=135842;
RN [1]
RN SEQUENCE FROM N.A.
RP PubMed=1252265; DOI=10.1073/pnas.023961100;
RA van Ham R.C.H.J., Kamerbeek U., Palacios C., Rauehl C., Abascal F.,
RA Baatolla U., Fernandez J.M., Jimenez L., Postigo M., Silva F.J.,
RA Tamames J., Viguera E., Latorre A., Valencia A., Moran F., Moya A.;
RT "Reductive genome evolution in Buchnera aphidicola."
RL Proc. Natl. Acad. Sci. U.S.A. 100:581-586(2003).
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CC or send an email to license@sib-sib.ch).
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CC EMBL; AE014016; AAO26903.1; -

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KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 279 AA; 31460 MW; 616FDB0C3821009D CRC64;

Query Match 85.7%; Score 30; DB 1; Length 279;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 6
DB 114 DISKRP 119

RESULT 21

070914 PRELIMINARY; PRT; 283 AA.

AC 070914
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Putative movement protein.
OS Prunus necrotic ringspot virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
OC Ilarvirus.
OX NCBI_TaxID=37733;

RN [1]
RP SEQUENCE FROM N.A.
RA Scott S.W., Zimmermann M.T., Ge X., Mackenzie D.J.;
RT "The coat proteins and putative movement proteins of isolates of Prunus necrotic ringspot virus from different host species and geographic origins are extensively conserved."
RL Eur. J. Plant Pathol. 104:155-161(1998).
DR EMBL; AF013285; AAC16498.1;
DR InterPro; IPR002538; Bromo_MP.
DR Pfam; PF01573; Bromo_MP.1;
SQ SEQUENCE 283 AA; 31568 MW; 4BA16CAD1F8B191A CRC64;

Query Match 85.7%; Score 30; DB 2; Length 283;
Best Local Similarity 85.7%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
DB 3 DVSKRPS 9

RESULT 22

070918 PRELIMINARY; PRT; 283 AA.

AC 070918
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Putative movement protein.
OS Prunus necrotic ringspot virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
OC Ilarvirus.
OX NCBI_TaxID=37733;

RN [1]
RP SEQUENCE FROM N.A.
RA Scott S.W., Zimmermann M.T., Ge X., Mackenzie D.J.;
RT "The coat proteins and putative movement proteins of isolates of Prunus necrotic ringspot virus from different host species and geographic origins are extensively conserved."
RL Eur. J. Plant Pathol. 104:155-161(1998).
DR EMBL; AF013287; AAC16502.1;
DR InterPro; IPR002538; Bromo_MP.
DR Pfam; PF01573; Bromo_MP.1;
SQ SEQUENCE 283 AA; 31459 MW; DEB6802B59309123 CRC64;

Query Match 85.7%; Score 30; DB 2; Length 283;
Best Local Similarity 85.7%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
DB 3 DVSKRPS 9

RESULT 23

071142 PRELIMINARY; PRT; 285 AA.

AC 071142
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Putative movement protein.
OS Prunus necrotic ringspot virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
OC Ilarvirus.
OX NCBI_TaxID=37733;

RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=CH71;
RX MEDLINE=98343741; PubMed=9680147;
RA Hammond R.W., Crosslin J.M.;
RT "Virulence and molecular polymorphism of Prunus necrotic ringspot virus isolates."
RL J. Gen. Virol. 79:1815-1823(1998).
DR EMBL; AF034995; AAC1036.1;
DR InterPro; IPR002538; Bromo_MP.
DR Pfam; PF01573; Bromo_MP.1;
SQ SEQUENCE 285 AA; 31795 MW; 3247584F7B73F506 CRC64;

Query Match 85.7%; Score 30; DB 2; Length 285;
Best Local Similarity 85.7%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
DB 3 DVSKRPS 9

RESULT 24

086V04 PRELIMINARY; PRT; 327 AA.

AC 086V04
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE KIA0285 protein (Fragment).
GN Name=KIA0285;

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE=Blood;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Tothiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loguigliano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McGwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Maitra W.A.;

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RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Strausberg R.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC052246; AAH52246.1; -.
FT NON TER
SQ SEQUENCE 327 AA; 34509 MW; D21FF6223ED711FC CRC64;

Query Match
Best Local Similarity 85.7%; Score 30; DB 2; Length 327;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSRRPS 7
Db 228 DISRRPS 234

RESULT 25
ID Q9XY82 PRELIMINARY; PRT; 378 AA.
AC Q9XY82;
DT 01-NOV-1999 (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Elongation factor 1-alpha (Fragment).
OS Enchytraeus sp. 'Enc'.
OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
OC Tubificata; Enchytraeidae; Enchytraeus.
OX NCBI_TaxID=89370;
RN [1]
RP SEQUENCE FROM N.A.
RA Register J.C., Shultz J.W.;
RT "Molecular phylogeny of arthropods and the significance of the
RT Cambrian 'explosion' for molecular systematics."
RL Am. Zoologist 38:918-928 (1998).
DR EMBL; AF063418; AAD21857.1; -.
DR HSSP; P02994; IFE0.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0003746; F:translation elongation factor activity; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR GO; GO:0006414; P:translational elongation; IEA.
DR InterPro; IPR004539; EFT_alpha.
DR InterPro; IPR004160; EFTU_Cterm.
DR InterPro; IPR009001; Elong_init_C.
DR InterPro; IPR000795; ProtSyn_GTPbind.
DR InterPro; IPR009000; Translat_Factor.
DR Pfam; PF00009; GTP_EFTU; 1.
DR Pfam; PF03144; GTP_EFTU_D2; 1.
DR Pfam; PF03143; GTP_EFTU_D3; 1.
DR PRINTS; PR00315; ELONGATNFCF.
DR TIGRfams; TIGR00483; EF-1_alpha; 1.
DR PROSITE; PS00301; ERCTOR_GTP; 1.
DR Elongation factor; GTP-binding; Protein biosynthesis.
KW NON TER
FT NON TER
SQ SEQUENCE 378 AA; 41429 MW; 1793787C653C5F5B CRC64;

Query Match
Best Local Similarity 85.7%; Score 30; DB 2; Length 378;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DVSRRPS 7
Db 191 DVSRRPS 197

RESULT 26

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Q7S098
ID Q7S098 PRELIMINARY; PRT; 385 AA.
AC Q7S098;
DT 01-MAR-2004 (TRENBLrel. 26, Created)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Predicted protein.
CN Name=NCU10037.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., Fitzhugh W., Ma L.-Y., Smirnov S., Purcell S., Rehm B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi W.,
RA Qiu D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA Seltremnikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Straben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnere S.,
RA Kamal M., Kamyselis M., Mauceli E., Bielke C., Rudd S., Frisman D.,
RA Krysstofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmani S.A.,
RA Desouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Nativig D.O., Alex L.A., Mannhaupt G., Ebbold D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nubbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa."
RL Nature 0:0-0 (2003).
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AA00100518; EAA28730.1; -.
SQ SEQUENCE 385 AA; 44471 MW; 6FF21B8053B0309B CRC64;

Query Match
Best Local Similarity 85.7%; Score 30; DB 2; Length 385;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DVSRRPS 7
Db 379 DVSRRPS 385

RESULT 27
ID Q6DHX1 PRELIMINARY; PRT; 401 AA.
AC Q6DHX1;
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedlin T.B., Toshitsuki S., Carrinci P., Prange C.,
RA Rahn S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

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RA Fahey J., Helton E., Kerteman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko I., Boultard G.G.,
 RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strauberg R.;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC075832; AAF75832.1; -
 DR InterPro; IPR008973; C2_CalB.
 KW Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 401 AA; 42633 MW; 80E3C52006A6DFPA CRC64;
 Query Match 85.7%; Score 30; DB 2; Length 401;
 Best Local Similarity 71.4%; Pred. No. 3.5e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DVSKRPS 7
 DB 302 DISERPS 308
 RESULT 28
 T2M2 MORBO STANDARD; PRT; 416 AA.
 ID T2M2 MORBO
 AC P23191.
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Type IIS restriction enzyme MboII (EC 3.1.21.4) (Endonuclease MboII)
 (R.MboII).
 GN Name=MboII;
 OS Moraxella boydii.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Moraxellaceae; Moraxella.
 OX NCBI_TaxID=476;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-5; 7-12 AND 15-19.
 RC STRAIN=ATCC 10900;
 RX MEDLINE=91212177; PubMed=2020540;
 RA Bocklage H., Heeger K., Mueller-Hill B.;
 RT "Cloning and characterization of the MboII restriction-modification
 RT system.";
 RL Nucleic Acids Res. 19:1007-1013 (1991).
 CC -1- FUNCTION: Recognizes the double-stranded sequences GAGA and TCCTC
 CC and cleaves respectively 13 bases after G-1 and 7 bases before T-
 CC 1, leaving a single 3' protruding nucleotide.
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give
 CC specific double-stranded fragments with terminal 5'-phosphates.
 CC -1- Cofactor: Magnesium.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL; X56977; CAA40298.1; -
 DR PIR; S26836; S26836.
 DR REBASE; 1205; MboII.
 KW Direct protein sequencing; Endonuclease; Hydrolase; Magnesium;
 KW Nuclease; Restriction system.
 SQ SEQUENCE 416 AA; 48617 MW; CSA0008775B635CP CRC64;

Query Match 85.7%; Score 30; DB 1; Length 416;
 Best Local Similarity 83.3%; Pred. No. 3.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DVSKRP 6
 DB 66 DISKRP 71
 RESULT 29
 Q80U48 PRELIMINARY; PRT; 508 AA.
 ID Q80U48
 AC Q80U48.
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE MKIA0285 protein (Fragment).
 GN Name=MKIA0285;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22579291; PubMed=12693553;
 RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Aizawa H., Yusa S.,
 RA Nakajima D., Nagase T., Ohara O., Koga H.;
 RT "Prediction of the coding sequences of mouse homologues of KIA gene:
 RT IT. The complete nucleotide sequences of 400 mouse KIAA-homologous
 RT cDNAs identified by screening of terminal sequences of cDNA clones
 RT randomly sampled from size-fractionated libraries.";
 RL DNA Res. 10:35-48 (2003).
 DR EMBL; AK122237; BAC65519.1; -
 FT NON TER 1
 SQ SEQUENCE 508 AA; 54979 MW; 2331C7AE26845EAI CRC64;
 Query Match 85.7%; Score 30; DB 2; Length 508;
 Best Local Similarity 71.4%; Pred. No. 4.4e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DVSKRPS 7
 DB 409 DISERPS 415
 RESULT 30
 Q6PHCO PRELIMINARY; PRT; 530 AA.
 ID Q6PHCO
 AC Q6PHCO.
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Tmem24 protein.
 GN Name=Tmem24;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Heien F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshitoki S., Carninci P., Prange C.,
 RA Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Muliyil S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.V., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalios D.E., Scherch J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Mammary tumor. C3;
 RA Strusberg R.;
 RA Submitted (Aug-2003) to the EMBL/Genbank/DBJ databases.
 DR EMBL, BC056612; AAH56612.1; -;
 DR InterPro: IPR008973; C2_CaLB.
 SQ SEQUENCE 530 AA; 5686 MW; PAAEE290EAF13504 CRC64;
 Query Match 85.7%; Score 30; DB 2; Length 530;
 Best Local Similarity 71.4%; Pred. No. 4.6e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 DVSKRPS 7
 Db 431 DISRPS 437
 RESULT 31
 ID Q8CA2 PRELIMINARY; PRT; 654 AA.
 AC Q8CA2;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Mus musculus adult male hypothalamus cDNA, RIKEN full-length enriched
 DE library, clone:A230109H5 product:hypothetical C2 domain
 DE (Calcium/lipid-binding domain, CaLB) structure containing protein,
 DE full insert sequence.
 GN Name=tmem24;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RT Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RT Nature 409:685-690(2001).
 RN [3]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;
 RA The FANTOM Consortium;
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RT Nature 420:563-573(2002).
 RN [4]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Suganara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to

RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Kitsuwa T., Tashiro H., Itoh M.,
 RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Katsukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Satoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (Jul-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL, AK039220; BAC30281.1; -;
 DR MGD: MGI:1919014; Tmem24.
 DR InterPro: IPR008973; C2_CaLB.
 KW Hypothetical protein.
 SQ SEQUENCE 654 AA; 70454 MW; 63472C1D12BAF05D CRC64;
 Query Match 85.7%; Score 30; DB 2; Length 654;
 Best Local Similarity 71.4%; Pred. No. 5.8e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 DVSKRPS 7
 Db 607 DISRPS 613
 RESULT 32
 ID Q9DBJ2 PRELIMINARY; PRT; 674 AA.
 AC Q9DBJ2;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Mus musculus adult male liver cDNA, RIKEN full-length enriched
 DE library, clone:130006023 product:hypothetical C2 domain
 DE (Calcium/lipid-binding domain, CaLB) structure containing protein,
 DE full insert sequence.
 GN Name=tmem24;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Liver;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RT Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Liver;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

RA RIKEN PANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 [3]
 RN SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6J; TISSUE=Liver;
 RC The PANTOM Consortium,
 RA The RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 [4]
 RN SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6J; TISSUE=Liver;
 RC MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carinini P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes."
 RL Genome Res. 10:1617-1630(2000).
 [5]
 RN SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6J; TISSUE=Liver;
 RC MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carinini P.,
 Kono H., Akiyama J., Nishi K., Katsunai T., Teshiro H., Itoh M.,
 Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki K.,
 Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer."
 RL Genome Res. 10:1757-1771(2000).
 [6]
 RN SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6J; TISSUE=Liver;
 RC Adachi J., Aizawa K., Akabira S., Akimura T., Arai A., Aono H.,
 Arakawa T., Bono H., Carinini P., Fukuda S., Fukunishi Y., Furuno M.,
 Haragaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
 Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
 Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kurihara C.,
 Muramatsu M., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
 Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
 Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
 Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
 Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK004920; BAB3671.1; -
 DR MGI; MGI:1919014; Tmem24.
 DR InterPro; IPR008973; C2_GaLB.
 KW Hypothetical protein.
 SQ SEQUENCE 674 AA; 72442 MW; BA290F25B6258E83 CRC64;
 Query Match 85.7%; Score 30; DB 2; Length 674;
 Best Local Similarity 71.4%; Pred. No. 6e+02; Indels 0; Gaps 0;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DVSXKPS 7
 Db 575 DISRPS 581
 RESULT 33
 ID TM24 HUMAN STANDARD: PRT. 706 AA.
 AC O14523; O86UT7; Q8NS22; Q8TBM4; Q96G10;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Transmembrane protein 24 (Dlnb23 protein).
 GN Name=TMEM24; Synonyms=KIAA0285;

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_Taxid=9606;
 [1]
 RN SEQUENCE FROM N.A.
 RP Kubo T., Arai Y., Ohira M., Gamou T., Maeno G., Sakiyama T.,
 Toyoda A., Hattori M., Sakaki Y., Nakagawara A., Ohki M.;
 RT "Identification of a 500-kb region of common allelic loss in
 chromosome 11q23 in non-MYC amplified type of neuroblastoma."
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 [2]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Brain, and Pancreas;
 RC MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 Rana S.S., Loughellano N.A., Peters G.J., Abramson R.D., Muliyil S.J.,
 Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W.,
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 Butlerfield A.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 Schermer A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [3]
 RN SEQUENCE OF 49-706 FROM N.A.
 RP TISSUE=Brain;
 RC MEDLINE=9732306; PubMed=9179496;
 RA Ohara O., Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N.,
 Nomura N.;
 RT "Construction and characterization of human brain cDNA libraries
 suitable for analysis of cDNA clones encoding relatively large
 proteins."
 RL DNA Res. 4:53-59(1997).
 [4]
 RN REVISIONS.
 RP Ohara O., Nagase T., Kikuno R., Nomura N.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
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 DR EMBL; AB094094; BAC76048.1; -
 DR EMBL; BC010071; AAH10071.1; ALT_INT.
 DR EMBL; BC021254; AAH21254.1; ALT_INT.
 DR EMBL; BC022219; AAH22219.1; -
 DR EMBL; BC033083; AAH33083.1; -
 DR EMBL; AB006623; BAA22954.2; -
 DR Genew; HGNC:29000; TMEM24.
 DR InterPro; IPR008973; C2_GaLB.
 KW Transmembrane.
 KM TRANSMEM 10
 FT CONFLICT 497 R -> Pg (in Ref. 1).
 SQ SEQUENCE 706 AA; 76180 MW; 9301ABBDFF6D4D5B6 CRC64;
 Query Match 85.7%; Score 30; DB 1; Length 706;
 Best Local Similarity 71.4%; Pred. No. 6.3e+02;

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Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 DVSKRPS 7
|:|:|
Db 607 DISERPS 613

RESULT 34
TM24_MOUSE STANDARD; PRT; 706 AA.
ID TM24_MOUSE
AC Q80X80.0
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Transmembrane protein 24.
GN Name=tmem24;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain, and Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggiano N.A., Peters G.J., Abramson R.D., Mullighy S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schultz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.T., Skalska U., Smallos D.E.,
RA Schermer A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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CC -----
CC EMBL; BC049875; AAH49875.1; -
DR EMBL; BC060156; AAH60156.1; -
DR MGD; MGI:1919014; 1300006023R1k.
DR InterPro; IPR008973; C2_CalB.
KM Transmembrane.
FT TRANSMEM 10 30 Potential.
FT CONFLICT 550 550 V -> A (in Ref. 1; AAH49875).
SQ SEQUENCE 706 AA; 76356 MW; 2F8B63D26FF1F91 CRC64;

Query Match 85.7%; Score 30; DB 1; Length 706;
Best Local Similarity 71.4%; Pred. No. 6.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 DVSKRPS 7
|:|:|
Db 607 DISERPS 613

RESULT 35
Q6D0L7

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ID Q6D0L7 PRELIMINARY; PRT; 747 AA.
AC Q6D0L7;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Tomb dependent siderophore receptor.
GN Name=FeprA; Synonyms=Fepr, Feub; OrderedLocustNames=BCA3781;
OS Erwinia carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pectobacterium.
OX NCBI_TaxId=29471;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SCRI 1043 / ATCC BAA-672;
RX PubMed=15263089; DOI=10.1073/pnas.0402424101;
RA Bell K.S., Sebaitia M., Pritchard L., Holden M.T.G., Hyman L.J.,
RA Holava M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K.,
RA Atkin R., Bacon N., Brooks K., Chillingworth T., Clark K., Doggett J.,
RA Fraser A., Hance Z., Hauser H., Jagels K., Moule S., Norbertczak H.,
RA Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
RA Salmond G.P.C., Birch P.R.J., Parkhill J., Toth I.K.;
RT "Genome sequence of the enterobacterial phytopathogen Erwinia
RT carotovora subsp. atroseptica and characterization of virulence
RT factors."
RT Proc. Natl. Acad. Sci. U.S.A. 101:11105-11110(2004).
RL EMBL; BX950851; CAG76680.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016469; C:proton-transporting two-sector ATPase complex; IEA.
DR GO; GO:0016820; F:hydrolase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0015992; P:proton transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002086; Alderhyd_dhydrg.
DR InterPro; IPR000568; ATPsyn_Asub.
DR InterPro; IPR010916; TONB_Box_N.
DR InterPro; IPR010917; TONB_recept_C.
DR InterPro; IPR010105; TONB_sdp_recept.
DR TIGRFAMs; TIGR01783; TONB-siderophor.1.
DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
DR PROSITE; PS00449; ATPASE_A; 1.
DR PROSITE; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
DR PROSITE; PS01156; TONB_DEPENDENT_REC_2; UNKNOWN_1.
KM Complete proteome; Receptor.
SQ SEQUENCE 747 AA; 81581 MW; 8E8A5D2505CBB065 CRC64;

Query Match 85.7%; Score 30; DB 2; Length 747;
Best Local Similarity 83.3%; Pred. No. 6.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 DVSKRP 6
|:|:|
Db 56 DISKRP 61

RESULT 36
Q6ADP4 PRELIMINARY; PRT; 833 AA.
ID Q6ADP4;
AC Q6ADP4;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Tetrahydro acid synthase.
GN Name=tagF; OrderedLocustNames=Lxx17460;
OS Leifsonia xyli (subsp. xyli).
OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;
OC Micrococciaceae; Microbacteriaceae; Leifsonia.
OX NCBI_TaxId=59736;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CTCB07;
RX PubMed=15305603;
Monteiro-Vitorello C.B., Camargo L.E.A., Van Sluys M.A.,

```

RA Kitaajima J.P., Truffi D., do Amaral A.M., Harakava R.,
RA de Oliveira J.C.F., Wood D., de Oliveira M.C., Miyaki C.Y.,
RA Taiteira M.A., da Silva A.C.R., Furian L.R., Carraro D.M., Camarotte G.,
RA Almeida N.F., Jr., Carreir H., Coutinho L.L., El-Dorri H.A.,
RA Ferro M.I.T., Gagliardi P.R., Gigliotti E., Goldman M.H.S.,
RA Goldman G.H., Kimura E.T., Ferro B.S., Kurama E.E., Lemos E.G.M.,
RA Lemos M.V.F., Mauro S.M.Z., Machado M.A., Marino C.L., Menck C.F.,
RA Nunes L.R., Oliveira A.C., Pereira G.G., Siqueira W., de Souza A.A.,
RA Tsai S.M., Zanca A.S., Simpson A.J.G., Brumley S.M., Setubal J.C.,
RT "the genome sequence of the Gram-positive sugarcane pathogen *Leifsonia*
RT *xyl* subsp. *xyl*.",
RL Mol. Plant Microbe Interact. 17:827-836(2004).
DR EMBL; AB016822; AAT89502.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0047355; F:CDP-glycerol 1-glycerophosphotransferase acti. ., IEA.
DR GO; GO:0009058; P:biogenesis; IEA.
DR GO; GO:0019350; P:teichoic acid biosynthesis; IEA.
DR InterPro; IPR001296; Glyco_trans_1.
DR InterPro; IPR007554; Glyphos_transf.
DR Pfam; PF00534; Glycos_transf_1.
DR Pfam; PF04464; Glyphos_transf; 1.
KW Complete proteome.
SQ SEQUENCE 833 AA; 92594 MW; 3C321CDAB67FC99 CRC64;

Query Match	85.7%	Score 30;	DB 2;	length 833;
Best Local Similarity	85.7%	Pred. No. 7.4e+02;		
Matches	6;	Conservative	0;	Mismatches 1;
				Indels 0;
				Gaps 0;
QY	1	DVSKRPS	7	
Db	119	DPSKRPS	125	

RESULT 37	
ID	06LMQ4
AC	06LMQ4; PRELIMINARY; PRT; 1036 AA.
DT	05-JUL-2004 (TREMBLrel. 27, Created)
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE	Hypothetical protein.
GN	OrderedLocustNames=MMP1653;
OS	Methanococcus maripaludis.
OC	Archaea; Buryarchaeota; Methanococci; Methanococcales;
OC	Methanococcaceae; Methanococcus.
OX	NCBI_TaxID=39152;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=52 / LL;
RA	Hendrickson E.L., Kaul R., Zhou Y., Bovee D., Chapman P., Chung J.,
RA	Conway de Macario E., Dodsworth J., Gillett W., Graham D.E.,
RA	Haydock A.K., Kang A., Land M.L., Levy R., Lie T.J., Major T.,
RA	Moore B., Porat I., Overbeek R., Palmeiri A., Rouse G.,
RA	Saenphitumachak C., Soll D., Whitman W.B., Larimer F.W., Olson M.V.,
RA	Leigh J.A.,
RT	"Complete genome sequence of the mesophilic hydrogenotrophic
RT	methanogen Methanococcus maripaludis."
RL	Submitted (FEB-2004) to the EMBL/Genbank/DBJ databases.
RL	EMBL; BX957223; CAF31209.1; -
DR	InterPro; IPR006938; ARM.
KM	Complete proteome.
Q0	SEQUENCE 1036 AA; 121756 MW; A79GCBF10B2060575 CRC64;

Query Match	85.7%	Score 30;	DB 2;	Length 1036;
Best Local Similarity	85.7%	Pred. No. 9.3e+02;		
Matches	6;	Conservative	0;	Mismatches 1;
				Indels 0;
				Gaps 0;
QY	1	DVSKRPS	7	
Db	808	DVSKRPS	814	

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ID      064001
AC      064001;
DT      25-OCT-2004 (TremblRel. 28, Created)
DT      25-OCT-2004 (TremblRel. 28, Last sequence update)
DT      25-OCT-2004 (TremblRel. 28, Last annotation update)
DE      Putative outer membrane protein probably involved in nutrient
DE      binding.
DE      ORFNames=BP3437;
OS      Bacteroides fragilis.
OC      Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC      Bacteroidaceae; Bacteroides.
OX      NCBI_TaxID=817;
RX      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=YCH46;
RA      Kuwahara T., Yamashita A., Hirakawa H., Nakayama H., Toh H., Okada N.,
RA      Kuhara S., Hattori M., Hayashi T., Ohnishi Y.;
RT      "Genomic analysis of Bacteroides fragilis reveals extensive DNA
RT      inversions regulating cell surface adaptation.";
RL      Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2004).
DQ      EMBL, AF006841; BAD50180.1;
SQ      SEQUENCE 1059 AA, 118250 MW, F15E945F7BFDPAAS CRC64;

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Query Match      85.7%;  Score 30;  DB 2;  Length 1059;
Best Local Similarity  83.3%;  Pred. No. 9.6e+02;
Matches      5;  Conservative      0;  Indels      0;  Gaps      0;
QY      1  DVSKRP 6
      : : : : :
      : : : : :
db      158  DISKRP 163

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RESULT 39		
08SX99		
ID	08SX99	PRELIMINARY; PRT; 1372 AA.
AC	08SX99;	
DT	01-JUN-2002 (TReMBLrel, 21, Created)	
DT1	01-JUN-2002 (TReMBLrel, 21, Last sequence update)	
DT2	01-MAR-2003 (TReMBLrel, 23, Last annotation update)	
DE	GH5780P.	
GN	Name=CG1054; ORFNames=CG31531;	
OS	Drosophila melanogaster (Fruit fly).	
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;	
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	
OC	Ephydroidea; Drosophilidae; Drosophila.	
OX	NCBI_TaxID=7227;	
RP	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=Berkley;	
RA	Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,	
RA	Champ M., Chavez C., Dorett V., Dresnek D., Farfan D., Frise E.,	
RA	George R., Gonzalez M., Guarin H., Krommler B., Li P., Lao G.,	
RA	Miranda A., Mungall C.J., Nunoo J., Pacleb J., Patagas V., Park S.,	
RA	Patel S., Phouanvong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,	
RA	Celniker S.;	
RA	Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.	
RL	EMBL; AY094730; AA011083.1; -	
DR	FLYBase; FBgn0051531; CG31531.	
SO	SEQUENCE 1372 AA; 149239 MW; 3B9B643E74C2658E CRC64;	

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Query Match      85.7%; Score 30; DB 2; Length 1372;
Best Local Similarity 85.7%; Pred. No. 1.3e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 DVSKRPS 7
    | | | | |
Db 722 DFKRPS 728

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RESULT 40	
Q9VN46	
ID Q9VN46	PRELIMINARY; PRT; 1372 AA

AC Q9VNA6; (TrEMBLrel. 13, Created)
 DT 01-MAR-2000 (TrEMBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE CG31531-PA (CG31531-pb).
 GN ORFNames=CG31531;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephyridae; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 RA Abell J.F., Agbayani A., An H.J., Andrews-Pfankuch C., Baldwin D.,
 RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Butlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Dudin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foslter C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glaeser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegam C.,
 RA Jatali M., Kalush F., Karpen G.H., Ke Z., Kemison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milhina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodager, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
 RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren B.J.,
 RA Svitskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
 melanogaster euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svitskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;
 RT "The transposable elements of the Drosophila melanogaster euchromatin:
 a genomic perspective.";
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).

RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Miya S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Bernan B.P.,
 RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 systematic review.";
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RG FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RG FlyBase;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB003605; AAF52105.2; -
 DR FlyBase; FBgn0051531; CG31531.
 SQ SEQUENCE 1372 AA; 149298 MW; 726436F41803F4D7 CRC64;

Query Match 85.7%; Score 30; DB 2; Length 1372;
 Best local similarity 85.7%; Pred. No. 1.3e+03;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DVSKRPS 7
 |||||
 DB 722 DFSKRPS 728

Search completed: March 31, 2005, 12:09:45
 Job time : 48.651 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 31, 2005, 11:42:18 ; Search time 85.25 Seconds
(without alignments)
49.905 Million cell updates/sec

Title: US-10-614-959-15
Perfect score: 58
Sequence: 1 AAWDSLSEFL 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	100.0	11	3	AA79073 Anti-fact
2	58	100.0	104	2	AA880087 Human der
3	58	100.0	104	2	AA95485 Human der
4	58	100.0	109	4	AAU02544 Anti-adip
5	58	100.0	110	4	AAU02558 Anti-adip
6	58	100.0	110	4	AAU02612 Anti-adip
7	58	100.0	110	4	AAU02627 Anti-adip
8	58	100.0	110	4	AAU02629 Anti-adip
9	58	100.0	111	2	AAW19883 CEA-speci
10	58	100.0	111	4	AAU02542 Anti-adip
11	58	100.0	111	4	AAU02551 Anti-adip
12	58	100.0	111	4	AAU02585 Anti-adip
13	58	100.0	111	4	AAU02606 Anti-adip
14	58	100.0	242	8	ADG34301 Neurokini
15	58	100.0	242	8	ADG34317 Neurokini
16	58	100.0	243	5	ABP45916 Human Bly
17	58	100.0	243	7	ADG96743 Single ch
18	58	100.0	243	7	ADG34310 Neurokini
19	58	100.0	244	8	ADG34306 Neurokini
20	58	100.0	244	8	ADG34303 Neurokini
21	58	100.0	245	5	ABP45915 Human Bly
22	58	100.0	245	7	ADG96742 Single ch
23	58	100.0	245	7	ADG98057 TNF proli
24	58	100.0	245	8	ADG83862 Chemokine
25	58	100.0	245	8	ADG34308 Neurokini

26	58	100.0	246	5	ABP45902 Human Bly
27	58	100.0	246	5	ABP45906 Human Bly
28	58	100.0	246	7	ADG96733 Single ch
29	58	100.0	246	7	ADG96729 Single ch
30	58	100.0	246	8	ADG83872 Chemokine
31	58	100.0	247	5	ABP45671 Human Bly
32	58	100.0	247	5	ABP45432 Human Bly
33	58	100.0	247	5	ABP45923 Human Bly
34	58	100.0	247	5	ABP45917 Human Bly
35	58	100.0	247	5	ABP45696 Human Bly
36	58	100.0	247	5	ABP45888 Human Bly
37	58	100.0	247	7	ADG30413 Human GMB
38	58	100.0	247	7	ADG30455 Human GMB
39	58	100.0	247	7	ADG96715 Single ch
40	58	100.0	247	7	ADG96498 Single ch
41	58	100.0	247	7	ADG96744 Single ch
42	58	100.0	247	7	ADG96259 Single ch
43	58	100.0	247	7	ADG96750 Single ch
44	58	100.0	247	7	ADG96523 Single ch
45	58	100.0	247	8	ADG83874 Chemokine

ALIGNMENTS

RESULT 1
AA79073
ID AA79073 standard; peptide; 11 AA.

AA79073;
12-JUN-2000 (first entry)

Anti-factor IX/IXa antibody L chain V domain CDR3 amino acid sequence.
Complementarity determining region 3, CDR3; antibody; Gla domain;
factor IX/IXa; blood coagulation; deep venous thrombosis; light chain;
arterial thrombosis; unstable angina; post myocardial infarction;
coronary artery bypass graft; CABG; stroke; tumour growth; metastasis;
percutaneous transluminal coronary angioplasty; PTCA; inflammation;
septic shock; hypotension; adult respiratory distress syndrome; ARDS;
arterial fibrillation; disseminated intravascular coagulopathy; DIC.

Homo sapiens.

WO200012562-A1.

09-MAR-2000.

26-AUG-1999; 99WO-US019453.

28-AUG-1998; 98US-0098233P.

03-MAR-1999; 99US-0122767P.

(GETH) GENENTECH INC.

Adams CW, Devaux B, Baton DL, Hase PE, Judice JK, Kirchofer D;
Suggett S;

WPI; 2000-256595/22.

Novel human anti-Factor IX/IXa antibodies against IX/IXa gamma-
carboxyglutamic acid domains useful as anti-coagulant in thrombosis,
stroke, and post myocardial infarction.

Claim 8, Fig 2; 84pp; English.

This sequence represents a complementarity determining region 3 (CDR3) of
the light chain variable domain of a human anti-factor IX/IXa Gla domain
antibody. Factor IXa is a vitamin K dependent plasma serine protease that
participates in the blood coagulation pathways. The Gla domain of factor
IXa and its zymogen factor IX contains important structural determinants
for interaction with high affinity binding sites on vascular endothelial

CC	cells and platelets. Compositions comprising the antibodies are used for
CC	the treatment or prophylaxis of thrombotic or coagulopathic diseases or
CC	disorders in a mammal for which inhibiting a FIX/FIXa mediated event is
CC	indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable
CC	angina, post myocardial infarction, post surgical thrombosis, coronary
CC	artery bypass graft (CABG), percutaneous transluminal coronary
CC	angioplasty (PTCA), stroke, tumour growth, invasion or metastasis,
CC	inflammation, septic shock, hypotension, adult respiratory distress
CC	syndrome (ARDS), arterial fibrillation and disseminated intravascular
CC	coagulation (DIC)
XX	
SQ	Sequence 11 AA;
Query Match	100.0%; Score 58; DB 3; Length 11;
Best Local Similarity	100.0%; Pred. NO. 0.0022;
Matches 11; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1 AAMDSSUSEPL 11
Dd	1 AAMDSSUSEFL 11
RESULT 2	
ID	AAR80087 standard; protein; 104 AA.
XX	
AC	AAR80087;
DT	23-MAY-1996 (first entry)
DE	Human derived light chain RT3 phage antibody.
XX	
KM	Light chain; RT3; human; catalytic antibody; bacteriophage.
XX	
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	Region 7..15
FT	/note= "framework region 1"
FT	Region 16..28
FT	/note= "complementarity determining region 1"
FT	Region 29..42
FT	/note= "framework region 2"
FT	Region 43..50
FT	/note= "complementarily determining region 2"
FT	Region 51..82
FT	/note= "framework region 3"
FT	Region 83..93
FT	/note= "complementarity determining region 3"
FT	Region 94..104
FT	/note= "framework region 4"
XX	
PN	WO9527045-A1.
XX	
DD	12-OCT-1995.
XX	
Pf	30-MAR-1994; 94WO-US003420.
XX	
PR	30-MAR-1994; 94WO-US003420.
XX	
PA	(IGEN-) IGEN INC.
PI	Smith RG, McCafferty J, Chiswell D, Darsley MJ, Fitzgerald K;
PI	Kenten JH, Martin MT, Tiltman RC, Williams RO;
DR	N-PDSB; NANT04634.
DR	WPI; 1995-358624/46.
XX	
PT	Production of catalytic antibodies displayed on phage - by generating a
PT	gene library of antibody-derived domains and expressing it in phage
PT	vectors.
DS	Disclosure; Fig 20; 133pp; English.

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XX  AAT04634 encodes AAR80087 human derived light chain RT3 phage antibody.
CC  The DNA was used in the prepn. of catalytic antibody (CA) producing
CC  bacteriophage. The CAs can be used to activate/deactivate a biological
CC  function in an animal by enhancing the rate of cleavage, or formation of
CC  a specific bond within a mol. in vivo
XX
SQ  Sequence 104 AA;

Query Match      100.0%; Score 58; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0

OY      1 AAMDLSLEFL 11
        |||||
Db       83 AAMDLSLEFL 93

RESULT 3
ID      AAW95485
AC      AAW95485;
DT      29-MAR-1999 (first entry)
DE      Human-derived RT3 phage antibody light chain genetic sequence.
XX
KW      Catalytic; antibody; phage display; immunising; phage expression vector;
XX      prodrg; scFv; RT3.
OS      Homo sapiens.
XX
FN      US5855885-A.
PD      05-JAN-1999.
PE      14-JUL-1994; 94US-00273146.
XX
PR      22-JAN-1993; 93US-00007684.
XX
PA      (MCCA/) MCCAFFERTY J.
PA      (CHIS/) CHISWELL D.
PA      (DARS/) DARSLEY M J.
PA      (TTTM/) TITMAS R C.
PA      (MART/) MARTIN M T.
PA      (KENT/) KENTEN J H.
PA      (SMIT/) SMITH R.
PA      (FITZ/) FITZGERALD K.
PA      (WILL/) WILLIAMS R O.
XX
P1      Fitzgerald K, Darsley MJ, Williams RO, Smith R, Martin MT;
P1      Kenten JH, Chiswell D, Mccafferty J, Titmas RC;
XX
DR      N-PSDB; AAX00884.
XX
WPI: 1999-105036/09.

XX  Production of catalytic antibodies displayed on bacteriophages -
PT  comprises generating a gene library of antibody-derived domains inserting
PT  coding into a phage expression vector and isolating the catalytic
PT  antibodies.

XX  Example; Fig 20B; 117p; English.

XX  The invention relates to methods for producing catalytic antibodies
XX  displayed on a phage. The method comprises: (a) generating a gene library
XX  of antibody-derived domains; (b) inserting coding for the domains into a
XX  phage expression vector; and (c) isolating the catalytic antibodies. The
XX  phage expression vector incorporates a histidine peptide in tandem with a
XX  myc peptide. The catalytic antibodies can be isolated by preparing an
XX  antigen; optionally immunising an animal with the antigen; generating a
XX  library of VH and VL domains from the immunised animal; cloning the VH
XX  and VL domains into a phage expression vector to generate phage display

```

CC antibodies; selecting phage display antibodies which bind specifically to
 CC the antigen; screening the selected phage display antibodies for
 CC catalytic activity to substrate; and isolating the catalytic antibodies,
 CC where the phage expression vector incorporates a histidine peptide in
 CC tandem with a myc peptide. The processes are used to produce catalytic
 CC antibodies, which can be used for in vivo activation of a prodrug.
 CC Sequences AA95444-489 represent genetic sequences of heavy and light
 CC chains of RT3 specific phage antibodies selected from a naive human phage
 CC antibody library
 CC
 SQ Sequence 104 AA;
 Query Match 100.0%; Score 58; DB 2; Length 104;
 Best Local Similarity 100.0%; Pred. No. 0.023;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAMDLSLEFL 11
 |||||
 DB 83 AAMDLSLEFL 93
 |||||
 RESULT 4
 AA02544
 ID AA02544 standard; protein; 109 AA.
 AC AA02544;
 XX
 DT 29-AUG-2001 (first entry)
 XX
 DE Anti-adipocyte monoclonal antibody light chain, FAT 31.
 XX
 KW Antibody; adipocyte; heavy chain; light chain; obesity; fat;
 KW heart disease; complementarity determining region; CDR.
 XX
 OS Homo sapiens.
 XX
 PN WO200127279-A1.
 XX
 PD 19-APR-2001.
 XX
 PF 11-OCT-2000; 2000WO-GB003900.
 XX
 PR 12-OCT-1999; 99US-0158812P.
 XX
 PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX
 PI Edwards BM, Main SH, Vaughan TJ;
 XX
 DR WPI; 2001-282031/29.
 DR N-PSDB; AAS03444.
 XX
 PT Panel of specific binding members of antibody molecules which bind to
 PT whole adipocytes is used in the treatment of obesity and obesity related
 PT diseases.
 PS
 PS Claim 1; Page 120; 182pp; English.
 CC AA02501-AA02635, and AA02641-AA02748 represent the amino acid
 CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
 CC and heavy chain complementarity determining regions (CDR) of the
 CC invention. The antibodies can be used in the treatment of obesity and
 CC obesity related diseases. The antibodies can be used to deliver drugs or
 CC pro-drugs directly to the fat mass of an obese patient or the antibody
 CC can be used as a therapeutic itself. Antibodies binding specifically to
 CC adipocytes can be used to activate the immune system to destroy the cells
 CC by complement mediated lysis. The antibodies may be labeled with a
 CC detectable label such as radiolabel, fluorescent or chemical group and
 CC used in methods of diagnosis in human subjects e.g. to determine the
 CC presence of adipocyte antigen on the surface of an adipocyte to detect or
 CC determine the presence or level of adipocytes in a cell or tissue sample.
 CC The antibodies can be used as an alternative means of treatment for obese
 CC patients other than undergoing surgery to remove excess fat. Antibodies
 CC for different types of fat deposits can also be produced e.g. intra-

CC abdominal fat associated with heart disease
 XX
 SQ Sequence 109 AA;
 Query Match 100.0%; Score 58; DB 4; Length 109;
 Best Local Similarity 100.0%; Pred. No. 0.024;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAMDLSLEFL 11
 |||||
 DB 90 AAMDLSLEFL 100
 |||||
 RESULT 5
 AA02558
 ID AA02558 standard; protein; 110 AA.
 AC AA02558;
 XX
 DT 29-AUG-2001 (first entry)
 XX
 DE Anti-adipocyte monoclonal antibody light chain, FAT 44.
 XX
 KW Antibody; adipocyte; heavy chain; light chain; obesity; fat;
 KW heart disease; complementarity determining region; CDR.
 XX
 OS Homo sapiens.
 XX
 PN WO200127279-A1.
 XX
 PD 19-APR-2001.
 XX
 PF 11-OCT-2000; 2000WO-GB003900.
 XX
 PR 12-OCT-1999; 99US-0158812P.
 XX
 PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX
 PI Edwards BM, Main SH, Vaughan TJ;
 XX
 DR WPI; 2001-282031/29.
 DR N-PSDB; AAS03458.
 XX
 PT Panel of specific binding members of antibody molecules which bind to
 PT whole adipocytes is used in the treatment of obesity and obesity related
 PT diseases.
 PS
 PS Claim 1; Page 128-129; 182pp; English.
 CC AA02501-AA02635, and AA02641-AA02748 represent the amino acid
 CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
 CC and heavy chain complementarity determining regions (CDR) of the
 CC invention. The antibodies can be used in the treatment of obesity and
 CC obesity related diseases. The antibodies can be used to deliver drugs or
 CC pro-drugs directly to the fat mass of an obese patient or the antibody
 CC can be used as a therapeutic itself. Antibodies binding specifically to
 CC adipocytes can be used to activate the immune system to destroy the cells
 CC by complement mediated lysis. The antibodies may be labeled with a
 CC detectable label such as radiolabel, fluorescent or chemical group and
 CC used in methods of diagnosis in human subjects e.g. to determine the
 CC presence of adipocyte antigen on the surface of an adipocyte to detect or
 CC determine the presence or level of adipocytes in a cell or tissue sample.
 CC The antibodies can be used as an alternative means of treatment for obese
 CC patients other than undergoing surgery to remove excess fat. Antibodies
 CC for different types of fat deposits can also be produced e.g. intra-
 CC abdominal fat associated with heart disease
 SQ Sequence 110 AA;
 Query Match 100.0%; Score 58; DB 4; Length 110;
 Best Local Similarity 100.0%; Pred. No. 0.024;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAWDSISEFL 11
 DB 90 AAWDSISEFL 100

RESULT 6
 AAU02612
 ID AAU02612 standard; protein; 110 AA.

AC AAU02612;
 DT 29-AUG-2001 (first entry)

DE Anti-adipocyte monoclonal antibody light chain, FAT 99.

XX Antibody; adipocyte; heavy chain; light chain; obesity; fat;
 KW heart disease; complementarity determining region; CDR.

OS Homo sapiens.

XX MO200127279-A1.

XX 19-APR-2001.

XX 11-OCT-2000; 2000WO-GB003900.

XX 12-OCT-1999; 99US-0158812P.

XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Edwards BM, Main SH, Vaughan TJ;

XX WPI; 2001-282031/29.

XX N-PSDB; AAS03512.

PT Panel of specific binding members of antibody molecules which bind to
 PT whole adipocytes is used in the treatment of obesity and obesity related
 PT diseases.

PS Claim 1; Page 163; 182pp; English.

XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
 CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
 CC and heavy chain complementarity determining regions (CDR) of the
 CC invention. The antibodies can be used in the treatment of obesity and
 CC obesity related diseases. The antibodies can be used to deliver drugs or
 CC pro-drugs directly to the fat mass of an obese patient or the antibody
 CC can be used as a therapeutic itself. Antibodies binding specifically to
 CC adipocytes can be used to activate the immune system to destroy the cells
 CC by complement mediated lysis. The antibodies may be labeled with a
 CC detectable label such as radiolabel, fluorescent or chemical group and
 CC used in methods of diagnosis in human subjects e.g. to determine the
 CC presence of adipocyte antigen on the surface of an adipocyte to detect or
 CC determine the presence or level of adipocytes in a cell or tissue sample.
 CC The antibodies can be used as an alternative means of treatment for obese
 CC patients other than undergoing surgery to remove excess fat. Antibodies
 CC for different types of fat deposits can also be produced e.g. intra-
 CC abdominal fat associated with heart disease

XX Sequence 110 AA;

Query Match 100.0%; Score 58; DB 4; Length 110;
 Best Local Similarity 100.0%; Pred. No. 0.024;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAWDSISEFL 11
 DB 90 AAWDSISEFL 100

RESULT 7
 AAU02627
 ID AAU02627 standard; protein; 110 AA.

XX AAU02627;
 AC
 DT 29-AUG-2001 (first entry)

DE Anti-adipocyte monoclonal antibody light chain, FAT 112.

XX Antibody; adipocyte; heavy chain; light chain; obesity; fat;
 KW heart disease; complementarity determining region; CDR.

OS Homo sapiens.

XX MO200127279-A1.

XX 19-APR-2001.

XX 11-OCT-2000; 2000WO-GB003900.

XX 12-OCT-1999; 99US-0158812P.

XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Edwards BM, Main SH, Vaughan TJ;

XX WPI; 2001-282031/29.

XX N-PSDB; AAS03527.

PT Panel of specific binding members of antibody molecules which bind to
 PT whole adipocytes is used in the treatment of obesity and obesity related
 PT diseases.

PS Claim 1; Page 172; 182pp; English.

XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
 CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
 CC and heavy chain complementarity determining regions (CDR) of the
 CC invention. The antibodies can be used in the treatment of obesity and
 CC obesity related diseases. The antibodies can be used to deliver drugs or
 CC pro-drugs directly to the fat mass of an obese patient or the antibody
 CC can be used as a therapeutic itself. Antibodies binding specifically to
 CC adipocytes can be used to activate the immune system to destroy the cells
 CC by complement mediated lysis. The antibodies may be labeled with a
 CC detectable label such as radiolabel, fluorescent or chemical group and
 CC used in methods of diagnosis in human subjects e.g. to determine the
 CC presence of adipocyte antigen on the surface of an adipocyte to detect or
 CC determine the presence or level of adipocytes in a cell or tissue sample.
 CC The antibodies can be used as an alternative means of treatment for obese
 CC patients other than undergoing surgery to remove excess fat. Antibodies
 CC for different types of fat deposits can also be produced e.g. intra-
 CC abdominal fat associated with heart disease

XX Sequence 110 AA;

Query Match 100.0%; Score 58; DB 4; Length 110;
 Best Local Similarity 100.0%; Pred. No. 0.024;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAWDSISEFL 11
 DB 90 AAWDSISEFL 100

RESULT 8
 AAU02629
 ID AAU02629 standard; protein; 110 AA.

XX AAU02629;

XX 29-AUG-2001 (first entry)

DE Anti-adipocyte monoclonal antibody light chain, FAT 113.

XX Antibody; adipocyte; heavy chain; light chain; obesity; fat;

KW heart disease; complementarity determining region; CDR.
 XX Homo sapiens.
 XX WO200127279-A1.
 PN 19-APR-2001.
 PD 11-OCT-2000; 2000WO-GB003900.
 PE 12-OCT-1999; 99US-0158812P.
 PR (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 PA Edwards BM, Main SH, Vaughan TJ;
 PI WPI, 2001-282031/29.
 DR N-PSDB; AAS03529.
 XX Panel of specific binding members of antibody molecules which bind to
 PT whole adipocytes is used in the treatment of obesity and obesity related
 PT diseases.
 PS Claim 1; Page 173; 182pp; English.
 XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
 CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
 CC and heavy chain complementarity determining regions (CDR) of the
 CC invention. The antibodies can be used in the treatment of obesity and
 CC obesity related diseases. The antibodies can be used to deliver drugs or
 CC pro-drugs directly to the fat mass of an obese patient or the antibody
 CC can be used as a therapeutic itself. Antibodies binding specifically to
 CC adipocytes can be used to activate the immune system to destroy the cells
 CC by complement mediated lysis. The antibodies may be labeled with a
 CC detectable label such as radiolabel, fluorescent or chemical group and
 CC used in methods of diagnosis in human subjects e.g. to determine the
 CC presence of adipocyte antigen on the surface of an adipocyte to detect or
 CC determine the presence or level of adipocytes in a cell or tissue sample.
 CC The antibodies can be used as an alternative means of treatment for obese
 CC patients other than undergoing surgery to remove excess fat. Antibodies
 CC for different types of fat deposits can also be produced e.g. intra-
 CC abdominal fat associated with heart disease
 CC XX
 SQ Sequence 110 AA;
 Query Match 100.0%; Score 58; DB 4; Length 110;
 Best Local Similarity 100.0%; Pred. No. 0.024;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAWDLSSEFL 11
 Db 90 AAWDLSSEFL 100
 RESULT 9
 AAU19883
 ID AAU19883 standard; protein; 111 AA.
 XX AAU19883;
 AC
 XX 07-DEC-1997 (first entry)
 DT
 XX CEA-specific antibody CEA1, CEA2, CEA3 VL sequence.
 DB
 XX Carcinoembryonic antigen; CEA; human; antibody; scFv; tumour marker;
 KW Lung cancer; breast cancer; colon cancer; adenocarcinoma; diagnosis.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT 23..35
 FT Region /label= CDR1
 FT /note= "complementarity determining region 1"

FT Region 50..56
 FT /label= CDR2
 FT /note= "complementarity determining region 2"
 FT Region 90..100
 FT /label= CDR3
 FT /note= "complementarity determining region 3"
 PN WO970932-A1.
 PD 12-JUN-1997.
 PE 09-DEC-1996; 96WO-GB003043.
 PR 07-DEC-1995; 95GB-00025004.
 PR 23-MAY-1996; 96GB-00010824.
 PR 11-OCT-1996; 96GB-00021295.
 XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 PA Osdounn JK, Allen DJ, McCafferty JG;
 PI WPI, 1997-319779/29.
 DR N-PSDB; AAT72133.
 XX Specific binding members for human carcinoembryonic antigen - bind to the
 PT A3-B3 extracellular domain of hCEA and are substantially non-cross-
 PT reactive with human liver cells; used for diagnosing cancer.
 PS Claim 14; Fig 1b; 128pp; English.
 XX This polypeptide sequence comprises the light chain variable region (VL)
 CC of human carcinoembryonic antigen (hCEA)-specific antibodies CEA1, CEA2
 CC and CEA3. VH (AAU72126-32) and VL (AAT72133-35) gene sequences were
 CC obtained for anti-hCEA antibodies CEA1-CEA3 (see AAU19876-85). A claimed
 CC specific binding member (A) comprises an hCEA specific antibody antigen
 CC binding domain that has a dissociation constant for hCEA of less than 1 x
 CC 10⁻⁸ M, is non-cross-reactive with human liver cells, and
 CC preferentially binds to the A3-B3 extracellular domain of hCEA and/or to
 CC cell-associated hCEA over hCEA over soluble hCEA. Preferred (A) include
 CC pairings of VH and VL sequences from CEA1-7, or their CDR sequences, as
 CC well as CEA6 VH and VL variants. (A) is used to detect cells expressing
 CC hCEA, in vivo or in vitro, especially tumour cells for diagnosing cancer,
 CC e.g. adenocarcinoma of the colon, lung or breast
 CC XX
 SQ Sequence 111 AA;
 Query Match 100.0%; Score 58; DB 2; Length 111;
 Best Local Similarity 100.0%; Pred. No. 0.025;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAWDLSSEFL 11
 Db 90 AAWDLSSEFL 100
 RESULT 10
 AAU02542
 ID AAU02542 standard; protein; 111 AA.
 XX AAU02542;
 AC
 XX 29-AUG-2001 (first entry)
 DT
 XX Anti-adipocyte monoclonal antibody light chain. PAT 30.
 DB
 XX Antibody; adipocyte; heavy chain; light chain; obesity; fat;
 KW heart disease; complementarity determining region; CDR.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT WO200127279-A1.
 FT 19-APR-2001.

XX 11-OCT-2000; 2000WO-GB003900.
PF 12-OCT-1999; 99US-0158812P.
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PA Edwards BM, Main SH, Vaughan TJ;
PI WPI; 2001-282031/29.
XX N-PSDB; AAS03442.
PT Panel of specific binding members of antibody molecules which bind to
PT whole adipocytes is used in the treatment of obesity and obesity related
PT diseases.
PS Claim 1; Page 118-119; 182pp; English.
XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
CC and heavy chain complementarity determining regions (CDR) of the
CC invention. The antibodies can be used in the treatment of obesity and
CC obesity related diseases. The antibodies can be used to deliver drugs or
CC pro-drugs directly to the fat mass of an obese patient or the antibody
CC can be used as a therapeutic itself. Antibodies binding specifically to
CC adipocytes can be used to activate the immune system to destroy the cells
CC by complement mediated lysis. The antibodies may be labeled with a
CC detectable label such as radiolabel, fluorescent or chemical group and
CC used in methods of diagnosis in human subjects e.g. to determine the
CC presence of adipocyte antigen on the surface of an adipocyte to detect or
CC determine the presence or level of adipocytes in a cell or tissue sample.
CC The antibodies can be used as an alternative means of treatment for obese
CC patients other than undergoing surgery to remove excess fat. Antibodies
CC for different types of fat deposits can also be produced e.g. intra-
CC abdominal fat associated with heart disease
XX Sequence 111 AA;
SQ
Query Match 100.0%; Score 58; DB 4; Length 111;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AAWDLSSEFL 11
DB 90 AAWDLSSEFL 100
RESULT 11
AAU02551
ID AAU02551 standard; protein; 111 AA.
XX AAU02551;
AC
XX 29-AUG-2001 (first entry)
DT
XX Anti-adipocyte monoclonal antibody light chain, FAT 37.
DE
XX Antibody; adipocyte; heavy chain; light chain; obesity; fat;
KW heart disease; complementarity determining region; CDR.
XX Homo sapiens.
OS
XX WO200127279-A1.
PN
XX 19-APR-2001.
PD
XX 11-OCT-2000; 2000WO-GB003900.
PF
XX 12-OCT-1999; 99US-0158812P.
PR
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PA Edwards BM, Main SH, Vaughan TJ;
PI

XX WPI; 2001-282031/29.
DR N-PSDB; AAS03451.
XX Panel of specific binding members of antibody molecules which bind to
PT whole adipocytes is used in the treatment of obesity and obesity related
PT diseases.
PS Claim 1; Page 124; 182pp; English.
XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
CC and heavy chain complementarity determining regions (CDR) of the
CC invention. The antibodies can be used in the treatment of obesity and
CC obesity related diseases. The antibodies can be used to deliver drugs or
CC pro-drugs directly to the fat mass of an obese patient or the antibody
CC can be used as a therapeutic itself. Antibodies binding specifically to
CC adipocytes can be used to activate the immune system to destroy the cells
CC by complement mediated lysis. The antibodies may be labeled with a
CC detectable label such as radiolabel, fluorescent or chemical group and
CC used in methods of diagnosis in human subjects e.g. to determine the
CC presence of adipocyte antigen on the surface of an adipocyte to detect or
CC determine the presence or level of adipocytes in a cell or tissue sample.
CC The antibodies can be used as an alternative means of treatment for obese
CC patients other than undergoing surgery to remove excess fat. Antibodies
CC for different types of fat deposits can also be produced e.g. intra-
CC abdominal fat associated with heart disease
XX Sequence 111 AA;
SQ
Query Match 100.0%; Score 58; DB 4; Length 111;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AAWDLSSEFL 11
DB 91 AAWDLSSEFL 101
RESULT 12
AAU02585
ID AAU02585 standard; protein; 111 AA.
XX AAU02585;
AC
XX 29-AUG-2001 (first entry)
DT
XX Anti-adipocyte monoclonal antibody light chain, FAT 72.
DE
XX Antibody; adipocyte; heavy chain; light chain; obesity; fat;
KW heart disease; complementarity determining region; CDR.
XX Homo sapiens.
OS
XX WO200127279-A1.
PN
XX 19-APR-2001.
PD
XX 11-OCT-2000; 2000WO-GB003900.
PF
XX 12-OCT-1999; 99US-0158812P.
PR
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PA Edwards BM, Main SH, Vaughan TJ;
PI WPI; 2001-282031/29.
XX N-PSDB; AAS03485.
DR
XX Panel of specific binding members of antibody molecules which bind to
PT whole adipocytes is used in the treatment of obesity and obesity related
PT diseases.

PS Claim 1; Page 146; 182pp; English.

AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid sequences of anti-adipocyte monoclonal antibody heavy chain, light chain, CC and heavy chain complementarity determining regions (CDR) of the CC invention. The antibodies can be used in the treatment of obesity and CC obesity related diseases. The antibodies can be used to deliver drugs or CC pro-drugs directly to the fat mass of an obese patient or the antibody CC can be used as a therapeutic itself. Antibodies binding specifically to CC adipocytes can be used to activate the immune system to destroy the cells CC by complement mediated lysis. The antibodies may be labeled with a CC detectable label such as radiolabel, fluorescent or chemical group and CC used in methods of diagnosis in human subjects e.g. to determine the CC presence of adipocyte antigen on the surface of an adipocyte to detect or CC the antibodies the presence or level of adipocytes in a cell or tissue sample. CC The antibodies can be used as an alternative means of treatment for obese CC patients other than undergoing surgery to remove excess fat. Antibodies CC for different types of fat deposits can also be produced e.g. intra-abdominal fat associated with heart disease

CC can be used as a therapeutic itself. Antibodies binding specifically to
CC adipocytes can be used to activate the immune system to destroy the cells
CC by complement mediated lysis. The antibodies may be labeled with a
CC detectable label such as radiolabel, fluorescent or chemical group and
CC used in methods of diagnosis in human subjects e.g. to determine the
CC presence of adipocyte antigen on the surface of an adipocyte to detect or
CC determine the presence or level of adipocytes in a cell or tissue sample.
CC The antibodies can be used as an alternative means of treatment for obese
CC patients other than undergoing surgery to remove excess fat. Antibodies
CC for different types of fat deposits can also be produced e.g. intra-
CC abdominal fat associated with heart disease

xx Sequence 111 AA;
SQ

Query Match: 100.0%; Score 58; DB 4; Length 111;
Best Local Similarity 100.0%; Pred. NO. 0.025;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 AAMDSDISEFL 11
DB 91 AAMDSDISEFL 101

50 Sequence 111 AA;

Query Match	100.0%;	Score 58;	DB 4;	Length 111;
Best Local Similarity	100.0%;	Pred. No. 0.025;		
Matches 11; Conservative	0;	Mismatches	0;	Gaps 0

```
QY      1 AAWDSLSEFL 11
        |||||
Db      91 AAWDSLSEFL 101
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```
Query Match      100.0%; Score 58; DB 4; Length 111;
Best local Similarity 100.0%; Pred No. 0.025;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 AAWDSLSEFL 11
        |||||
Db      90 AAWDSLSEFL 100
```

RESULT 13
AAU02606
ID AAU02606 standard; protein: 111 AA.

AC	AAU02606;
XX	
DT	29-AUG-2001 (first entry)

DE Anti-adipocyte monoclonal antibody light chain, FAT 95.

KM Antibody; adipocyte; heavy chain; light chain; obesity; fat;
 KW heart disease; complementarity determining region; CDR.

OS Homo sapiens.

PN WO2001.27279-A1.

PD 19-APR-2001.

11-OCT-2000; 2000WO-GB003900.

PR 12-OCT-1999; 99US-0158812P.

PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

PI Edwards BM, Main SH, Vaughan TJ;

DR WPI; 2001-282031/29.

DR N-PSDB; AAS03506.

Panel of specific binding members of antibody molecules which bind to PT whole adipocytes is used in the treatment of obesity and obesity related PT diseases.

PS Claim 1; Page 159; 182pp; English.

CC AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
CC sequences of anti-idiotypic monoclonal antibody heavy chain, light chain
CC and heavy chain complementarily determining regions (CDR) of the
CC invention. The antibodies can be used in the treatment of obesity and
CC obesity related diseases. The antibodies can be used to deliver drugs or
CC pro-drugs directly to the fat mass of an obese patient or the antibody

RESULT 14
ADG34301
ID ADG34301 standard; protein: 242 AA.

ADG34301;

DT 26-FEB-2004 (first entry)

DE Neurokinin B antibody SEQ ID NO:24.

antibody; neurokinin B; hypotensive; gynaecological; gene therapy;
hypertension; pre-eclampsia; NKB.

Synthetic.

AA WO2003102136-A2.
PN

PD 11-DEC-2003

29-MAY-2003: 2003WO-US016802.

AA 30-MAY-2002; 2002US-0383802P.
PR

PA (HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Ruben SM:

AA
DR WPI: 2004-053456/05.

DN N-ESDB; AUG34202.
XX

PT composition for treating or preventing hypertension or preeclampsia.

Claim 2: SEO ID NO 24: 127bp; English.

The invention relates to a novel antibody specifically binding neurokinin B. An antibody of the invention has hypertensive, and gynecological activity, and may have a use in gene therapy. The antibody is useful for preparing a composition for treating or preventing hypertension or pre-eclampsia. The present sequence is used in the exemplification of the invention.

Sequence 242 AA:

Query Match	100.0%;	Score 58;	DB 8;	Length 242;
Best Local Similarity	100.0%;	Pred. No. 0.056;		
Matches 11;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

QY 1 AAWDDSLSEFL 11
|||||

Db 221 AAWDLSSEFL 231

RESULT 15
ADG34317 standard; protein; 242 AA.
AC ADG34317;
DT 26-FEB-2004 (first entry)
DE Neurokinin B antibody SEQ ID NO:40.
XX antibody; neurokinin B; hypotensive; gynaecological; gene therapy;
KM hyperextension; pre-eclampsia; NKB.
XX Synthetic.
OS WO2003102136-A2.
XX 11-DEC-2003.
XX 29-MAY-2003; 2003WO-US016802.
XX 30-MAY-2002; 2002US-038802P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Ruben SM;
XX WPI; 2004-053456/05.
XX N-PSDB; ADG34298.
XX New antibody that specifically binds neurokinin B, useful for preparing a
PT composition for treating or preventing hypertension or pre-eclampsia.
XX Claim 2; SEQ ID NO 40; 127bp; English.
XX The invention relates to a novel antibody specifically binding neurokinin
CC B. An antibody of the invention has hypotensive, and gynaecological
CC activity, and may have a use in gene therapy. The antibody is useful for
CC preparing a composition for treating or preventing hypertension or pre-
CC eclampsia. The present sequence is used in the exemplification of the
CC invention.
XX Sequence 242 AA;
SQ

Query Match 100.0%; Score 58; DB 8; Length 242;
Best Local Similarity 100.0%; Pred. NO. 0.056;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAWDLSSEFL 11
Db 221 AAWDLSSEFL 231

RESULT 16
ABP45916 standard; protein; 243 AA.
AC ABP45916;
DT 19-AUG-2002 (first entry)
DE Human Blys binding scFv SEQ ID 1927.
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KM tumour necrosis factor; B cell proliferation; B cell differentiation;
KM immunosuppressive; immunostimulant; immunomodulatory; antineumatic;
KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS.
XX Common variable immunodeficiency; acquired immunodeficiency syndrome.

OS Homo sapiens.
XX WO200202641-A1.
XX 10-JAN-2002.
XX 15-JUN-2001; 2001WO-US019110.
XX 16-JUN-2000; 2000US-0212210P.
XX 17-OCT-2000; 2000US-0240816P.
XX 16-MAR-2001; 2001US-0276248P.
XX 21-MAR-2001; 2001US-0277379P.
XX 25-MAY-2001; 2001US-0293499P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI; 2002-114799/15.
XX Antibodies against B lymphocyte stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.
XX Claim 1; Page 2700-2701; 3148pp; English.
XX This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antineumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention.
XX Sequence 243 AA;
SQ

Query Match 100.0%; Score 58; DB 5; Length 243;
Best Local Similarity 100.0%; Pred. NO. 0.056;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAWDLSSEFL 11
Db 222 AAWDLSSEFL 232

RESULT 17
ADG36743 standard; protein; 243 AA.
AC ADG36743;
DT 11-MAR-2004 (first entry)
DE Single chain antibody that immunospecifically binds Blys SeqID 1927.
XX antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
KM B cell proliferation; differentiation; scFv; myasthenia gravis;
KM multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
KM carcinoma; lymphoma; antineumatic; antiarthritic; neuroprotective;
KM antiinflammatory; antiallergic; cytostatic.
XX Unidentified.

CC preparing a composition for treating or preventing hypertension or pre-eclampsia. The present sequence is used in the exemplification of the invention.

CC Sequence 243 AA;

Query Match 100.0%; Score 58; DB 8; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDLSSEFL 11
|||
DB 222 AAMDLSSEFL 232

RESULT 20
ADG34303
ID ADG34303 standard; protein; 244 AA.

AC ADG34303;

DT 26-FEB-2004 (first entry)

DE Neurokinin B antibody SEQ ID NO:26.

KM antibody; neurokinin B; hypotensive; gynaecological; gene therapy;
KM hypertension; pre-eclampsia; NKB.

OS Synthetic.

PN WO2003102136-A2.

PD 11-DEC-2003.

PF 29-MAY-2003; 2003WO-US016802.

PR 30-MAY-2002; 2002US-0383802P.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Ruben SM;

DR WPI, 2004-053456/05.

DR N-PSDB; ADG34284.

PT New antibody that specifically binds neurokinin B, useful for preparing a composition for treating or preventing hypertension or pre-eclampsia.

PS Claim 2; SEQ ID NO 26; 127pp; English.

CC The invention relates to a novel antibody specifically binding neurokinin B. An antibody of the invention has hypotensive, and gynaecological activity, and may have a use in gene therapy. The antibody is useful for preparing a composition for treating or preventing hypertension or pre-eclampsia. The present sequence is used in the exemplification of the invention.

CC Sequence 244 AA;

Query Match 100.0%; Score 58; DB 8; Length 244;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDLSSEFL 11
|||
DB 223 AAMDLSSEFL 233

RESULT 21
ABP45915
ID ABP45915 standard; protein; 245 AA.

AC ABP45915;

XX 19-AUG-2002 (first entry)
DT Human Blys binding scFv SEQ ID 1926.

KM Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KM tumour necrosis factor; B cell proliferation; B cell differentiation;
KM immunosuppressive; immunostimulant; immunomodulatory; antineutritic;
KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KM common variable immunodeficiency; acquired immunodeficiency syndrome.

OS Homo sapiens.

PN WO200202641-A1.

PD 10-JAN-2002.

PF 15-JUN-2001; 2001WO-US019110.

PR 16-JUN-2000; 2000US-0212210P.

PR 17-OCT-2000; 2000US-0240816P.

PR 16-MAR-2001; 2001US-0276248P.

PR 21-MAR-2001; 2001US-0277379P.

PR 25-MAY-2001; 2001US-0293499P.

PA (HUMA-) HUMAN GENOME SCI INC.

PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

DR WPI; 2002-114799/15.

PT Antibodies against B lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.

PS Claim 1; Page 2699-2700; 314pp; English.

CC This invention describes novel antibodies that immunospecifically bind to B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antineutritic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of Blys. The antibodies bind to Blys and so may be used to detect and quantitate the presence of Blys in biological samples and may be used in this way to diagnose disease associated with aberrant expression of Blys. They may also be administered to treat diseases associated with aberrant Blys expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method of the invention.

CC Sequence 245 AA;

Query Match 100.0%; Score 58; DB 5; Length 245;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDLSSEFL 11
|||
DB 224 AAMDLSSEFL 234

RESULT 22
ADG96742
ID ADG96742 standard; protein; 245 AA.

AC ADG96742;

DT 11-MAR-2004 (first entry)
 XX Single chain antibody that immunospecifically binds Blys Segid 1926.
 XX
 KW antibody, B lymphocyte stimulator; Blys; tumour necrosis factor;
 KW B cell proliferation; differentiation; scfv; myasthenia gravis;
 KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
 KW carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;
 KW antiinflammatory; antiasthmatic; antiallergic; cytostatic.
 XX
 OS Unidentified.
 XX
 PN WO2003055979-A2.
 XX
 PD 10-JUL-2003.
 XX
 PF 14-NOV-2002; 2002WO-US036496.
 XX
 PR 16-NOV-2001; 2001US-0331469P.
 PR 19-DEC-2001; 2001US-0340817P.
 XX
 PA (HUMA-) HUMAN GENOME SCT INC.
 XX
 PI Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;
 XX
 DR WPI; 2003-505530/47.
 XX
 PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator
 PT (Blys), useful for detecting and treating diseases or disorders e.g.
 PT rheumatoid arthritis, asthma and leukemia.
 XX
 PS Example 1; SEQ ID NO 1926; 394pp; English.
 XX
 CC This invention relates to novel antibodies that immunospecifically bind
 CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
 CC chromosome 13q34 and encodes a protein that is a member of the tumour
 CC necrosis factor superfamily and induces both in vivo and in vitro B cell
 CC proliferation and differentiation. Specifically, it refers to single
 CC chain antibody molecules (scFvs) derived, preferably, from the variable
 CC heavy CDR3 region that immunospecifically bind to a polypeptide, or
 CC fragment thereof, of either human, murine, rat or monkey Blys. The
 CC present invention refers to the use of such antibodies in various methods
 CC for the detection, diagnosis and prognosis of diseases related to the
 CC aberrant expression or inappropriate function of Blys or its receptor. As
 CC such, these compositions are useful for identifying immune disorders
 CC including myasthenia gravis and multiple sclerosis, inflammatory
 CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
 CC as AIDS and proliferative disorders including leukaemia, carcinoma and
 CC lymphoma. Accordingly, they can be described as exhibiting various
 CC activities such as antirheumatic, antiarthritic, neuroprotective,
 CC antiinflammatory, antiasthmatic, antiallergic and cytostatic. This
 CC polypeptide sequence is a single chain antibody that binds Blys of the
 CC invention. NOTE: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published/pct_sequences.
 XX
 SQ Sequence 245 AA;
 QY
 Db 1 AAWDSLSEFL 11
 224 AAWDSLSEFL 234
 100.0%; Score 58; DB 7; Length 245;
 Best Local Similarity 100.0%; Pred. No. 0.056;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 23
 ID ADG98057 standard; protein; 245 AA.
 AC ADG98057;
 XX

DT 11-MAR-2004 (first entry)
 XX TNF proliferation inducing protein ligand (APRIL) Segid 3241.
 DE
 KW human; B lymphocyte stimulator; Blys; tumour necrosis factor;
 KW B cell proliferation; differentiation; myasthenia gravis;
 KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
 KW carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;
 KW antiinflammatory; antiasthmatic; antiallergic; cytostatic; APRIL; TNF;
 KW ligand.
 XX
 OS Unidentified.
 XX
 PN WO2003055979-A2.
 XX
 PD 10-JUL-2003.
 XX
 PF 14-NOV-2002; 2002WO-US036496.
 XX
 PR 16-NOV-2001; 2001US-0331469P.
 PR 19-DEC-2001; 2001US-0340817P.
 XX
 PA (HUMA-) HUMAN GENOME SCT INC.
 XX
 PI Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;
 XX
 DR WPI; 2003-505530/47.
 XX
 PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator
 PT (Blys), useful for detecting and treating diseases or disorders e.g.
 PT rheumatoid arthritis, asthma and leukemia.
 XX
 PS Claim 1; SEQ ID NO 3241; 394pp; English.
 XX
 CC This invention relates to novel antibodies that immunospecifically bind
 CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
 CC chromosome 13q34 and encodes a protein that is a member of the tumour
 CC necrosis factor superfamily and induces both in vivo and in vitro B cell
 CC proliferation and differentiation. Specifically, it refers to single
 CC chain antibody molecules (scFvs) derived, preferably, from the variable
 CC heavy CDR3 region that immunospecifically bind to a polypeptide, or
 CC fragment thereof, of either human, murine, rat or monkey Blys. The
 CC present invention refers to the use of such antibodies in various methods
 CC for the detection, diagnosis and prognosis of diseases related to the
 CC aberrant expression or inappropriate function of Blys or its receptor. As
 CC such, these compositions are useful for identifying immune disorders
 CC including myasthenia gravis and multiple sclerosis, inflammatory
 CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
 CC as AIDS and proliferative disorders including leukaemia, carcinoma and
 CC lymphoma. Accordingly, they can be described as exhibiting various
 CC activities such as antirheumatic, antiarthritic, neuroprotective,
 CC antiinflammatory, antiasthmatic, antiallergic and cytostatic. This
 CC polypeptide sequence is an APRIL protein, a TNF proliferation inducing
 CC ligand that can form a fusion protein with a Blys protein of the
 CC invention.
 XX
 SQ Sequence 245 AA;
 QY
 Db 1 AAWDSLSEFL 11
 224 AAWDSLSEFL 234
 100.0%; Score 58; DB 7; Length 245;
 Best Local Similarity 100.0%; Pred. No. 0.056;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 24
 ID ADE83862 standard; protein; 245 AA.
 AC ADE83862;
 XX

DT 29-JAN-2004 (first entry)
XX Chemokine beta-4 binding antibody F081C09 protein SEQ ID NO:21.
DE
XX antibody; chemokine beta-4; CK-B4; single chain Fvs; scFvs;
XX antiproliferative; dermatological; antiinflammatory; immunosuppressive;
XX antineoplastic; antirheumatic; cerebroprotective; cytostatic; anti-HIV;
XX vulnery; dermatitis; autoimmune disease; rheumatoid arthritis;
XX systemic lupus erythematosus; autoimmune encephalitis; cancer;
XX HIV infection; wound; inflammatory disorder; human; psoriasis.
XX
OS Synthetic.
OS Homo sapiens.
XX WO2003092597-A2.
XX
XX 13-NOV-2003.
XX
XX 30-APR-2003; 2003WO-US013414.
XX
XX 01-MAY-2002; 2002US-0376561P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM;
XX WPI; 2004-022614/02.
XX N-PSDB; ADE83845.
XX
XX New antibody that specifically binds to a chemokine beta-4 polypeptide,
XX useful for diagnosing, treating, preventing or ameliorating psoriasis,
XX rheumatoid arthritis, systemic lupus erythematosus, cancer, HIV infection
XX and wounds.
XX
XX Claim 1; SEQ ID NO 21; 181bp; English.
XX
XX The present invention describes an antibody (I) that specifically binds
XX to a chemokine beta-4 (CK-B4) polypeptide. Where (I) comprises a first
XX amino acid sequence at least 95% identical to a second amino acid
XX sequence comprising a VH complementarily determining region (CDR) or VL
XX CDR of any of the single chain Fvs (scFvs) from any of 17 fully defined
XX sequences of 245-253 amino acids (ADE83861 to ADE83877). Also described:
XX (1) a kit comprising (1); (2) an isolated nucleic acid molecule encoding
XX (1); (3) a vector comprising the isolated nucleic acid of (2); (4) a host
XX cell comprising the vector of (3); (5) a cell line engineered to express
XX (1); (6) an antibody that binds the same epitope as (1); (7) an antibody
XX that competitively inhibits the binding (1) to a CK-B4 polypeptide; (8) a
XX method for detecting aberrant expression of CK-B4 polypeptide; (9) a
XX assay of the level of CK-B4 polypeptide expression in a first biological
XX sample of an individual using at least one of (1) and comparing the
XX level of CK-B4 polypeptide assayed in the biological sample with a
XX standard level of CK-B4 polypeptide expression or level of CK-B4
XX polypeptide in a second, normal biological sample, where an increase or
XX decrease in the assayed level of CK-B4 polypeptide in the first
XX biological sample compared to the standard level is indicative of
XX aberrant expression; and (9) a method of treating, preventing or
XX ameliorating psoriasis, dermatitis or an autoimmune disease, comprising
XX administering (1) to the animal. (I) has antipsoriatic, dermatologic,
XX antiinflammatory, immunosuppressive, antineoplastic, antirheumatic,
XX cerebroprotective, cytostatic, anti-HIV and vulnery activities. The
XX methods and compositions of the present invention are useful for
XX diagnosing, treating, preventing or ameliorating psoriasis, dermatitis or
XX an autoimmune disease such as rheumatoid arthritis, systemic lupus
XX erythematosus and autoimmune encephalitis. They can also be used in
XX cancer, HIV infection, wounds and inflammatory disorders. The present
XX sequence is used in the exemplification of the present invention.
XX
XX Sequence 245 AA;

Query Match 100.0%; Score 58; DB 8; Length 245;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDDSLSEFL 11
DB 224 AAWDDSLSEFL 234
RESULT 25
ID ADG34308 standard; protein; 245 AA.
XX ADG34308
XX
XX ADG34308;
XX
XX 26-FEB-2004 (first entry)
XX
XX
XX Neurokinin B antibody SEQ ID NO:31.
XX
XX antibody; neurokinin B; hypotensive; gynaecological; gene therapy;
XX hypertension; pre-eclampsia; NKB.
XX
XX Synthetic.
XX
XX WO2003102136-A2.
XX
XX 11-DEC-2003.
XX
XX 29-MAY-2003; 2003WO-US016802.
XX
XX 30-MAY-2002; 2002US-0383802P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM;
XX WPI; 2004-053456/05.
XX N-PSDB; ADG34289.
XX
XX New antibody that specifically binds neurokinin B, useful for preparing a
XX composition for treating or preventing hypertension or preeclampsia.
XX
XX Claim 2; SEQ ID NO 31; 127bp; English.
XX
XX The invention relates to a novel antibody specifically binding neurokinin
XX B. An antibody of the invention has hypotensive, and gynaecological
XX activity, and may have a use in gene therapy. The antibody is useful for
XX preparing a composition for treating or preventing hypertension or pre-
XX eclampsia. The present sequence is used in the exemplification of the
XX invention.
XX
XX Sequence 245 AA;

QY 1 AAWDDSLSEFL 11
DB 224 AAWDDSLSEFL 234
RESULT 26
ID ABP45902 standard; protein; 246 AA.
XX ABP45902
XX
XX ABP45902;
XX
XX 19-AUG-2002 (first entry)
XX
XX Human Blys binding scFv SEQ ID 1913.
XX
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
XX tumour necrosis factor; B cell proliferation; B cell differentiation;
XX immunosuppressive; immunostimulant; immunomodulatory; antineoplastic;
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;

XX common variable immunodeficiency; acquired immunodeficiency syndrome.
OS Homo sapiens.
XX WO200202641-A1.
PN
PD 10-JAN-2002.
XX
XX 15-JUN-2001; 2001WO-US019110.
PF
XX 16-JUN-2000; 2000US-0212210P.
PR 17-OCT-2000; 2000US-0240816P.
PR 16-MAR-2001; 2001US-0276248P.
PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PX
PI Ruben SM, Barash SC, Choi GH, Vaughan T, Halbert D;
XX WPI; 2002-114799/15.
DR
PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
XX diagnosis and treatment of cancers and immune disorders.
XX
PS Claim 1; Page 2683-2684; 3148p; English.

This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antihermetic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and actively such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43950-ABP47228 represent the antibodies and fragments of the antibodies described in the method of the invention

Sequence 246 AA;

Query Match 100.0%; Score 58; DB 5; Length 246;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 AAMDLSLEFL 11
|||
DB 225 AAMDLSLEFL 235

RESULT 27
ABP45906
ID ABP45906 standard; protein; 246 AA.
XX
XX ABP45906;
AC
XX
XX 19-AUG-2002 (first entry)
DT
DE Human BLyS binding scfv SEQ ID 1917.
XX
XX
XX BLyS: B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; Rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.

```

XX XX Homo sapiens.
XX XX WO200202641-A1.
XX XX 10-JAN-2002.
XX XX 15-JUN-2001; 2001WO-US019110.
XX XX 16-JUN-2000; 2000US-0212210P.
XX XX 17-OCT-2000; 2000US-0240816P.
XX XX 16-MAR-2001; 2001US-0276248P.
XX XX 21-MAR-2001; 2001US-0277379P.
XX XX 25-MAY-2001; 2001US-0293499P.
XX XX (HUMA-) HUMAN GENOME SCI INC.
XX XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX XX WPI; 2002-114799/15.
XX XX
XX XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
XX XX diagnosis and treatment of cancers and immune disorders.
XX XX
XX XX Claim 1; Page 2688-2689; 314bpb; English.
XX XX
XX XX This invention describes novel antibodies that immunospecifically bind to
XX XX B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
XX XX tumour necrosis factor (TNF) super family and induces B cell
XX XX proliferation and differentiation. The antibodies of the invention have
XX XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
XX XX antirheumatic and antiAIDS activity and can be used in vaccines to
XX XX inhibit the expression and activity of BLyS. The antibodies bind to BLyS
XX XX and so may be used to detect and quantitate the presence of BLyS in
XX XX biological samples and may be used in this way to diagnose disease
XX XX associated with aberrant expression of BLyS. They may also be
XX XX administered to treat diseases associated with aberrant BLyS expression
XX XX and actively such as cancer, immune, and autoimmune disorders and
XX XX diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
XX XX immunodeficiency (e.g. common variable immunodeficiency (CVID) and
XX XX acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
XX XX the antibodies and fragments of the antibodies described in the method of
XX XX the invention
XX XX
XX XX Sequence 246 AA;
XX XX
XX XX Query Match 100.0%; Score 58; DB 5; Length 246;
XX XX Best Local Similarity 100.0%; Pred. No. 0.057;
XX XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX XX
XX XX 1 AAMDSDLSEPL 11
XX XX |||||
XX XX 225 AAMDSDLSEFL 235
XX XX
XX XX
XX XX RESULT 28
XX XX ADG96733
XX XX ID ADG96733 standard; protein, 246 AA.
XX XX
XX XX ADG96733;
XX XX
XX XX 11-MAR-2004 (first entry)
XX XX
XX XX Single chain antibody that immunospecifically binds BLyS SeqID 1917.
XX XX
XX XX antibody; B lymphocyte stimulator; BLyS; tumour necrosis factor;
XX XX B cell proliferation; differentiation; scFv; myasthenia gravis;
XX XX multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
XX XX carcinoma; lymphoma; antirheumatic; antiautarchic; neuroprotective;
XX XX antiinflammatory; antiaesthetic; antiallergic; cytostatic.
XX XX
XX XX Unidentified.

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XX PN WO2003055979-A2.
XX PN
XX PD 10-JUL-2003.
XX PD
XX PF 14-NOV-2002; 2002WO-US036496.
XX PF
XX PR 16-NOV-2001; 2001US-0331469P.
XX PR 19-DEC-2001; 2001US-0340817P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PA
XX PI Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;
XX PI WPI; 2003-505530/47.
XX DR
XX PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator
XX PT (Blys), useful for detecting and treating diseases or disorders e.g.
XX PT rheumatoid arthritis, asthma and leukemia.
XX PS Example 1; SEQ ID NO 1917; 394bp; English.
XX PS
XX CC This invention relates to novel antibodies that immunospecifically bind
XX CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
XX CC chromosome 13q34 and encodes a protein that is a member of the tumour
XX CC necrosis factor superfamily and induces both in vivo and in vitro B cell
XX CC proliferation and differentiation. Specifically, it refers to single
XX CC chain antibody molecules (scFvs) derived, preferably, from the variable
XX CC heavy CDR3 region that immunospecifically bind to a polypeptide, or
XX CC fragment thereof, of either human, murine, rat or monkey Blys. The
XX CC present invention refers to the use of such antibodies in various methods
XX CC for the detection, diagnosis and prognosis of diseases related to the
XX CC aberrant expression or inappropriate function of Blys or its receptor. As
XX CC such, these compositions are useful for identifying immune disorders
XX CC including myasthenia gravis and multiple sclerosis, inflammatory
XX CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
XX CC as AIDS and proliferative disorders including leukaemia, carcinoma and
XX CC lymphoma. Accordingly, they can be described as exhibiting various
XX CC activities such as antirheumatic, antiarthritic, neuroprotective,
XX CC antiinflammatory, antiallergic, antitoxic and cytostatic. This
XX CC polypeptide sequence is a single chain antibody that binds Blys of the
XX CC invention. NOTE: The sequence data for this patent did not form part of
XX CC the printed specification, but was obtained in electronic format
XX CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX SQ
XX Sequence 246 AA:
SQ
Query Match 100.0%; Score 58; DB 7; Length 246;
Best Local Similarity 100.0%; Pred. NO. 0.057;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAMWDSISEFL 11
Db 225 AAMWDSISEFL 235
RESULT 29
ADG96729
ID ADG96729 standard; protein; 246 AA.
XX AC
XX AC ADG96729;
XX DT
XX DT 11-MAR-2004 (first entry)
XX DE
XX DE Single chain antibody that immunospecifically binds Blys SegID 1913.
XX KM antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
XX KM B cell proliferation; differentiation; scFv; myasthenia gravis;
XX KM multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
XX KM carcinoma; lymphoma; antirheumatic; antitoxic; neuroprotective;
XX KM antiinflammatory; antiallergic; antitoxic; cytostatic.
XX KM
XX SQ Unidentified.

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XX PN WO2003055979-A2.
XX PN
XX PD 10-JUL-2003.
XX PD
XX PF 14-NOV-2002; 2002WO-US036496.
XX PF
XX PR 16-NOV-2001; 2001US-0331469P.
XX PR 19-DEC-2001; 2001US-0340817P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PA
XX PI Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;
XX PI WPI; 2003-505530/47.
XX DR
XX PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator
XX PT (Blys), useful for detecting and treating diseases or disorders e.g.
XX PT rheumatoid arthritis, asthma and leukemia.
XX PS Example 1; SEQ ID NO 1913; 394bp; English.
XX PS
XX CC This invention relates to novel antibodies that immunospecifically bind
XX CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
XX CC chromosome 13q34 and encodes a protein that is a member of the tumour
XX CC necrosis factor superfamily and induces both in vivo and in vitro B cell
XX CC proliferation and differentiation. Specifically, it refers to single
XX CC chain antibody molecules (scFvs) derived, preferably, from the variable
XX CC heavy CDR3 region that immunospecifically bind to a polypeptide, or
XX CC fragment thereof, of either human, murine, rat or monkey Blys. The
XX CC present invention refers to the use of such antibodies in various methods
XX CC for the detection, diagnosis and prognosis of diseases related to the
XX CC aberrant expression or inappropriate function of Blys or its receptor. As
XX CC such, these compositions are useful for identifying immune disorders
XX CC including myasthenia gravis and multiple sclerosis, inflammatory
XX CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
XX CC as AIDS and proliferative disorders including leukaemia, carcinoma and
XX CC lymphoma. Accordingly, they can be described as exhibiting various
XX CC activities such as antirheumatic, antiarthritic, neuroprotective,
XX CC antiinflammatory, antiallergic, antitoxic and cytostatic. This
XX CC polypeptide sequence is a single chain antibody that binds Blys of the
XX CC invention. NOTE: The sequence data for this patent did not form part of
XX CC the printed specification, but was obtained in electronic format
XX CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX SQ
XX Sequence 246 AA:
SQ
Query Match 100.0%; Score 58; DB 7; Length 246;
Best Local Similarity 100.0%; Pred. NO. 0.057;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAMWDSISEFL 11
Db 225 AAMWDSISEFL 235
RESULT 30
ADE83872
ID ADE83872 standard; protein; 246 AA.
XX AC
XX AC ADE83872;
XX DT
XX DT 29-JAN-2004 (first entry)
XX DE
XX DE Chemokine beta-4 binding antibody F002C08 protein SEQ ID NO:31.
XX KM antibody; chemokine beta-4; CK-β4; single chain Fvs; scFvs;
XX KM antiproliferative; dermatological; antiinflammatory; immunosuppressive;
XX KM antirheumatic; antitoxic; neuroprotective; cytostatic; anti-HIV;
XX KM vulnery; dermatitis; autoimmune disease; rheumatoid arthritis;
XX KM systemic lupus erythematosus; autoimmune encephalitis; cancer;
XX KM HIV infection; wound; inflammatory disorder; human; psoriasis.
XX KM

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OS Synthetic.
OS Homo sapiens.
XX
PN WO2003092597-A2.
XX
PD 13-NOV-2003.
XX
PF 30-APR-2003; 2003WO-US013414.
XX
PR 01-MAY-2002; 2002US-0376561P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
PI WPI: 2004-022614/02.
XX
DR N-P8DB; ADE83855.
XX
PT New antibody that specifically binds to a chemokine beta-4 polypeptide,
PT useful for diagnosing, treating, preventing or ameliorating psoriasis,
PT rheumatoid arthritis, systemic lupus erythematosus, cancer, HIV infection
PT and wounds.
XX
PS Claim 1; SEQ ID NO 31; 181bp; English.
XX
CC The present invention describes an antibody (I) that specifically binds
CC to a chemokine beta-4 (CK-B4) polypeptide. Where (I) comprises a first
CC amino acid sequence at least 95% identical to a second amino acid
CC sequence comprising a VH complementarity determining region (CDR) or VL
CC CDR of any of the single chain Fvs (scFvs) from any of 17 fully defined
CC sequences of 245-253 amino acids (ADE83861 to ADE83877). Also described:
CC (1) a kit comprising (I); (2) an isolated nucleic acid molecule encoding
CC (I); (3) a vector comprising the isolated nucleic acid of (2); (4) a host
CC cell comprising the vector of (3); (5) a cell line engineered to express
CC (I); (6) an antibody that binds the same epitope as (I); (7) an antibody
CC that competitively inhibits the binding (I) to a CK-B4 polypeptide; (8) a
CC method for detecting aberrant expression of CK-B4 polypeptide; (9) a
CC assay of the level of CK-B4 polypeptide expression in a first biological
CC sample of an individual using at least one of (I), and comparing the
CC level of CK-B4 polypeptide assayed in the biological sample with a
CC standard level of CK-B4 polypeptide expression or level of CK-B4
CC polypeptide in a second, normal biological sample, where an increase or
CC decrease in the assayed level of CK-B4 polypeptide in the first
CC biological sample compared to the standard level is indicative of
CC aberrant expression; and (9) a method of treating, preventing or
CC ameliorating psoriasis, dermatitis or an autoimmune disease, comprising
CC administering (I) to the animal. (I) has antipsoriatic, dermatological,
CC antiinflammatory, immunosuppressive, antirheumatic, antiarthritic,
CC cerebroprotective, cytostatic, anti-HIV and vulnery activites. The
CC methods and compositions of the present invention are useful for
CC diagnosing, treating, preventing or ameliorating psoriasis, dermatitis or
CC an autoimmune disease such as rheumatoid arthritis, systemic lupus
CC erythematosus and autoimmune encephalitis. They can also be used in
CC cancer, HIV infection, wounds and inflammatory disorders. The present
CC sequence is used in the exemplification of the present invention.
XX
SQ Sequence 246 AA;
Query Match 100.0%; Score 58; DB 8; Length 246;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAMDLSLEFL 11
DB 225 AAMDLSLEFL 235

RESULT 31
ID ABP45671 standard; protein; 247 AA.
XX
AC ABP45671;
XX

DT 19-AUG-2002 (first entry)
XX
XX Human Blys binding scFv SEQ ID 1682.
XX
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
XX tumor necrosis factor; B cell proliferation; B cell differentiation;
XX immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
XX common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
OS Homo sapiens.
XX
XX WO200202641-A1.
XX
XX 10-JAN-2002.
XX
XX 15-JUN-2001; 2001WO-US019110.
XX
XX 16-JUN-2000; 2000US-0212210P.
XX
XX 17-OCT-2000; 2000US-0240816P.
XX
XX 16-MAR-2001; 2001US-0276248P.
XX
XX 21-MAR-2001; 2001US-0277379P.
XX
XX 25-MAY-2001; 2001US-0293499P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
XX WPI: 2002-114799/15.
XX
XX Antibodies against B lymphocyte stimulating polypeptides, useful for the
XX diagnosis and treatment of cancers and immune disorders.
XX
XX Claim 1; Page 2409-2410; 3148bp; English.
XX
XX This invention describes novel antibodies that immunospecifically bind to
XX B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
XX tumor necrosis factor (TNF) super family and induces B cell
XX proliferation and differentiation. The antibodies of the invention have
XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
XX antirheumatic and antiAIDS activity and can be used in vaccines to
XX inhibit the expression and activity of Blys. The antibodies bind to Blys
XX and so may be used to detect and quantitate the presence of Blys in
XX biological samples and may be used in this way to diagnose disease
XX associated with aberrant expression of Blys. They may also be
XX administered to treat diseases associated with aberrant Blys expression
XX and actively such as cancer, immune, and autoimmune disorders and
XX diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
XX immunodeficiency (e.g. common variable immunodeficiency (CVID) and
XX acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
XX the antibodies and fragments of the antibodies described in the method of
XX the invention
XX
SQ Sequence 247 AA;
Query Match 100.0%; Score 58; DB 5; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAMDLSLEFL 11
DB 226 AAMDLSLEFL 236

RESULT 32
ID ABP45432 standard; protein; 247 AA.
XX
AC ABP45432;
XX
DT 19-AUG-2002 (first entry)

XX	Human Blys binding scFv SEQ ID 1443.
DE	
XX	
XX	
KW	Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW	tumour necrosis factor; B cell proliferation; B cell differentiation;
KW	immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW	antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW	systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW	common variable immunodeficiency; acquired immunodeficiency syndrome.
XX	
OS	Homo sapiens.
XX	
PN	WO200202641-A1.
XX	
PD	10-JAN-2002.
XX	
PF	15-JUN-2001; 2001WO-US019110.
XX	
PR	16-JUN-2000; 2000US-0212210P.
PR	17-OCT-2000; 2000US-0240816P.
PR	16-MAR-2001; 2001US-0276248P.
PR	21-MAR-2001; 2001US-0277379P.
PR	25-MAY-2001; 2001US-0293499P.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
PA	(CAME-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX	
PI	Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX	
DR	WPI; 2002-114799/15.
XX	
PT	Antibodies against B lymphocyte Stimulating polypeptides, useful for the
PT	diagnosis and treatment of cancers and immune disorders.
XX	
PS	Claim 1; Page 2124-2125; 3148pp; English.
XX	
CC	This invention describes novel antibodies that immunospecifically bind to
CC	B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC	tumour necrosis factor (TNF) super family and induces B cell
CC	proliferation and differentiation. The antibodies of the invention have
CC	cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC	antirheumatic and antiAIDS activity and can be used in vaccines to
CC	inhibit the expression and activity of Blys. The antibodies bind to Blys
CC	and so may be used to detect and quantitate the presence of Blys in
CC	biological samples and may be used in this way to diagnose disease
CC	associated with aberrant expression of Blys. They may also be
CC	administered to treat diseases associated with aberrant Blys expression
CC	and actively such as cancer, immune, and autoimmune disorders and
CC	diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC	immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC	acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC	the antibodies and fragments of the antibodies described in the method of
CC	the invention
XX	
SO	Sequence 247 AA;
QY	1 AAMDLSLEPL 11
DB	226 AAMDLSLEPL 236
Query Match	100.0%; Score 58; DB 5; Length 247;
Best Local Similarity	100.0%; Pred. No. 0.057;
Matches 11; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
RESULT 33	
ABP45923	
ID	ABP45923 standard; protein; 247 AA.
XX	
AC	ABP45923;
XX	
PT	19-AUG-2002 (first entry)
XX	

DE	Human Blys binding scFv SEQ ID 1934.
XX	
KM	Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KM	tumour necrosis factor; B cell proliferation; B cell differentiation;
KM	immunopressive; immunostimulant; immunomodulatory; antirheumatic;
XX	antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KM	systemic lupus erythematosus; rheumatoid arthritis; COVID; AIDS;
KM	common variable immunodeficiency; acquired immunodeficiency syndrome.
XX	
OS	Homo sapiens.
XX	
PN	WO200202641-A1.
XX	
PD	10-JAN-2002.
XX	
PF	15-JUN-2001; 2001WO-US019110.
XX	
PR	16-JUN-2000; 2000US-0212210P.
PR	17-OCT-2000; 2000US-0240816P.
XX	16-MAR-2001; 2001US-0276248P.
PR	21-MAR-2001; 2001US-0277379P.
PR	25-MAY-2001; 2001US-0293499P.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
PA	(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PI	Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX	
DR	WPI; 2002-114799/15.
XX	
PT	Antibodies against B lymphocyte Stimulating polypeptides, useful for the
XX	diagnosis and treatment of cancers and immune disorders.
PS	Claim 1; Page 2708-2709; 3148pp; English.
XX	
XX	This invention describes novel antibodies that immunospecifically bind to
CC	B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
CC	tumour necrosis factor (TNF) super family and induces B cell
CC	proliferation and differentiation. The antibodies of the invention have
CC	cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC	antirheumatic and antiAIDS activity and can be used in vaccines to
CC	inhibit the expression and activity of Blys. The antibodies bind to Blys
CC	and so may be used to detect and quantitate the presence of Blys in
CC	biological samples and may be used in this way to diagnose disease
CC	associated with aberrant expression of Blys. They may also be
CC	administered to treat diseases associated with aberrant Blys expression
CC	and activity such as cancer, immune, and autoimmune disorders and
CC	diseases e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC	immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC	acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC	the antibodies and fragments of the antibodies described in the method of
XX	the invention
XX	
XX	Sequence 247 AA;
QY	
Query Match	100.0%; Score 58; DB 5; Length 247;
Best Local Similarity	100.0%; Pred. No. 0.057;
Matches 11; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
1 AAWDSTSEFL 11	
Db 226 AAWDSTSEFL 236	
RESULT 34	
ABP45917	
ID ABP45917 standard; protein; 247 AA.	
XX	
XX	ABP45917;
XX	
DT 19-AUG-2002 (first entry)	
XX	
DE Human Blys binding scFv SEQ ID 1928.	

KM	tumour necrosis factor; B cell proliferation; B cell differentiation;
KM	immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KM	antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KM	systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW	common variable immunodeficiency; acquired immunodeficiency syndrome.
XX	
OS	Homo sapiens.
XX	
PN	WO200202641-A1.
PD	10-JAN-2002.
XX	
PF	15-JUN-2001; 2001WO-US019110.
XX	
PR	16-JUN-2000; 2000US-0212210P.
PR	17-OCT-2000; 2000US-0240816P.
PR	16-MAR-2001; 2001US-0276248P.
PR	21-MAR-2001; 2001US-0277379P.
PR	25-MAY-2001; 2001US-0293499P.
XX	
PA	(HUMA-) HUMAN GENOME SCT INC.
XX	(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PI	Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX	
DR	WPI; 2002-114799/15.
PT	Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
XX	diagnosis and treatment of cancers and immune disorders.
PS	Claim 1; Page 2667-2668; 3148pp; English.
XX	
CC	This invention describes novel antibodies that immunospecifically bind to
CC	B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the
CC	tumour necrosis factor (TNF) super family and induces B cell
CC	proliferation and differentiation. The antibodies of the invention have
CC	cycostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC	antirheumatic and antiAIDS activity and can be used in vaccines to
CC	inhibit the expression and activity of BLyS. The antibodies bind to BLyS
CC	and so may be used to detect and quantitate the presence of BLyS in
CC	biological samples and may be used in this way to diagnose disease
CC	associated with aberrant expression of BLyS. They may also be
CC	administered to treat diseases associated with aberrant BLyS expression
CC	and acitivity such as cancer, immune, and autoimmune disorders and
CC	diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, and
CC	immunodeficiency (e.g. common variable immunodeficiency (CVID)) and
CC	acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC	the antibodies and fragments of the antibodies described in the method of
CC	the invention
XX	
SQ	Sequence 247 AA;
XX	
Query Match	100.0%; Score 58; DB 5; Length 247;
Best Local Similarity	100.0%; Pred. No. 0.057;
Matches 11; Conservative	0; Mismatches 0; Indels 0; Gaps 0
OY	1 AAMDLSLEFL 11
DB	226 AAMDSLSEFL 236
RESULT 37	
ADG30413	
ID	ADG30413 standard; protein; 247 AA.
AC	ADG30413;
DT	26-FEB-2004 (first entry)
DE	Human GMBC609 scFv protein.
GMD;	VH; CDR complementarity determining region; VL; scFv;
single chain antibody; antidiabetic;	type II diabetes; human; GMBC609.

XX	OS	Homo sapiens.
XX	PN	WO2003085093-A2.
XX	PD	16-OCT-2003.
XX	PF	28-MAR-2003; 2003WO-US009625.
XX	PR	01-APR-2002; 2002US-0368813P.
XX	PA	(HUMA-) HUMAN GENOME SCI INC.
XX	PI	Baker KP, Albert VR, Chowdhury P;
XX	DR	WPI; 2003-804305/75.
XX	DR	N-PSDB; ADG30510.
XX	PT	New antibody that specifically binds to GMAD polypeptide, useful for
XX	PT	diagnosing, monitoring, treating, preventing or ameliorating type II
XX	PT	diabetes.
XX	PS	Claim 2; SEQ ID NO 46; 410pp; English.
XX	CC	The invention relates to a novel antibody that specifically binds to a
XX	CC	GMAD polypeptide comprising a first amino acid sequence that is at least
XX	CC	95% identical to a second amino acid sequence of a VH CDR (single chain
XX	CC	(complementarity determining region) or VL CDR of an scFv (single chain
XX	CC	antibody molecule). The antibody of the invention demonstrates
XX	CC	antidiabetic activity and may be useful for diagnosing, monitoring,
XX	CC	treating, preventing or ameliorating type II diabetes. The current
XX	CC	sequence is that of the human scFv protein of the invention.
XX	SQ	Sequence 247 AA;
QY	Query Match	100.0%; Score 58; DB 7; Length 247;
DB	Best Local Similarity	100.0%; Pred. NO. 0.057;
DB	Matches	11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB		1 AAWDDSLSEFL 11
DB		
DB		226 AAWDDSLSEFL 236
RESULT 38		
ADG30455		
ID	ADG30455	standard; protein; 247 AA.
XX	AC	ADG30455;
XX	DT	26-FEB-2004 (first entry)
XX	DE	Human GMBC666 scFv protein.
XX	GMAD; VH; CDR; complementarity determining region; VL; scFv;	
XX	single chain antibody; antidiabetic; type II diabetes; human; GMBC666.	
XX	Homo sapiens.	
XX	WO2003085093-A2.	
XX	16-OCT-2003.	
XX	28-MAR-2003; 2003WO-US009625.	
XX	01-APR-2002; 2002US-0368813P.	
XX	(HUMA-) HUMAN GENOME SCI INC.	
XX	Baker KP, Albert VR, Chowdhury P;	
XX	WPI; 2003-804305/75.	
XX	N-PSDB; ADG30552.	

XX New antibody that specifically binds to GMD polypeptide, useful for
PT diagnosing, monitoring, treating, preventing or ameliorating type II
PT diabetes.
XX
XX Claim 2; SEQ ID NO 88; 410pp; English.
XX
XX The invention relates to a novel antibody that specifically binds to a
CC GMD polypeptide comprising a first amino acid sequence that is at least
CC 95% identical to a second amino acid sequence of a VH CDR of an scFv (single chain
CC (complementarity determining region) or VL CDR of an scFv (single chain
CC antibody molecule). The antibody of the invention demonstrates
CC antidiabetic activity and may be useful for diagnosing, monitoring,
CC treating, preventing or ameliorating type II diabetes. The current
CC sequence is that of the human scFv protein of the invention.
XX
SQ Sequence 247 AA;
Query Match 100.0%; Score 58; DB 7; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAMDLSSEFL 11
Db 226 AAMDLSSEFL 236
RESULT 39
ADG96715
ID ADG96715 standard; protein; 247 AA.
XX
XX ADG96715;
XX
DT 11-MAR-2004 (first entry)
XX
XX Single chain antibody that immunospecifically binds Blys segid 1899.
XX
XX antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
KM B cell proliferation; differentiation; scFv; myasthenia gravis;
KM multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukemia;
KM carcinoma; lymphoma; antineumatic; antiallergic; neuroprotective;
KM antineumatic; antiallergic; antiallergic; cystostatic.
XX
OS Unidentified.
XX
XX WO2003055979-A2.
XX
PD 10-JUL-2003.
XX
PE 14-NOV-2002; 2002MO-US036496.
XX
PR 16-NOV-2001; 2001US-0331469P.
PR 19-DEC-2001; 2001US-0340817P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;
XX
XX WPI; 2003-505530/47.
XX
PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator
PT (Blys), useful for detecting and treating diseases or disorders e.g.
PT rheumatoid arthritis, asthma and leukemia.
XX
XX Example 1; SEQ ID NO 1899; 394pp; English.
XX
XX This invention relates to novel antibodies that immunospecifically bind
CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
CC chromosome 13q34 and encodes a protein that is a member of the tumour
CC necrosis factor superfamily and induces both in vivo and in vitro B cell
CC proliferation and differentiation. Specifically, it refers to single
CC chain antibody molecules (scFvs) derived, preferably, from the variable
CC heavy CDR3 region that immunospecifically bind to a polypeptide, or

CC fragment thereof, of either human, murine, rat or monkey Blys. The
CC present invention refers to the use of such antibodies in various methods
CC for the detection, diagnosis and prognosis of diseases related to the
CC aberrant expression or inappropriate function of Blys or its receptor. As
CC such, these compositions are useful for identifying immune disorders
CC including myasthenia gravis and multiple sclerosis, inflammatory
CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
CC as AIDS and proliferative disorders including leukaemia, carcinoma and
CC lymphoma. Accordingly, they can be described as exhibiting various
CC activities such as antineumatic, antiallergic and neuroprotective,
CC antineumatic, antiallergic, antiallergic and cystostatic. This
CC polypeptide sequence is a single chain antibody that binds Blys of the
CC invention. NOTE: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 247 AA;
Query Match 100.0%; Score 58; DB 7; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAMDLSSEFL 11
Db 226 AAMDLSSEFL 236
RESULT 40
ADG96498
ID ADG96498 standard; protein; 247 AA.
XX
XX ADG96498;
XX
DT 11-MAR-2004 (first entry)
XX
XX Single chain antibody that immunospecifically binds Blys segid 1682.
XX
XX antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
KM B cell proliferation; differentiation; scFv; myasthenia gravis;
KM multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukemia;
KM carcinoma; lymphoma; antineumatic; antiallergic; neuroprotective;
KM antineumatic; antiallergic; antiallergic; cystostatic.
XX
OS Unidentified.
XX
XX WO2003055979-A2.
XX
PD 10-JUL-2003.
XX
PE 14-NOV-2002; 2002MO-US036496.
XX
PR 16-NOV-2001; 2001US-0331469P.
PR 19-DEC-2001; 2001US-0340817P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;
XX
XX WPI; 2003-505530/47.
XX
PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator
PT (Blys), useful for detecting and treating diseases or disorders e.g.
PT rheumatoid arthritis, asthma and leukemia.
XX
XX Example 1; SEQ ID NO 1682; 394pp; English.
XX
XX This invention relates to novel antibodies that immunospecifically bind
CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
CC chromosome 13q34 and encodes a protein that is a member of the tumour
CC necrosis factor superfamily and induces both in vivo and in vitro B cell
CC proliferation and differentiation. Specifically, it refers to single
CC chain antibody molecules (scFvs) derived, preferably, from the variable
CC heavy CDR3 region that immunospecifically bind to a polypeptide, or

CC fragment thereof, of either human, murine, rat or monkey Blys. The
 CC present invention refers to the use of such antibodies in various methods
 CC for the detection, diagnosis and prognosis of diseases related to the
 CC aberrant expression or inappropriate function of Blys or its receptor. As
 CC such, these compositions are useful for identifying immune disorders
 CC including myasthenia gravis and multiple sclerosis, inflammatory
 CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
 CC as AIDS and proliferative disorders including leukaemia, carcinoma and
 CC lymphoma. Accordingly, they can be described as exhibiting various
 CC activities such as antirheumatic, antiarthritic, neuroprotective,
 CC antiinflammatory, antiallergic, antiallergic and cytostatic. This
 CC polypeptide sequence is a single chain antibody that binds Blys of the
 CC invention. NOTE: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 247 AA;

Query Match 100.0%; Score 58; DB 7; Length 247;
 Best Local Similarity 100.0%; Pred. No. 0.057;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDDSLSEFL 11
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 Db 226 AAWDDSLSEFL 236

Search completed: March 31, 2005, 12:02:32
 Job time : 86.25 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 31, 2005, 11:51:44 ; Search time 21.4844 Seconds
(without alignments)
38.220 Million cell updates/sec

Title: US-10-614-959-15
Perfect score: 58
Sequence: 1 AAMDLSSEFL 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: Issued Patents_AA: *
2: /cgn2_6/ptodata/1/1aa/5A_COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/5B_COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/6A_COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/6B_COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/backfill1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	100.0	11	4	US-09-383-667-15
2	58	100.0	104	2	US-08-273-146-63
3	58	100.0	111	2	US-08-652-816A-15
4	46	79.3	11	2	US-08-350-260A-374
5	46	79.3	11	4	US-09-104-337A-374
6	44	75.9	11	2	US-08-350-260A-346
7	44	75.9	11	4	US-09-104-337A-346
8	43	74.1	9	2	US-08-665-202-60
9	43	74.1	9	4	US-09-315-574-60
10	43	74.1	10	2	US-08-350-260A-339
11	43	74.1	10	2	US-08-350-260A-497
12	43	74.1	10	4	US-09-104-337A-339
13	43	74.1	10	4	US-09-104-337A-497
14	43	74.1	11	2	US-08-350-260A-441
15	43	74.1	11	2	US-08-665-202-6
16	43	74.1	11	4	US-09-104-337A-441
17	43	74.1	11	4	US-09-315-574-6
18	43	74.1	98	1	US-08-211-202-111
19	43	74.1	98	4	US-08-665-202-38
20	43	74.1	98	4	US-09-315-574-38
21	43	74.1	109	3	US-09-240-274-59
22	43	74.1	110	3	US-09-240-274-60
23	43	74.1	111	2	US-08-665-202-35
24	43	74.1	111	2	US-08-665-202-43
25	43	74.1	111	4	US-09-315-574-36
26	43	74.1	111	4	US-09-315-574-43
27	43	74.1	112	2	US-08-665-202-39

28	43	74.1	112	4	US-09-315-574-39	Sequence 39, Appl
29	43	74.1	113	1	US-08-211-202-112	Sequence 112, App
30	43	74.1	113	1	US-08-211-202-113	Sequence 113, App
31	43	74.1	113	1	US-08-211-202-114	Sequence 114, App
32	43	74.1	258	2	US-08-665-202-5	Sequence 5, Appli
33	43	74.1	258	4	US-09-315-574-5	Sequence 5, Appli
34	43	74.1	262	3	US-09-069-821-4	Sequence 4, Appli
35	43	74.1	262	4	US-09-956-086-4	Sequence 4, Appli
36	43	74.1	262	4	US-09-956-087-4	Sequence 4, Appli
37	43	74.1	282	3	US-09-420-592A-7	Sequence 7, Appli
38	43	74.1	282	4	US-09-985-442-7	Sequence 7, Appli
39	43	74.1	282	4	US-09-983-580-7	Sequence 7, Appli
40	41	70.7	111	2	US-08-665-202-40	Sequence 40, Appl
41	41	70.7	111	4	US-09-315-574-40	Sequence 40, Appl
42	40	69.0	10	2	US-08-350-260A-361	Sequence 361, App
43	40	69.0	10	2	US-08-350-260A-446	Sequence 446, App
44	40	69.0	10	2	US-08-350-260A-514	Sequence 514, App
45	40	69.0	10	4	US-09-104-337A-361	Sequence 361, App

ALIGNMENTS

```
RESULT 1
US-09-383-667-15
; Sequence 15, Application US/09383667
; Patent No. 6624295
; GENERAL INFORMATION:
; APPLICANT: Adams, Camelia W.
; APPLICANT: Devaux, Brigitte
; APPLICANT: Baton, Dan L.
; APPLICANT: Haas, Philip E.
; APPLICANT: Kirchofer, Daniel
; APPLICANT: Suggest, Shelley
; APPLICANT: Human Anti-Factor IX/IXa Antibodies
; TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
; FILE REFERENCE: P1661R2
; CURRENT APPLICATION NUMBER: US/09/383,667
; CURRENT FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098,233
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: US 60/122,767
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 15
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-383-667-15

Query Match      100.0%; Score 58; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 AAMDLSSEFL 11
Db      1 AAMDLSSEFL 11

RESULT 2
US-08-273-146-63
; Sequence 63, Application US/08273146
; Patent No. 5855885
; GENERAL INFORMATION:
; APPLICANT: Smith, Rodger
; APPLICANT: McCafferty, John
; APPLICANT: Chiswell, David
; APPLICANT: Darsley, Michael J.
; APPLICANT: Fitzgerald, Kevin
; APPLICANT: Kenten, John H.
; APPLICANT: Martin, Mark T.
; APPLICANT: Titmas, Richard C.
; APPLICANT: Williams, Richard O.
```

TITLE OF INVENTION: The Isolation and Production of
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: IGEN, Inc.
STREET: 1530 East Jefferson St.
CITY: Rockville
STATE: MD
COUNTRY: USA
ZIP: 20852
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/273,146
FILING DATE: 14-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ryan, John W.
REGISTRATION NUMBER: 33,771
REFERENCE/DOCKET NUMBER: 09000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-984-8000
TELEFAX: 301-230-0158
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-273-146-63

Query Match 100.0%; Score 58; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDSISEFL 11
Db 83 AAWDSISEFL 93

RESULT 3
US-08-652-816A-15
Sequence 15, Application US/08652816A
GENERAL INFORMATION:
PATENT NO. 5872215
APPLICANT: Osbourn, JK
APPLICANT: Allen, DJ
APPLICANT: McCallerty, JG
TITLE OF INVENTION: Specific binding members, materials and
METHODS OF INVENTION: methods.
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,816A
FILING DATE: 23-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.4
FILING DATE: 02-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9125579.8

FILING DATE: 02-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 23-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9525004.9
FILING DATE: 07-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9610824.6
FILING DATE: 23-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/02240
FILING DATE: 02-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/244,597
FILING DATE: 01-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/33308
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-652-816A-15

Query Match 100.0%; Score 58; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDSISEFL 11
Db 90 AAWDSISEFL 100

RESULT 4
US-08-350-260A-374
Sequence 374, Application US/08350260A
GENERAL INFORMATION:
PATENT NO. 5962255
APPLICANT: Winter, Gregory Paul
APPLICANT: Griffiths, Andrew David
APPLICANT: Williams, Samuel Cameron
APPLICANT: Waterhouse, Peter
APPLICANT: Nissim, Ahuva
APPLICANT: Johnson, Kevin Stuart
TITLE OF INVENTION: Methods for producing members of specific
TITLE OF INVENTION: binding pairs
NUMBER OF SEQUENCES: 602
CORRESPONDENCE ADDRESS:
ADDRESSEE: David W. Clough
STREET: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/350,260A
FILING DATE: 05-DEC-1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB91/01134
FILING DATE: 10-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/32372
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 374:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-350-260A-374

Query Match 79.3%; Score 46; DB 2; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.05;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAWDSLSEFL 11
Db 1 AAWDSLSEFL 11

RESULT 5
US-09-104-337A-374
Sequence 374, Application US/09104337A
Patent No. 6492160
GENERAL INFORMATION:
APPLICANT: Winter, Gregory Paul
Griffiths, Andrew David
Williams, Samuel Cameron
Waterhouse, Peter
Nissim, Ahuva
Johnson, Kevin Stuart
Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific
NUMBER OF SEQUENCES: 600
CORRESPONDENCE ADDRESS:
ADDRESSEE: Audrey L. Bartnicki
STREET: Marshall, Gerstein & Borun
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/104,337A
FILING DATE: 25-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/350,260
FILING DATE: 05-DEC-1994
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1993
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bartnicki, Audrey L.
REGISTRATION NUMBER: 40,499
REFERENCE/DOCKET NUMBER: 28111/32372A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 374:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-104-337A-374

Query Match 79.3%; Score 46; DB 4; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.05;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAWDSLSEFL 11
Db 1 AAWDSLSEFL 11

RESULT 6
US-08-350-260A-346
Sequence 346, Application US/08350260A
Patent No. 5962255
GENERAL INFORMATION:
APPLICANT: Winter, Gregory Paul
Griffiths, Andrew David
Williams, Samuel Cameron
Waterhouse, Peter
Nissim, Ahuva
Johnson, Kevin Stuart
Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific
NUMBER OF SEQUENCES: 602
CORRESPONDENCE ADDRESS:
ADDRESSEE: David W. Clough
STREET: Marshall, O'Toole, Gerstein, Murray & Borun
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/350,260A
FILING DATE: 05-DEC-1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB91/01134
FILING DATE: 10-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/32372
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 346:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-350-260A-346

Query Match 75.9%; Score 44; DB 2; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.11;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAWDDSLSEFL 11
Db 1 AAWDDSLAWFV 11

RESULT 7
US-09-104-337A-346
Sequence 346, Application US/09104337A
Patent No. 6492160
GENERAL INFORMATION:
APPLICANT: Winer, Gregory Paul
Griffiths, Andrew David
Williams, Samuel Cameron
Waterhouse, Peter
Nissim, Ahuva
Johnson, Kevin Stuart
Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific
binding pairs
NUMBER OF SEQUENCES: 600
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Audrey L. Bartnicki
STREET: Marshall, Gerstein & Borun
6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/104,337A
FILING DATE: 25-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/350,260
FILING DATE: 05-DEC-1994
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1993
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bartnicki, Audrey L.
REGISTRATION NUMBER: 40,499
REFERENCE/DOCKET NUMBER: 28111/32372A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 346:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 346:
US-09-104-337A-346

Query Match 75.9%; Score 44; DB 4; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.11;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAWDDSLSEFL 11
Db 1 AAWDDSLAWFV 11

RESULT 8
US-08-665-202-60
Sequence 60, Application US/08665202
Patent No. 5977322
GENERAL INFORMATION:
APPLICANT: Marks, James D.
TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995

ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-665-202-60

Query Match 74.1%; Score 43; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDSIS 8
Db 1 AAWDSIS 8

RESULT 9
US-09-315-574-60
Sequence 60. Application US/09315574
Patent No. 6512897
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 6512097e1 High Affinity Human Antibodies to
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.
STREET: Four Embarcadero Center, Suite 1100
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear

MOLECULE TYPE: peptide
US-09-315-574-60

Query Match 74.1%; Score 43; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDSIS 8
Db 1 AAWDSIS 8

RESULT 10
US-08-350-260A-339
Sequence 339. Application US/08350260A
Patent No. 5962255
GENERAL INFORMATION:
APPLICANT: Winter, Gregory Paul
APPLICANT: Griffiths, Andrew David
APPLICANT: Williams, Samuel Cameron
APPLICANT: Waterhouse, Peter
APPLICANT: Nissem, Ahuva
APPLICANT: Johnson, Kevin Stuart
APPLICANT: Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific
NUMBER OF SEQUENCES: 602
CORRESPONDENCE ADDRESSES:
ADDRESSEE: David W. Clough
STREET: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/350,260A
FILING DATE: 05-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB91/01134
FILING DATE: 10-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/32372
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 339:
SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-350-260A-339

Query Match 74.1%; Score 43; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAMDSSLIS 8
Db 1 AAMDSSLIS 8

RESULT 11
US-08-350-260A-497
Sequence 497, Application US/08350260A
Patent No. 5962255
GENERAL INFORMATION:
APPLICANT: Winter, Gregory Paul
APPLICANT: Griffiths, Andrew David
APPLICANT: Williams, Samuel Cameron
APPLICANT: Waterhouse, Peter
APPLICANT: Nissim, Ahuva
APPLICANT: Johnson, Kevin Stuart
TITLE OF INVENTION: Methods for producing members of specific
NUMBER OF SEQUENCES: 602
CORRESPONDENCE ADDRESS:
ADDRESSEE: David W. Clough
STREET: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/350,260A
FILING DATE: 05-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB91/01114
FILING DATE: 10-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/32372
TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 497:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-350-260A-497

Query Match 74.1%; Score 43; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAMDSSLIS 8
Db 1 AAMDSSLIS 8

RESULT 12
US-09-104-337A-339
Sequence 339, Application US/09104337A
Patent No. 6492160
GENERAL INFORMATION:
APPLICANT: Winter, Gregory Paul
APPLICANT: Griffiths, Andrew David
APPLICANT: Williams, Samuel Cameron
APPLICANT: Waterhouse, Peter
APPLICANT: Nissim, Ahuva
APPLICANT: Johnson, Kevin Stuart
TITLE OF INVENTION: Methods for producing members of specific
NUMBER OF SEQUENCES: 600
CORRESPONDENCE ADDRESS:
ADDRESSEE: Andrew L. Bartnicki
STREET: Marshall, Gerstein & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/104,337A
FILING DATE: 25-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/350,260
FILING DATE: 05-DEC-1994
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1993
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bartnicki, Audrey L.
REGISTRATION NUMBER: 40,499
REFERENCE/DOCKET NUMBER: 28111/32372A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 339:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 339:
US-09-104-337A-339

Query Match 74.1%; Score 43; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDSSLIS 8
Db 1 AAMDSSLIS 8

RESULT 13
US-09-104-337A-497
Sequence 497, Application US/09104337A
Patent No. 6492160
GENERAL INFORMATION:
APPLICANT: Winter, Gregory Paul
Griffiths, Andrew David
Williams, Samuel Cameron
Waterhouse, Peter
Nissim, Ahuva
Johnson, Kevin Stuart
Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific binding pairs
NUMBER OF SEQUENCES: 600
CORRESPONDENCE ADDRESS:
ADDRESSEE: Audrey L. Bartnicki
STREET: Marshall, Gerstein & Borun
6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/104,337A
FILING DATE: 25-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/350,260
FILING DATE: 05-DEC-1994
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1993
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bartnicki, Audrey L.
REGISTRATION NUMBER: 40,499
REFERENCE/DOCKET NUMBER: 28111/32372A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 497:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 497:
US-09-104-337A-497

Query Match 74.1%; Score 43; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDSSLIS 8
Db 1 AAMDSSLIS 8

RESULT 14
US-08-350-260A-441
Sequence 441, Application US/08350260A
Patent No. 5962255
GENERAL INFORMATION:
APPLICANT: Winter, Gregory Paul
Griffiths, Andrew David
Williams, Samuel Cameron
Waterhouse, Peter
Nissim, Ahuva
Johnson, Kevin Stuart
APPLICANT: Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific binding pairs
NUMBER OF SEQUENCES: 602
CORRESPONDENCE ADDRESS:
ADDRESSEE: David W. Clough
STREET: Marshall, O'Toole, Gerstein, Murray & Borun
6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/350,260A
FILING DATE: 05-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB91/01134
FILING DATE: 10-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/32372
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 441:
SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-350-260A-441

Query Match 74.1%; Score 43; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDSLS 8
Db 1 AAWDSLS 8

RESULT 15
US-08-665-202-6
Sequence 6, Application US/08665202
Patent No. 597322

GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schler, Robert
TITLE OF INVENTION: No. 597322e1 High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995

ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear

MOLECULE TYPE: peptide
US-08-665-202-6

Query Match 74.1%; Score 43; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDSLS 8
Db 1 AAWDSLS 8

RESULT 16

US-09-104-337A-441
Sequence 441, Application US/09104337A
Patent No. 6492160

GENERAL INFORMATION:
APPLICANT: Winter, Gregory Paul

Griffiths, Andrew David
Williams, Samuel Cameron
Waterhouse, Peter
Nissim, Ahuva
Johnson, Kevin Stuart

TITLE OF INVENTION: Methods for producing members of specific
binding pairs
NUMBER OF SEQUENCES: 600
CORRESPONDENCE ADDRESS:
ADDRESSER: Audrey L. Bartnicki
STREET: Marshall, Gerstein & Borum
6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
ZIP: 60606-6402

COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/104,337A
FILING DATE: 25-Jun-1998

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/350,260
FILING DATE: 05-DEC-1994

APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991

APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992

APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992

APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1993

APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994

APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994

ATTORNEY/AGENT INFORMATION:
NAME: Bartnicki, Audrey L.
REGISTRATION NUMBER: 40,499

REFERENCE/DOCKET NUMBER: 28111/32372A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300

INFORMATION FOR SEQ ID NO: 441:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 441:
US-09-104-337A-441

Query Match 74.1%; Score 43; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDSLS 8
Db 1 AAWDSLS 8

RESULT 17

US-09-315-574-6
Sequence 6, Application US/09315574
Patent No. 6512097

```

; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
; TITLE OF INVENTION: Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Huse P.C.
; STREET: Four Embarcadero Center, Suite 1100
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4106
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/315,574
; FILING DATE: 20-MAY-99
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/665,202
; FILING DATE: 13-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 02307E-061411
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-315-574-6

Query Match 74.1%; Score 43; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDSLS 8
Db 1 AAWDSLS 8

RESULT 18
US-08-211-202-111
; Sequence 111, Application US/08211202
; Patent No. 5565332
; GENERAL INFORMATION:
; APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Matreus
; APPLICANT: BAIRER, Michael
; APPLICANT: JESPERSEN, Laurent Stephane Anne Therese
; APPLICANT: WINTER, Gregory Paul
; TITLE OF INVENTION: Production of chimeric antibodies - a
; TITLE OF INVENTION: combinatorial approach
; NUMBER OF SEQUENCES: 144
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
; ADDRESSEE: Botum
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
```

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; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/211,202
; FILING DATE: 23-SEP-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9120252.3
; FILING DATE: 23-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9120377.8
; FILING DATE: 25-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206372.6
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: David W. Clough
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/31960
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 111:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-211-202-111

Query Match 74.1%; Score 43; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDSLS 8
Db 90 AAWDSLS 97

RESULT 19
US-08-665-202-38
; Sequence 38, Application US/08665202
; Patent No. 5977322
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
; TITLE OF INVENTION: Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-665-202-38

Query Match 74.1%; Score 43; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAWDSLS 8
Db 90 AAWDSLS 97

RESULT 20
US-09-315-574-38
Sequence 38, Application US/09315574
Patent No. 6512097
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
NUMBER OF INVENTIONS: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Majestic, Parsons, Siebert & Hane P.C.
STREET: Four Embarcadero Center, Suite 1100
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom

REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-315-574-38

Query Match 74.1%; Score 43; DB 4; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAWDSLS 8
Db 90 AAWDSLS 97

RESULT 21
US-09-240-274-59
Sequence 59, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 59
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: anti-Rh(D) chain M02
US-09-240-274-59

Query Match 74.1%; Score 43; DB 3; Length 109;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAWDSLS 8
Db 89 AAWDSLS 96

RESULT 22
US-09-240-274-60
Sequence 60, Application US/09240274
Patent No. 6255455
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
FILE REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224

SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 60
 LENGTH: 110
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: anti-Rh(D) chain M03
 US-09-240-274-60

Query Match 74.1%; Score 43; DB 3; Length 110;
 Best Local Similarity 100.0%; Pred. No. 2;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAMDLS 8
 |||||
 Db 89 AAMDLS 96

RESULT 23
 US-08-665-202-36
 Sequence 36, Application US/08665202
 Patent No. 5977322
 GENERAL INFORMATION:
 APPLICANT: Marks, James D.
 APPLICANT: Schier, Robert
 TITLE OF INVENTION: No. 5977322e1 High Affinity Human Antibodies to
 TITLE OF INVENTION: Tumor Antigens
 NUMBER OF SEQUENCES: 141
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/665,202
 FILING DATE: 13-JUN-1996
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/000,238
 FILING DATE: 14-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/000,250
 FILING DATE: 15-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Hunter, Tom
 REGISTRATION NUMBER: 38,498
 REFERENCE/DOCKET NUMBER: 02307E-061410
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 36:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 111 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-665-202-36

Query Match 74.1%; Score 43; DB 2; Length 111;
 Best Local Similarity 100.0%; Pred. No. 2;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AAMDLS 8
 |||||
 Db 90 AAMDLS 97

RESULT 24
 US-08-665-202-43
 Sequence 43, Application US/08665202
 Patent No. 5977322
 GENERAL INFORMATION:
 APPLICANT: Marks, James D.
 APPLICANT: Schier, Robert
 TITLE OF INVENTION: No. 5977322e1 High Affinity Human Antibodies to
 TITLE OF INVENTION: Tumor Antigens
 NUMBER OF SEQUENCES: 141
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/665,202
 FILING DATE: 13-JUN-1996
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/000,238
 FILING DATE: 14-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/000,250
 FILING DATE: 15-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Hunter, Tom
 REGISTRATION NUMBER: 38,498
 REFERENCE/DOCKET NUMBER: 02307E-061410
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 43:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 111 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-665-202-43

Query Match 74.1%; Score 43; DB 2; Length 111;
 Best Local Similarity 100.0%; Pred. No. 2;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AAMDLS 8
 |||||
 Db 90 AAMDLS 97

RESULT 25
 US-09-315-574-36
 Sequence 36, Application US/09315574
 Patent No. 6512097
 GENERAL INFORMATION:
 APPLICANT: Marks, James D.
 APPLICANT: Schier, Robert
 TITLE OF INVENTION: No. 6512097e1 High Affinity Human Antibodies to
 TITLE OF INVENTION: Tumor Antigens
 NUMBER OF SEQUENCES: 141
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Majestic, Parsons, Siebert & Haue P.C.
 STREET: Four Embarcadero Center, Suite 1100
 CITY: San Francisco

```
STATE: California.
COUNTRY: USA
ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-315-574-36

Query Match      74.1%; Score 43; DB 4; Length 111;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 AAWDSLS 8
Db      90 AAWDSLS 97

RESULT 26
US-09-315-574-43
; Sequence 43, Application US/09315574
; Patent No. 6512097
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
; TITLE OF INVENTION: Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.
; STREET: Four Embarcadero Center, Suite 1100
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4106
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/315,574
; FILING DATE: 20-MAY-99
; CLASSIFICATION: 530
; INFORMATION FOR SEQ ID NO: 36:
; PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-315-574-43

Query Match      74.1%; Score 43; DB 4; Length 111;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 AAWDSLS 8
Db      90 AAWDSLS 97

RESULT 27
US-08-665-202-39
; Sequence 39, Application US/08665202
; Patent No. 5977322
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
; TITLE OF INVENTION: Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3634
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,202
; FILING DATE: 13-JUN-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 02307E-061410
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 39:
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SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-665-202-39

Query Match 74.1%; Score 43; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDSLS 8
|||||||
Db 90 AAMDSLS 97

RESULT 28
US-09-315-574-39
Sequence 39, Application US/09315574
Patent No. 6512097
GENERAL INFORMATION:
APPLICANT: Marks, James D.
TITLE OF INVENTION: No. 6512097e1 High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.
STREET: Four Embarcadero Center, Suite 1100
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-315-574-39

Query Match 74.1%; Score 43; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAMDSLS 8

Db 90 AAMDSLS 97
|||||||

RESULT 29
US-08-211-202-112
Sequence 112, Application US/08211202
Patent No. 5565332
GENERAL INFORMATION:
APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Matreus
APPLICANT: BAIRER, Michael
APPLICANT: JESPER, Laurent Stephane Anne Therese
APPLICANT: WINTER, Gregory Paul
TITLE OF INVENTION: Production of chimeric antibodies - a
TITLE OF INVENTION: combinatorial approach
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211,202
FILING DATE: 23-SEP-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120252.3
FILING DATE: 23-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120377.8
FILING DATE: 25-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/31960
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-211-202-112

Query Match 74.1%; Score 43; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAMDSLS 8
|||||||
Db 90 AAMDSLS 97

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RESULT 30
US-08-211-202-113
; Sequence 113, Application US/08211202
; Patent No. 5565332
; GENERAL INFORMATION:
; APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Matheus
; APPLICANT: BAIRER, Michael
; APPLICANT: JESPEERS, Laurent Stephane Anne Therese
; APPLICANT: WINTER, Gregory Paul
; TITLE OF INVENTION: Production of chimeric antibodies - a
; NUMBER OF SEQUENCES: 144
; CORRESPONDENCE ADDRESS:
; ADDRESS: David W. Clough, Marshall O'Toole Gerstein Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/211,202
; FILING DATE: 23-SEP-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9120252.3
; FILING DATE: 23-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9120377.8
; FILING DATE: 25-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206372.6
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: David W. Clough
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/31960
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-211-202-113

Query Match      74.1%; Score 43; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

CY      1 AAWDSLS 8
Db      90 AAWDSLS 97

RESULT 31
US-08-211-202-114
; Sequence 114, Application US/08211202
; Patent No. 5565332
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; GENERAL INFORMATION:
; APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Matheus
; APPLICANT: BAIRER, Michael
; APPLICANT: JESPEERS, Laurent Stephane Anne Therese
; APPLICANT: WINTER, Gregory Paul
; TITLE OF INVENTION: Production of chimeric antibodies - a
; NUMBER OF SEQUENCES: 144
; CORRESPONDENCE ADDRESS:
; ADDRESS: David W. Clough, Marshall O'Toole Gerstein Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/211,202
; FILING DATE: 23-SEP-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9120252.3
; FILING DATE: 23-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9120377.8
; FILING DATE: 25-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206372.6
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: David W. Clough
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/31960
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-211-202-114

Query Match      74.1%; Score 43; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

CY      1 AAWDSLS 8
Db      90 AAWDSLS 97

RESULT 32
US-08-665-202-5
; Sequence 5, Application US/08665202
; Patent No. 597322
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 597322el High Affinity Human Antibodies to
```

TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 258 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-665-202-5

Query Match 74.1%; Score 43; DB 2; Length 258;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAMDLS 8
Db 234 AAMDLS 241

RESULT 33
US-09-315-574-5
Sequence 5, Application US/09315574
GENERAL INFORMATION:
APPLICANT: Marks, James D.
APPLICANT: Schlier, Robert
TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Majestic, Parsons, Siebert & Huse P.C.
STREET: Four Embarcadero Center, Suite 1100
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,574
FILING DATE: 20-MAY-99

CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061411
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 258 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-315-574-5

Query Match 74.1%; Score 43; DB 4; Length 258;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAMDLS 8
Db 234 AAMDLS 241

RESULT 34
US-09-069-821-4
Sequence 4, Application US/09069821
Patent No. 6323322
GENERAL INFORMATION:
APPLICANT: PILRULA, DAVID
APPLICANT: WANG, MAOLIAN
APPLICANT: SHORR, ROBERT
APPLICANT: WHITLOW, MARC
APPLICANT: LEE, LHSYNG S.
TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
TITLE OF INVENTION: CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/069,821
FILING DATE: 30-APR-1998
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/067,341
FILING DATE: 02-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/063,074
FILING DATE: 27-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/050,472
FILING DATE: 23-JUN-1997
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/044,449
FILING DATE: 30-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 0977.2280003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 262 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-09-069-821-4

Query Match 74.1%; Score 43; DB 3; Length 262;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAMDLS 8
Db 90 AAMDLS 97

RESULT 35
US-09-956-086-4
Sequence 4, Application US/09956086
Patent No. 6743896
GENERAL INFORMATION:
APPLICANT: FILIPULA, DAVID
WANG, MAOLIANG
SHORR, ROBERT
WHITLOW, MARC
LEE, LIHSYNG S.
COUNTRY: USA
ZIP: 20005
TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/956,086
FILING DATE: 20-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/069,821
FILING DATE: <Unknown>
APPLICATION NUMBER: US 60/063,074
FILING DATE: 27-OCT-1997
APPLICATION NUMBER: US 60/050,472
FILING DATE: 23-JUN-1997
APPLICATION NUMBER: US 60/044,449
FILING DATE: 30-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 0977.2280003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 262 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: No. 6743896 Relevant
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-956-086-4

Query Match 74.1%; Score 43; DB 4; Length 262;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAMDLS 8
Db 90 AAMDLS 97

RESULT 36
US-09-956-087-4
Sequence 4, Application US/09956087
Patent No. 6743908
GENERAL INFORMATION:
APPLICANT: FILIPULA, DAVID
WANG, MAOLIANG
SHORR, ROBERT
WHITLOW, MARC
LEE, LIHSYNG S.
COUNTRY: USA
ZIP: 20005
TITLE OF INVENTION: SINGLE-CHAIN ANTIGEN-BINDING PROTEINS
CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/956,087
FILING DATE: 20-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/069,821
FILING DATE: 1998-04-30
APPLICATION NUMBER: US 60/063,074
FILING DATE: 27-OCT-1997
APPLICATION NUMBER: US 60/050,472
FILING DATE: 23-JUN-1997
APPLICATION NUMBER: US 60/044,449
FILING DATE: 30-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 0977.2280003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 262 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-956-087-4

Query Match 74.1%; Score 43; DB 4; Length 262;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDLS 8
Db 90 AAMDLS 97

RESULT 37
US-09-420-592A-7

; Sequence 7, Application US/09420592A
; Patent No. 6333396
; GENERAL INFORMATION:
; APPLICANT: Filpula, David R.
; APPLICANT: Wang, Maoliang
; APPLICANT: Whitlow, Marc D.
; TITLE OF INVENTION: No. 6333396el Method for Targeted Delivery of Nucleic Acids
; FILE REFERENCE: 0977.2300001
; CURRENT APPLICATION NUMBER: US/09/420,592A
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/104,949
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 7
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: C6.5/218 sfv
US-09-420-592A-7

Query Match 74.1%; Score 43; DB 3; Length 282;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDLS 8
Db 90 AAMDLS 97

RESULT 38
US-09-985-442-7

; Sequence 7, Application US/09985442
; Patent No. 6692942
; GENERAL INFORMATION:
; APPLICANT: Filpula, David R.
; APPLICANT: Wang, Maoliang
; APPLICANT: Whitlow, Marc D.
; TITLE OF INVENTION: No. 6692942el Method for Targeted Delivery of Nucleic Acids
; FILE REFERENCE: 0977.2300003
; CURRENT APPLICATION NUMBER: US/09/985,442
; PRIOR FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 09/420,592
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/104,949
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 7
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: C6.5/218 sfv
US-09-985-442-7

Query Match 74.1%; Score 43; DB 4; Length 282;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDLS 8

Db 90 AAMDLS 97

RESULT 39
US-09-983-580-7

; Sequence 7, Application US/09983580
; Patent No. 6764853
; GENERAL INFORMATION:
; APPLICANT: Filpula, David R.
; APPLICANT: Wang, Maoliang
; APPLICANT: Whitlow, Marc D.
; TITLE OF INVENTION: No. 6764853el Method for Targeted Delivery of Nucleic Acids
; FILE REFERENCE: 0977.2300002
; CURRENT APPLICATION NUMBER: US/09/983,580
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: 09/420,592
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/104,949
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 7
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: C6.5/218 sfv
US-09-983-580-7

Query Match 74.1%; Score 43; DB 4; Length 282;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDLS 8
Db 90 AAMDLS 97

RESULT 40
US-08-665-202-40

; Sequence 40, Application US/08665202
; Patent No. 5977322
; GENERAL INFORMATION:
; APPLICANT: Marko, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,202
; FILING DATE: 13-JUN-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom

```

?      REGISTRATION NUMBER: 38.498
?      REFERENCE/DOCKET NUMBER: 02307E-061410
?      TELECOMMUNICATION INFORMATION:
?      TELEPHONE: (415) 576-0200
?      TELEFAX: (415) 576-0300
?      INFORMATION FOR SEQ ID NO: 40:
?      SEQUENCE CHARACTERISTICS:
?      LENGTH: 111 amino acids
?      TYPE: amino acid
?      STRANDEDNESS:
?      TOPOLOGY: linear
?      MOLECULE TYPE: peptide
US-08-665-202-40

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Query Match	70.7%	Score 41	DB 2	Length 11
Best Local Similarity	63.6%	Pred. No. 4.6		
Matches	7	Conservative	3	Mismatches 1
				Indels 0
				Gaps 0
Qy	1	AAWDDSLSEFL	11	
		:::		
Db	90	AAWDDSLNGMM	100	

Search completed: March 31, 2005, 12:13:28
Job time : 22.4844 Secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: March 31, 2005, 12:10:00 ; Search time 61.5312 Seconds
(without alignments)
59.279 Million cell updates/sec

Title: US-10-614-959-15
Perfect score: 58
Sequence: 1 AAMDLSLEFL 11

Scoring table: BLOSUM62
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Total number of hits satisfying chosen parameters: 1413372

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications_AA:*

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- 19: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	58	100.0	243	15	US-10-293-418-1927 Sequence 1927, Ap
3	58	100.0	245	10	US-09-880-748-1926 Sequence 1926, Ap
4	58	100.0	245	15	US-10-293-418-1926 Sequence 1926, Ap
5	58	100.0	245	15	US-10-293-418-1926 Sequence 1926, Ap
6	58	100.0	246	10	US-09-880-748-1913 Sequence 1913, Ap
7	58	100.0	246	10	US-09-880-748-1913 Sequence 1913, Ap
8	58	100.0	246	15	US-10-293-418-1913 Sequence 1913, Ap
9	58	100.0	246	15	US-10-293-418-1917 Sequence 1917, Ap
10	58	100.0	247	10	US-09-880-748-1443 Sequence 1443, Ap
11	58	100.0	247	10	US-09-880-748-1682 Sequence 1682, Ap
12	58	100.0	247	10	US-09-880-748-1707 Sequence 1707, Ap
13	58	100.0	247	10	US-09-880-748-1899 Sequence 1899, Ap

14	58	100.0	247	10	US-09-880-748-1928 Sequence 1928, Ap
15	58	100.0	247	15	US-09-880-748-1934 Sequence 1934, Ap
16	58	100.0	247	15	US-10-293-418-1443 Sequence 1443, Ap
17	58	100.0	247	15	US-10-293-418-1682 Sequence 1682, Ap
18	58	100.0	247	15	US-10-293-418-1707 Sequence 1707, Ap
19	58	100.0	247	15	US-10-293-418-1899 Sequence 1899, Ap
20	58	100.0	247	15	US-10-293-418-1928 Sequence 1928, Ap
21	58	100.0	247	15	US-10-293-418-1934 Sequence 1934, Ap
22	58	100.0	249	10	US-09-880-748-1419 Sequence 1419, Ap
23	58	100.0	249	10	US-09-880-748-1618 Sequence 1618, Ap
24	58	100.0	249	10	US-09-880-748-2049 Sequence 2049, Ap
25	58	100.0	249	15	US-09-880-748-2065 Sequence 2065, Ap
26	58	100.0	249	15	US-10-293-418-1419 Sequence 1419, Ap
27	58	100.0	249	15	US-10-293-418-1618 Sequence 1618, Ap
28	58	100.0	249	15	US-10-293-418-2049 Sequence 2049, Ap
29	58	100.0	249	15	US-10-293-418-2065 Sequence 2065, Ap
30	58	100.0	251	10	US-09-880-748-1309 Sequence 1309, Ap
31	58	100.0	251	10	US-09-880-748-1671 Sequence 1671, Ap
32	58	100.0	251	10	US-09-880-748-1809 Sequence 1809, Ap
33	58	100.0	251	15	US-10-293-418-1309 Sequence 1309, Ap
34	58	100.0	251	15	US-10-293-418-1671 Sequence 1671, Ap
35	58	100.0	251	15	US-10-293-418-1809 Sequence 1809, Ap
36	58	100.0	252	10	US-09-880-748-1698 Sequence 1698, Ap
37	58	100.0	252	15	US-10-293-418-1698 Sequence 1698, Ap
38	58	100.0	253	10	US-09-880-748-935 Sequence 935, Ap
39	58	100.0	253	10	US-09-880-748-935 Sequence 935, Ap
40	58	100.0	253	10	US-09-880-748-939 Sequence 939, Ap
41	58	100.0	253	10	US-09-880-748-1611 Sequence 1611, Ap
42	58	100.0	253	10	US-09-880-748-1936 Sequence 1936, Ap
43	58	100.0	253	15	US-10-293-418-929 Sequence 929, Ap
44	58	100.0	253	15	US-10-293-418-935 Sequence 935, Ap
45	58	100.0	253	15	US-10-293-418-939 Sequence 939, Ap

ALIGNMENTS

RESULT 1
US-09-880-748-1927
; Sequence 1927, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1927
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-880-748-1927

Query Match 100.0%; Score 58; DB 10; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.036;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 AAMDLSLEFL 11
DB 222 AAMDLSLEFL 232

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RESULT 2
US-10-293-418-1927
; Sequence 1927, Application US/10293418
; Publication No. US2003022396A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1927
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1927

Query Match          100.0%; Score 58; DB 15; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.036;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AAMDLSSEFL 11
Db      222 AAMDLSSEFL 232

RESULT 3
US-09-880-748-1926
; Sequence 1926, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1926
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1926

Query Match          100.0%; Score 58; DB 10; Length 245;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AAMDLSSEFL 11
Db      224 AAMDLSSEFL 234

RESULT 4
US-10-293-418-1926
; Sequence 1926, Application US/10293418
; Publication No. US2003022396A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1926
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1926

Query Match          100.0%; Score 58; DB 15; Length 245;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AAMDLSSEFL 11
Db      224 AAMDLSSEFL 234

RESULT 5
US-10-293-418-3241
; Sequence 3241, Application US/10293418
; Publication No. US2003022396A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
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;; PRIOR APPLICATION NUMBER: 60/212,210
;; PRIOR FILING DATE: 2000-06-16
;; NUMBER OF SEQ ID NOS: 3247
;; SEQ ID NO 3241
;; LENGTH: 245
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-293-418-3241

Query Match 100.0%; Score 58; DB 15; Length 245;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDSTSEFL 11
|||
Db 225 AAMDSTSEFL 234

RESULT 6
US-09-880-748-1913
;; Sequence 1913, Application US/09880748
;; Publication No. US20030059937A1
;; GENERAL INFORMATION:
;; APPLICANT: Ruben et al.
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
;; FILE REFERENCE: PF523
;; CURRENT APPLICATION NUMBER: US/09/880,748
;; CURRENT FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/212,210
;; PRIOR FILING DATE: 2000-06-15
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; NUMBER OF SEQ ID NOS: 3239
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 1913
;; LENGTH: 246
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-880-748-1913

Query Match 100.0%; Score 58; DB 10; Length 246;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDSTSEFL 11
|||
Db 225 AAMDSTSEFL 235

RESULT 7
US-09-880-748-1917
;; Sequence 1917, Application US/09880748
;; Publication No. US20030059937A1
;; GENERAL INFORMATION:
;; APPLICANT: Ruben et al.
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
;; FILE REFERENCE: PF523
;; CURRENT APPLICATION NUMBER: US/09/880,748
;; CURRENT FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/212,210
;; PRIOR FILING DATE: 2000-06-15
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21

;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; NUMBER OF SEQ ID NOS: 3239
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 1917
;; LENGTH: 246
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-880-748-1917

Query Match 100.0%; Score 58; DB 10; Length 246;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDSTSEFL 11
|||
Db 225 AAMDSTSEFL 235

RESULT 8
US-10-293-418-1913
;; Sequence 1913, Application US/10293418
;; Publication No. US20030223996A1
;; GENERAL INFORMATION:
;; APPLICANT: Ruben et al.
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
;; FILE REFERENCE: PF523p2
;; CURRENT APPLICATION NUMBER: US/10/293,418
;; CURRENT FILING DATE: 2002-11-27
;; PRIOR APPLICATION NUMBER: 60/331,469
;; PRIOR FILING DATE: 2001-11-16
;; PRIOR APPLICATION NUMBER: 60/340,817
;; PRIOR FILING DATE: 2001-12-19
;; PRIOR APPLICATION NUMBER: 09/880,748
;; PRIOR FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; PRIOR APPLICATION NUMBER: 60/212,210
;; PRIOR FILING DATE: 2000-06-16
;; NUMBER OF SEQ ID NOS: 3247
;; SEQ ID NO 1913
;; LENGTH: 246
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-293-418-1913

Query Match 100.0%; Score 58; DB 15; Length 246;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDSTSEFL 11
|||
Db 225 AAMDSTSEFL 235

RESULT 9
US-10-293-418-1917
;; Sequence 1917, Application US/10293418
;; Publication No. US20030223996A1
;; GENERAL INFORMATION:
;; APPLICANT: Ruben et al.
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
;; FILE REFERENCE: PF523p2
;; CURRENT APPLICATION NUMBER: US/10/293,418
;; CURRENT FILING DATE: 2002-11-27
;; PRIOR APPLICATION NUMBER: 60/331,469
;; PRIOR FILING DATE: 2001-11-16

```

; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1917
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1917
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```

Query Match          100.0%; Score 58; DB 15; Length 246;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 AAWDLSSEFL 11
        |||||
Db       225 AAWDLSSEFL 235
```

```

RESULT 10
US-09-880-748-1443
; Sequence 1443, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1443
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1443
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```

Query Match          100.0%; Score 58; DB 10; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 AAWDLSSEFL 11
        |||||
Db       226 AAWDLSSEFL 236
```

```

RESULT 11
US-09-880-748-1682
; Sequence 1682, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
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; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1682
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1682
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```

Query Match          100.0%; Score 58; DB 10; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 AAWDLSSEFL 11
        |||||
Db       226 AAWDLSSEFL 236
```

```

RESULT 12
US-09-880-748-1707
; Sequence 1707, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1707
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1707
```

```

Query Match          100.0%; Score 58; DB 10; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 AAWDLSSEFL 11
        |||||
Db       226 AAWDLSSEFL 236
```

```

RESULT 13
US-09-880-748-1899
; Sequence 1899, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
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RESULT 16
US-10-293-418-1443
; Sequence 1443, Application US/10293418
; Publication No. US2003022396A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P5523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1443
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1443

Query Match 100.0%; Score 58; DB 15; Length 247;
Best Local Similarity 100.0%; Pctd. No. 0.037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

Cy 1 AAWDDSLSEFL 11
Db 226 AAWDDSLSEFL 236

```

```
RESULT 17
US-10-293-418-1682
; Sequence 1682, Application US/10293418
; Publication No. US2003022396A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1682
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1682

Query Match          100.0%; Score 58; DB 15; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AAMDLSSEFL 11
Db      226 AAMDLSSEFL 236

RESULT 18
US-10-293-418-1707
; Sequence 1707, Application US/10293418
; Publication No. US2003022396A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1707
; LENGTH: 247
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1707

Query Match          100.0%; Score 58; DB 15; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AAMDLSSEFL 11
Db      226 AAMDLSSEFL 236

RESULT 19
US-10-293-418-1899
; Sequence 1899, Application US/10293418
; Publication No. US2003022396A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1899
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1899

Query Match          100.0%; Score 58; DB 15; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AAMDLSSEFL 11
Db      226 AAMDLSSEFL 236

RESULT 20
US-10-293-418-1928
; Sequence 1928, Application US/10293418
; Publication No. US2003022396A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
```

PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1928
LENGTH: 247
TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-418-1928

Query Match 100.0%; Score 58; DB 15; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAMDSEFL 11
Db 226 AAMDSEFL 236

RESULT 21

US-10-293-418-1934
Sequence 1934, Application US/10293418
Publication No. US2003023996A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523P2
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1934
LENGTH: 247
TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-418-1934

Query Match 100.0%; Score 58; DB 15; Length 247;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAMDSEFL 11
Db 226 AAMDSEFL 236

RESULT 22

US-09-880-748-1419
Sequence 1419, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1419
LENGTH: 249
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-1419

Query Match 100.0%; Score 58; DB 10; Length 249;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAMDSEFL 11
Db 228 AAMDSEFL 238

RESULT 23

US-09-880-748-1618
Sequence 1618, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1618
LENGTH: 249
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-1618

Query Match 100.0%; Score 58; DB 10; Length 249;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAMDSEFL 11
Db 228 AAMDSEFL 238

RESULT 24

US-09-880-748-2049
Sequence 2049, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.

```
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
;; FILE REFERENCE: P523
;; CURRENT APPLICATION NUMBER: US/09/880,748
;; PRIOR FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/212,210
;; PRIOR FILING DATE: 2000-06-15
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; NUMBER OF SEQ ID NOS: 3239
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 2049
;; LENGTH: 249
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-880-748-2049
```

```
Query Match      100.0%; Score 58; DB 10; Length 249;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 AAWDSLSEFL 11
        |||||
Db      228 AAWDSLSEFL 238
```

```
RESULT 25
```

```
;; Sequence 2065, Application US/09880748
;; Publication No. US2003005937A1
;; GENERAL INFORMATION:
```

```
;; APPLICANT: Ruben et al.
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
;; FILE REFERENCE: P523
;; CURRENT APPLICATION NUMBER: US/09/880,748
;; PRIOR FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/212,210
;; PRIOR FILING DATE: 2000-06-15
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; NUMBER OF SEQ ID NOS: 3239
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 2065
;; LENGTH: 249
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-880-748-2065
```

```
Query Match      100.0%; Score 58; DB 10; Length 249;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 AAWDSLSEFL 11
        |||||
Db      228 AAWDSLSEFL 238
```

```
RESULT 26
US-10-293-418-1419
;; Sequence 1419, Application US/10293418
;; Publication No. US20030223996A1
;; GENERAL INFORMATION:
```

```
;; APPLICANT: Ruben et al.
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
;; FILE REFERENCE: P523P2
;; CURRENT APPLICATION NUMBER: US/10/293,418
;; PRIOR FILING DATE: 2002-11-27
;; PRIOR APPLICATION NUMBER: 60/331,469
;; PRIOR FILING DATE: 2001-11-16
;; PRIOR APPLICATION NUMBER: 60/340,817
;; PRIOR FILING DATE: 2001-12-19
;; PRIOR APPLICATION NUMBER: 09/880,748
;; PRIOR FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; PRIOR APPLICATION NUMBER: 60/212,210
;; PRIOR FILING DATE: 2000-06-16
;; NUMBER OF SEQ ID NOS: 3247
;; SEQ ID NO 1419
;; LENGTH: 249
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-293-418-1419
```

```
Query Match      100.0%; Score 58; DB 15; Length 249;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 AAWDSLSEFL 11
        |||||
Db      228 AAWDSLSEFL 238
```

```
RESULT 27
```

```
;; Sequence 1618, Application US/10293418
;; Publication No. US20030223996A1
;; GENERAL INFORMATION:
```

```
;; APPLICANT: Ruben et al.
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
;; FILE REFERENCE: P523P2
;; CURRENT APPLICATION NUMBER: US/10/293,418
;; PRIOR FILING DATE: 2002-11-27
;; PRIOR APPLICATION NUMBER: 60/331,469
;; PRIOR FILING DATE: 2001-11-16
;; PRIOR APPLICATION NUMBER: 60/340,817
;; PRIOR FILING DATE: 2001-12-19
;; PRIOR APPLICATION NUMBER: 09/880,748
;; PRIOR FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; PRIOR APPLICATION NUMBER: 60/212,210
;; PRIOR FILING DATE: 2000-06-16
;; NUMBER OF SEQ ID NOS: 3247
;; SEQ ID NO 1618
;; LENGTH: 249
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-293-418-1618
```

```
Query Match      100.0%; Score 58; DB 15; Length 249;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```


QY 1 AAMDLSSEFL 11
 |||||
 Db 228 AAMDLSSEFL 238

RESULT 28
 US-10-293-418-2049
 ; Sequence 2049, Application US/10293418
 ; Publication No. US2003022396A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 ; FILE REFERENCE: PF523P2
 ; CURRENT APPLICATION NUMBER: US/10/293,418
 ; CURRENT FILING DATE: 2002-11-27
 ; PRIOR APPLICATION NUMBER: 60/331,469
 ; PRIOR FILING DATE: 2001-11-16
 ; PRIOR APPLICATION NUMBER: 60/340,817
 ; PRIOR FILING DATE: 2001-12-19
 ; PRIOR APPLICATION NUMBER: 09/880,748
 ; PRIOR FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: 60/293,499
 ; PRIOR FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: 60/277,379
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/276,248
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/240,816
 ; PRIOR FILING DATE: 2000-10-17
 ; PRIOR APPLICATION NUMBER: 60/212,210
 ; PRIOR FILING DATE: 2000-06-16
 ; NUMBER OF SEQ ID NOS: 3247
 ; SEQ ID NO 2049
 ; LENGTH: 249
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-293-418-2049

Query Match 100.0%; Score 58; DB 15; Length 249;
 Best Local Similarity 100.0%; Pred. No. 0.037;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDLSSEFL 11
 |||||
 Db 228 AAMDLSSEFL 238

RESULT 29
 US-10-293-418-2065
 ; Sequence 2065, Application US/10293418
 ; Publication No. US2003022396A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 ; FILE REFERENCE: PF523P2
 ; CURRENT APPLICATION NUMBER: US/10/293,418
 ; CURRENT FILING DATE: 2002-11-27
 ; PRIOR APPLICATION NUMBER: 60/331,469
 ; PRIOR FILING DATE: 2001-11-16
 ; PRIOR APPLICATION NUMBER: 60/340,817
 ; PRIOR FILING DATE: 2001-12-19
 ; PRIOR APPLICATION NUMBER: 09/880,748
 ; PRIOR FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: 60/293,499
 ; PRIOR FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: 60/277,379
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/276,248
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/240,816
 ; PRIOR FILING DATE: 2000-10-17
 ; PRIOR APPLICATION NUMBER: 60/212,210

; PRIOR FILING DATE: 2000-06-16
 ; NUMBER OF SEQ ID NOS: 3247
 ; SEQ ID NO 2065
 ; LENGTH: 249
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-293-418-2065

Query Match 100.0%; Score 58; DB 15; Length 249;
 Best Local Similarity 100.0%; Pred. No. 0.037;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDLSSEFL 11
 |||||
 Db 228 AAMDLSSEFL 238

RESULT 30
 US-09-880-748-1309
 ; Sequence 1309, Application US/09880748
 ; Publication No. US20030059937A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 ; FILE REFERENCE: PF523
 ; CURRENT APPLICATION NUMBER: US/09/880,748
 ; CURRENT FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: 60/212,210
 ; PRIOR FILING DATE: 2000-06-15
 ; PRIOR APPLICATION NUMBER: 60/240,816
 ; PRIOR FILING DATE: 2000-10-17
 ; PRIOR APPLICATION NUMBER: 60/276,248
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/277,379
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/293,499
 ; PRIOR FILING DATE: 2001-05-25
 ; NUMBER OF SEQ ID NOS: 3239
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1309
 ; LENGTH: 251
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-880-748-1309

Query Match 100.0%; Score 58; DB 10; Length 251;
 Best Local Similarity 100.0%; Pred. No. 0.038;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDLSSEFL 11
 |||||
 Db 230 AAMDLSSEFL 240

RESULT 31
 US-09-880-748-1671
 ; Sequence 1671, Application US/09880748
 ; Publication No. US20030059937A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 ; FILE REFERENCE: PF523
 ; CURRENT APPLICATION NUMBER: US/09/880,748
 ; CURRENT FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: 60/212,210
 ; PRIOR FILING DATE: 2000-06-15
 ; PRIOR APPLICATION NUMBER: 60/240,816
 ; PRIOR FILING DATE: 2000-10-17
 ; PRIOR APPLICATION NUMBER: 60/276,248
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/277,379
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/293,499

;; PRIOR FILING DATE: 2001-05-25
;; NUMBER OF SEQ ID NOS: 3239
;; SOFTWARE: Patentin Ver. 2.0
;; SEQ ID NO 1671
;; LENGTH: 251
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-880-748-1671

Query Match 100.0%; Score 58; DB 10; Length 251;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDSLSEFL 11
Db 230 AAMDSLSEFL 240

RESULT 32
US-09-880-748-1809
; Sequence 1809, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1809
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1809

Query Match 100.0%; Score 58; DB 10; Length 251;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDSLSEFL 11
Db 230 AAMDSLSEFL 240

RESULT 33
US-10-293-418-1309
; Sequence 1309, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25

;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; PRIOR APPLICATION NUMBER: 60/212,210
;; PRIOR FILING DATE: 2000-06-16
;; NUMBER OF SEQ ID NOS: 3247
;; SEQ ID NO 1309
;; LENGTH: 251
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-293-418-1309

Query Match 100.0%; Score 58; DB 15; Length 251;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDSLSEFL 11
Db 230 AAMDSLSEFL 240

RESULT 34
US-10-293-418-1671
; Sequence 1671, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1671
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1671

Query Match 100.0%; Score 58; DB 15; Length 251;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDSLSEFL 11
Db 230 AAMDSLSEFL 240

RESULT 35
US-10-293-418-1809
; Sequence 1809, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

```
FILE REFERENCE: PF523p2
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1809
LENGTH: 251
TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-418-1809

Query Match
Best Local Similarity 100.0%; Score 58; DB 15; Length 251;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDLSSEFL 11
|||||
Db 230 AAMDLSSEFL 240

RESULT 36
US-09-880-748-1698
Sequence 1698, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1698
LENGTH: 252
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-1698

Query Match
Best Local Similarity 100.0%; Score 58; DB 10; Length 252;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDLSSEFL 11
|||||
Db 231 AAMDLSSEFL 241

RESULT 37
```

```
US-10-293-418-1698
Sequence 1698, Application US/10293418
Publication No. US20030223996A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523p2
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/212,210
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1698
LENGTH: 252
TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-418-1698

Query Match
Best Local Similarity 100.0%; Score 58; DB 15; Length 252;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDLSSEFL 11
|||||
Db 231 AAMDLSSEFL 241

RESULT 38
US-09-880-748-929
Sequence 929, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 929
LENGTH: 253
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-929

Query Match
Best Local Similarity 100.0%; Score 58; DB 10; Length 253;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 AAWDLSSEFL 11
 |||||
 Db 232 AAWDLSSEFL 242

RESULT 39
 US-09-880-748-935
 ; Sequence 935, Application US/09880748
 ; Publication No. US20030059937A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 ; FILE REFERENCE: PF523
 ; CURRENT APPLICATION NUMBER: US/09/880,748
 ; CURRENT FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: 60/212,210
 ; PRIOR FILING DATE: 2000-06-15
 ; PRIOR APPLICATION NUMBER: 60/240,816
 ; PRIOR FILING DATE: 2000-10-17
 ; PRIOR APPLICATION NUMBER: 60/276,248
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/277,379
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/293,499
 ; PRIOR FILING DATE: 2001-05-25
 ; NUMBER OF SEQ ID NOS: 3239
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 935
 ; LENGTH: 253
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-880-748-935

Query Match 100.0%; Score 58; DB 10; Length 253;
 Best Local Similarity 100.0%; Pred. No. 0.038;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAWDLSSEFL 11
 |||||
 Db 232 AAWDLSSEFL 242

RESULT 40
 US-09-880-748-939
 ; Sequence 939, Application US/09880748
 ; Publication No. US20030059937A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 ; FILE REFERENCE: PF523
 ; CURRENT APPLICATION NUMBER: US/09/880,748
 ; CURRENT FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: 60/212,210
 ; PRIOR FILING DATE: 2000-06-15
 ; PRIOR APPLICATION NUMBER: 60/240,816
 ; PRIOR FILING DATE: 2000-10-17
 ; PRIOR APPLICATION NUMBER: 60/276,248
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/277,379
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/293,499
 ; PRIOR FILING DATE: 2001-05-25
 ; NUMBER OF SEQ ID NOS: 3239
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 939
 ; LENGTH: 253
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-880-748-939

Query Match 100.0%; Score 58; DB 10; Length 253;
 Best Local Similarity 100.0%; Pred. No. 0.038;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAWDLSSEFL 11
 |||||
 Db 232 AAWDLSSEFL 242

Search completed: March 31, 2005, 12:46:10
 Job time : 61.5312 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 31, 2005, 11:51:19 ; Search time 15.6406 Seconds
(without alignments)
67.669 Million cell updates/sec

Title: US-10-614-959-15
Perfect score: 58
Sequence: 1 AAWDSLSRFL 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	74.1	98	2	S36048 Ig lambda chain -
2	43	74.1	129	2	S78058 Ig lambda chain pr
3	43	74.1	235	2	S25750 Ig lambda chain -
4	41	70.7	112	1	L1HUMM Ig lambda chain V-
5	40	69.0	95	2	S49571 Ig lambda chain pr
6	40	69.0	98	2	S36047 Ig lambda chain -
7	40	69.0	98	2	S36046 Ig lambda chain -
8	40	69.0	109	1	L1HUMA Ig lambda chain V-
9	40	69.0	117	2	S23627 Ig lambda chain pr
10	40	69.0	149	2	S23626 Ig lambda chain V
11	40	69.0	233	2	S25752 Ig lambda chain -
12	40	69.0	234	2	S25757 Ig lambda chain -
13	40	69.0	235	2	S25754 Ig lambda chain -
14	40	69.0	355	2	B87394 conserved hypotet
15	40	69.0	497	2	G95983 probable glycerol
16	40	69.0	502	2	S49113 hypothetical prote
17	40	69.0	4367	1	B54802 dynein heavy chain
18	39	67.2	110	2	S57428 Ig light chain V-J
19	39	67.2	112	2	D44151 Ig lambda chain V
20	39	67.2	130	2	S78057 Ig lambda chain pr
21	39	67.2	397	1	OKBOB2 protein kinase (EC
22	39	67.2	1995	2	T08166 dynein heavy chain
23	39	67.2	4344	1	A53489 hypothetical prote
24	38	65.5	210	2	G84751 hypothetical prote
25	38	65.5	329	2	T18622 hypothetical prote
26	38	65.5	423	2	S41389 probable serine/thr
27	38	65.5	443	2	T30619 outer membrane ush
28	38	65.5	842	2	B55853 ribonucleoside-dip
29	38	65.5	885	1	WMBY31

30	37.5	64.7	166	2	C83366 hypothetical prote
31	37	63.8	259	2	T40104 conserved hypotet
32	37	63.8	371	2	AH0147 outer membrane pro
33	37	63.8	395	2	T40102 conserved hypotet
34	37	63.8	476	2	H84228 thiamin biosynthes
35	37	63.8	644	2	F84698 probable thiamin b
36	37	63.8	655	2	A70931 probable PPE prote
37	37	63.8	857	2	B69798 hypothetical prote
38	37	63.8	1485	2	S23756 CFTF protein - Afr
39	36	62.1	184	1	IVHOA1 interferon alpha-1
40	36	62.1	184	1	IVHOA2 interferon alpha-1
41	36	62.1	184	1	IVHOA3 interferon alpha-1
42	36	62.1	184	1	IVHOA4 interferon alpha-1
43	36	62.1	227	2	F81855 insertion element
44	36	62.1	280	2	C98208 probable sugar tra
45	36	62.1	280	2	AF3078 hypothetical prote

ALIGNMENTS

RESULT 1
S36048
Ig lambda chain - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
C/Accession: S36048; S36049
R.Williams, S.C.
Submitted to the EMBL Data Library, April 1993
A/Reference number: S36046
A/Accession: S36048
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-98 <MTL>
A/Cross-references: EMBL:Z22189; NID:g312294; PIDN:CAA80199.1; PID:g312295; EMBL:Z22190
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/15-91/Domain: immunoglobulin homology <IMW>

Query Match 74.1%; Score 43; DB 2; Length 98;
Best Local Similarity 100.0%; Pred.No. 1.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDSLS 8
Db 90 AAWDSLS 97

RESULT 2
S78058
Ig lambda chain precursor V-J region (clone mAb 67VL) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C/Accession: S78058; S23723
R.Harindranath, N.
Submitted to the EMBL Data Library, August 1990
A/Reference number: S78051
A/Accession: S78058
A/Molecule type: mRNA
A/Residues: 1-129 <HAR>
A/Cross-references: EMBL:X54446; NID:g37923; PIDN:CAA38313.1; PID:g930121
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: immunoglobulin
F/1-18/Domain: signal sequence (fragment) #status predicted <SIG>

F:19-129/Product: Ig lambda chain (fragment) #status predicted <MAT>
F:33-109/Domain: immunoglobulin homology <IMM>

Query Match 74.1%; Score 43; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDLS 8
|||||
DB 108 AAMDLS 115

RESULT 3

S25750
Ig lambda chain - human
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S25750
R/Contributor: G.; Kiobeck, H.G.
Bur. J. Immunol. 21, 1513-1522, 1991
A/Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A/Reference number: S16439; MUID:91257162; PMID:1904362
A/Accession: S25750
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-235 <COM>
A/Cross-references: EMBL:X57815; NID:G33729; PIDN:CAA0592.1; PID:G33730
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:150-218/Domain: immunoglobulin homology <IMM>

Query Match 74.1%; Score 43; DB 2; Length 235;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDLS 8
|||||
DB 109 AAMDLS 116

RESULT 4

LIHUM
Ig lambda chain V-I region (Mem) - human
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C/Accession: A25479
R/Mihaesco, E.; Roy, J.P.; Congy, N.; Peran-Rivat, L.; Mihaesco, C.
Eur. J. Biochem. 150, 349-357, 1985
A/Title: The amino acid sequence of a lambda light chain presenting abnormal physicochem
A/Reference number: A25479; MUID:85257662; PMID:2410269
A/Accession: A25479
A/Molecule type: protein
A/Residues: 1-112 <MIH>
A/Cross-references: UNIPROT:P06887
A/Note: residues 33-36 and some of the sequenced peptides were positioned by homology
C/Comment: The C region of this chain has the Mgr+ and Kern+ markers.
C/Genetics:
A/Gene: GDB:IGLV@
A/Cross-references: GDB:119342; OMIM:147240
A/Map position: 22q11.2-22q11.2
C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin; pyroglyutamic acid
F:15-92/Domain: immunoglobulin homology <IMM>
F:1/Modified site: pyroglutamic acid (Gln) #status experimental
F:22-90/Disulfide bonds: #status predicted

Query Match 70.7%; Score 41; DB 1; Length 112;
Best Local Similarity 63.6%; Pred. No. 3.4;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAMDLS EFL 11

|||||
DB 91 AAMDLS LGIV 101

RESULT 5
S49571
Ig lambda chain precursor V region - human (fragment)

C/Species: Homo sapiens (man)
C/Date: 05-Mar-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999
C/Accession: S49571
R/Giachino, C.; Padovan, B.; Lanzavecchia, A.
submitted to the EMBL Data Library, November 1994
A/Description: k+l+ dual receptor B cells are present in the human peripheral repertoire
A/Reference number: S49571
A/Accession: S49571
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-95 <GIA>

A/Cross-references: EMBL:Z46625; NID:G575259; PIDN:CAA6595.1; PID:G575260
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

Query Match 69.0%; Score 40; DB 2; Length 95;
Best Local Similarity 87.5%; Pred. No. 4.2;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDLS 8
|||||
DB 76 AAMDLS 83

RESULT 6

S36047
Ig lambda chain - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
C/Accession: S36047
R/Williams, S.C.
submitted to the EMBL Data Library, April 1993
A/Reference number: S36046
A/Accession: S36047
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-98 <WIL>
A/Cross-references: EMBL:Z22188; NID:G312291; PIDN:CAA60198.1; PID:G312292
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:15-91/Domain: immunoglobulin homology <IMM>

Query Match 69.0%; Score 40; DB 2; Length 98;
Best Local Similarity 87.5%; Pred. No. 4.4;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDLS 8
|||||
DB 90 AAMDLS 97

RESULT 7

S36046
Ig lambda chain - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S36046
R/Williams, S.C.
submitted to the EMBL Data Library, April 1993
A/Reference number: S36046
A/Accession: S36046
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-98 <WIL>

A/Cross-references: EMBL:Z22187; NID:G312312; PIDN:CAA60197.1; PID:G312313
C/Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 69.0%; Score 40; DB 2; Length 98;
Best Local Similarity 87.5%; Pred. No. 4.4;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAMDLSL 8
Db 90 AAMDLSLN 97

RESULT 8

Ig lambda chain V-I region (Vah) - human

C:Species: Homo sapiens (man)
C>Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 03-Jul-2004
C:Accession: A01967

R:Takehashi, Y.; Takehashi, N.; Tetaert, D.; Putnam, F.W.

Proc. Natl. Acad. Sci. U.S.A. 80, 3686-3690, 1983

A:Title: Complete covalent structure of a human immunoglobulin D: sequence of the lambda

A:Reference number: A01967; MUID:83221661; PMID:6407018

A:Accession: A01967

A:Molecule type: protein

A:Residues: 1-109 <TAK>

A:Cross-references: UNIPROT:P04208

C:Genetics:

A:Gene: GDB:IGLV@

A:Cross-references: GDB:119342; OMIM:147240

A:Map position: 22q11.2-22q11.2

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-91/Region: V segment

F:15-91/Domain: immunoglobulin homology <IMM>

F:98-109/Region: J segment

F:22-89/Disulfide bonds: #status predicted

Query Match 69.0%; Score 40; DB 1; Length 109;
Best Local Similarity 80.0%; Pred. No. 4.9;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAMDLSL 10
Db 90 AAMDLSLWF 99

RESULT 9

Ig lambda chain precursor - human

C:Species: Homo sapiens (man)

C>Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C:Accession: S23627

R:Ole, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Defetos, M.; Kozin, F.; Carson, D.A.;

J. Exp. Med. 175, 831-842, 1992

A:Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from

A:Reference number: S23627; MUID:92156804; PMID:1740665

A:Accession: S23627

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-117 <OLB>

A:Cross-references: EMBL:X59707; NID:G34426; PIDN:CAA42228.1; PID:G34427

C:Genetics:

A:Introns: 16/1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-110/Domain: immunoglobulin homology <IMM>

Query Match 69.0%; Score 40; DB 2; Length 117;
Best Local Similarity 87.5%; Pred. No. 5.3;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAMDLSL 8

Db 109 AAMDLSLN 116

RESULT 10

Ig lambda chain V region - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000

C:Accession: S23626

R:Ole, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Defetos, M.; Kozin, F.; Carson, D.A.;

J. Exp. Med. 175, 831-842, 1992

A:Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from

A:Reference number: S23623; MUID:92156804; PMID:1740665

A:Accession: S23626

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-149 <OLB>

A:Cross-references: EMBL:X59706; NID:G34204; PIDN:CAA42227.1; PID:G34205

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-110/Domain: immunoglobulin homology <IMM>

Query Match 69.0%; Score 40; DB 2; Length 149;
Best Local Similarity 87.5%; Pred. No. 6.9;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAMDLSL 8
Db 109 AAMDLSLN 116

RESULT 11

Ig lambda chain - human

C:Species: Homo sapiens (man)

C>Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S25752

R:Combratio, G.; Klobeck, H.G.

Eur. J. Immunol. 21, 1513-1522, 1991

A:Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin

A:Reference number: S16439; MUID:91257162; PMID:1904362

A:Accession: S25752

A:Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-233 <COM>

A:Cross-references: EMBL:X57817; NID:G33733; PIDN:CAA40954.1; PID:G33734

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:148-216/Domain: immunoglobulin homology <IMM>

Query Match 69.0%; Score 40; DB 2; Length 233;
Best Local Similarity 87.5%; Pred. No. 11;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAMDLSL 8
Db 107 AAMDLSLN 114

RESULT 12

Ig lambda chain - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S25757

R:Combratio, G.; Klobeck, H.G.

Eur. J. Immunol. 21, 1513-1522, 1991

A:Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin

A:Reference number: S16439; MUID:91257162; PMID:1904362

A:Accession: S25757

A:Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-234 <COM>
A:Cross-references: EMBL:X57822; NID:g33743; PIDD:CAA40959.1; PID:g33744
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:149-217/Domain: immunoglobulin homology <IMM>

Query Match 69.0%; Score 40; DB 2; Length 234;
Best Local Similarity 87.5%; Pred. No. 11;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAMDSTLS 8
 |||||
Db 108 AAMDSTLS 115

RESULT 13
IG lambda chain - human (fragment)
S25754
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S25754
R:Combiarto, G.; Klobeck, H.G.
Bur. J. Immunol. 21, 1513-1522, 1991
A:Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lat
A:Reference number: S16439; MUID:91257162; PMID:1904362
A:Accession: S25754
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-235 <COM>
A:Cross-references: EMBL:X57819; NID:g33737; PIDD:CAA40956.1; PID:g33738
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:150-218/Domain: immunoglobulin homology <IMM>

Query Match 69.0%; Score 40; DB 2; Length 235;
Best Local Similarity 87.5%; Pred. No. 11;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAMDSTLS 8
 |||||
Db 108 AAMDSTLS 115

RESULT 14
conserved hypothetical protein CC1169 [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: E87394
R:Nierman, W.C.; Feldblym, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kjol
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: E87394
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-355 <STO>
A:Cross-references: UNIPROT:Q9A925; GB:AEO05673; NID:g13422491; PIDD:AAK23153.1; GSPDB:C
C:Genetic8;
A:Gene: CC1169

Query Match 69.0%; Score 40; DB 2; Length 355;
Best Local Similarity 87.5%; Pred. No. 18;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAMDSTLS 8
 |||||
Db 138 SAMDSTLS 145

RESULT 15

G95983
Probable glycerol kinase (EC 2.7.1.30) [imported] - Sinorhizobium meliloti (strain 1021)
C:Species: Sinorhizobium meliloti
C>Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C:Accession: G95983
R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrester, J.; Chain, P.; Vorholter, F.J.; Hernan
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A:Title: The complete sequence of the 1,683-kb pSymb megaplasmid from the N2-fixing endo
A:Reference number: A95842; MUID:21396508; PMID:11481431
A:Accession: G95983
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-497 <KUR>
A:Cross-references: UNIPROT:O86033; GB:A4591985; PIDD:CA49535.1; PID:g15141022; GSPDB:G
A:Experimental source: strain 1021, megaplasmid pSymb
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Apola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: g1pk; SMD21009
A:Genome: plasmid
C:Superfamily: xylokinase
C:Keywords: phosphotransferase

Query Match 69.0%; Score 40; DB 2; Length 497;
Best Local Similarity 70.0%; Pred. No. 26;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 AAMDSTSEFL 11
 |||||
Db 197 AAMDSTSEFL 206

RESULT 16
S49113
hypothetical protein 2 - Microcystis aeruginosa
C:Species: Microcystis aeruginosa
C>Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C:Accession: S49113
R:Juerchott, K.; Boerner, T.
submitted to the EMBL Data Library, November 1993
A:Description: Sequence of the cyanobacterial plasmid pMA1 from Microcystis aeruginosa H
A:Reference number: S49112
A:Accession: S49113
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-502 <JNB>
A:Cross-references: UNIPROT:Q48904; EMBL:Z28337; NID:g509352; PIDD:CAA82191.1; PID:g5093
C:Superfamily: Microcystis aeruginosa hypothetical protein 2

Query Match 69.0%; Score 40; DB 2; Length 502;
Best Local Similarity 60.0%; Pred. No. 26;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 AAMDSTSEFL 11
 |||||
Db 434 SWEDELAFL 443

RESULT 17
B54802
dynein heavy chain, cytosolic - Neurospora crassa
N:Contains: dynein ATPase (EC 3.6.4.2)
C:Species: Neurospora crassa
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: B54802
R:Pliemann, M.; Minke, P.F.; Tinsley, J.H.; Bruno, K.S.

J. Cell Biol. 127, 139-149, 1994
 A:Title: Cytoplasmic dynein and actin-related protein Arp1 are required for normal nucleocytoplasmic transport
 A:Reference number: A54802; MUID:95014704; PMID:7929559
 A:Accession: B54802
 A:Molecule type: DNA
 A:Residues: 1-4367 <PLA>
 A:Cross-references: UNIPROT:P45443; GB:L31504; NID:G473489; PDB:AAA64908.1; PID:G473490
 C:Genetics:
 A:Introns: 104/1; 4205/3
 C:Superfamily: dynein heavy chain, cytosolic
 C:Keywords: ATP; heterotetramer; hydrolyase; microtubule binding; nucleotide binding; P-1
 F:1943-1950/Region: nucleotide-binding motif A (P-loop)
 F:2240-2247/Region: nucleotide-binding motif A (P-loop)
 F:2605-2612/Region: nucleotide-binding motif A (P-loop)
 F:2947-2954/Region: nucleotide-binding motif A (P-loop)
 F:1949/Binding site: ATP (Lys) #status predicted
 F:2246/Binding site: ATP (Lys) #status predicted
 F:2611/Binding site: ATP (Lys) #status predicted
 F:2953/Binding site: ATP (Lys) #status predicted

Query Match 69.0%; Score 40; DB 1; Length 4367;
 Best Local Similarity 66.7%; Pred. No. 2.8e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AAMDLSRF 10
 |||||
 Db 455 AAMDSEIKF 463

RESULT 18
 S57428
 Ig light chain V-J region - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 10-Oct-1995 #sequence revision 17-Nov-1995 #text_change 21-Jan-2000
 C:Accession: S57428
 R:Paterson, G.; Wilson, G.; Kennedy, P.G.E.; Willison, H.J.
 submitted to the EMBL Data Library, June 1995
 A:Description: Analysis of anti-GM1 ganglioside IGM antibodies cloned from motor neurons
 A:Reference number: S57408
 A:Accession: S57428
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-110 <PAR>
 A:Cross-references: EMBL:X87690; NID:G871271; PDB:CAA61141.1; PID:G871272
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:15-91/Domain: immunoglobulin homology <IMM>

Query Match 67.2%; Score 39; DB 2; Length 110;
 Best Local Similarity 100.0%; Pred. No. 7.4;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAMDLSL 7
 |||||
 Db 90 AAMDLSL 96

RESULT 19
 D44151
 Ig lambda chain V region (BO-12) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 27-Jun-1994 #sequence revision 27-Jun-1994 #text_change 21-Jan-2000
 C:Accession: D44151
 R:Zebedes, S.L.; Barbash, C.F.; Hom, Y.L.; Caochien, R.H.; Graff, R.; Degraw, J.; Pys
 Proc. Natl. Acad. Sci. U.S.A. 89, 3175-3179, 1992
 A:Title: Human combinatorial antibody libraries to hepatitis B surface antigen.
 A:Reference number: A44151; MUID:92228746; PMID:1373487
 A:Accession: D44151
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-112 <ZEB>
 A>Note: nucleotide translation is not given
 C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin
 F:14-90/Domain: immunoglobulin homology <IMM>

Query Match 67.2%; Score 39; DB 2; Length 112;
 Best Local Similarity 100.0%; Pred. No. 7.6;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAMDLSL 7
 |||||
 Db 89 AAMDLSL 95

RESULT 20
 S78057
 Ig lambda chain precursor V-J region (clone mAb 61VL) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 19-Nov-1997 #sequence revision 05-Dec-1997 #text_change 23-Jul-1999
 C:Accession: S78057; S23722
 R:Harindranath, N.
 submitted to the EMBL Data Library, August 1990
 A:Reference number: S78051
 A:Accession: S78057
 A:Molecule type: mRNA
 A:Residues: 1-130 <HAR>
 A:Cross-references: EMBL:X54438; NID:G37920; PDB:CAA8307.1; PID:G37921
 R:Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burnstero, S.E.; Wilder, R.L.; Norkins
 Int. Immunol. 3, 865-875, 1991
 A:Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h
 patient.
 A:Reference number: S23716; MUID:92031262; PMID:1718404
 A:Accession: S23722
 A:Molecule type: mRNA
 A:Residues: 20-130 <HAM>
 A:Cross-references: EMBL:X54438
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-130/Product: Ig lambda chain (fragment) #status predicted <MAT>
 F:34-110/Domain: immunoglobulin homology <IMM>

Query Match 67.2%; Score 39; DB 2; Length 130;
 Best Local Similarity 87.5%; Pred. No. 8.9;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAMDLSL 8
 |||||
 Db 109 AAMDLSL 116

RESULT 21
 OKR082
 protein kinase (EC 2.7.1.37), CAMP-dependent, beta-2 catalytic chain - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #text_change 09-Jul-2004
 C:Accession: A23716
 R:Wiemann, S.; Kinzel, V.; Peyerin, W.
 J. Biol. Chem. 266, 5140-5146, 1991
 A:Title: Isoform Cbeta2, an unusual form of the bovine catalytic subunit of CAMP-depend
 A:Reference number: A23716; MUID:91161607; PMID:2002051
 A:Accession: A23716
 A:Molecule type: mRNA
 A:Residues: 1-397 <MIE>
 A:Cross-references: UNIPROT:P24256; GB:M60482; NID:G162786; PDB:AAA30424.1; PID:G162787
 C:Comment: The inactive enzyme contains two regulatory chains and two catalytic chains.
 C:Two types found in mammalian tissue are distinguished by having either type I or type
 C:Comment: Both alpha and beta catalytic chains are found in many tissues, with the alpha
 C:Superfamily: kinase-related transforming protein; protein kinase homology
 C:Keywords: alternative splicing; ATP; CAMP binding; heterotetramer; magnesium; phospho
 F:2-397/Product: protein kinase, CAMP-dependent, beta-2 catalytic chain #status predicte
 F:88-344/Domain: protein kinase homology <KIN>
 F:96-104/Region: protein kinase ATP-binding motif
 F:101,102,166,174,217,230/Binding site: Mg-ATP (Phe, Gly, Glu, Glu, Thr) #status pr
 F:119,138,213,215/Active site: Lys, Glu, Asp, Lys #status predicted

F:218.231/Binding site: magnesium (Asn, Arg) #status predicted
F:244/Binding site: phosphate (Thr) (covalent) #status predicted
F:38/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 67.2%; Score 39; DB 1; Length 397;
Best Local Similarity 63.6%; Pred. No. 31;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 AAMDLSLEFL 11
|||:|
Db 56 ALMDRSMKEFL 66

RESULT 22

T08166
Probable membrane protein 1995 - Chlamydomonas reinhardtii chloroplast
C:Species: chloroplast Chlamydomonas reinhardtii
C:Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 09-Jul-2004
C:Accession: T08166; A24829
R:Boudreau, E.; Tumele, M.; Goldschmidt-Clermont, M.; Rochaix, J.D.; Sivan, S.; Michaela
Mol. Gen. Genet. 253, 649-653, 1997
A:Title: A large unidentified open reading frame (ORF1995) in Chlamydomonas reinhardtii
A:Reference number: Z16392; MUID:97218038; PMID:9065699
A:Accession: T08166

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1995 <BOU>
A:Cross-references: UNIPROT:P36495; EMBL:X92726; NID:g1054719; PID:CAA63385.1; PID:g105
R:Moessner, J.P.; Gillham, N.W.; Boynton, J.E.
Gene 44, 17-28, 1986

A:Title: The sequence of the chloroplast atpB gene and its flanking regions in Chlamydom
A:Reference number: A24829; MUID:87031585; PMID:2876928
A:Accession: A24829

A:Molecule type: DNA
A:Residues: 1925-1995 <MOB>
A:Cross-references: GB:M13704; NID:g33666; PID:AAA84144.1; PID:g895614
A>Note: the authors translated the codon GAA for residue 1957 as Gly
A:Genetics:
A:Genome: chloroplast
C:Keywords: chloroplast; membrane protein

Query Match 67.2%; Score 39; DB 2; Length 1995;
Best Local Similarity 54.5%; Pred. No. 1.8e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 AAMDLSLEFL 11
|||:|
Db 1581 AGWDESLKFLV 1591

RESULT 23

A53489
dynein heavy chain, cytosolic - Emeritella nidulans
N:Contains: dynein ATPase (RC 3.6.4.2)
C:Species: Emeritella nidulans, Aspergillus nidulans
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A53489

R:Xiang, X.; Beckwith, S.M.; Morris, N.R.
Proc. Natl. Acad. Sci. U.S.A. 91, 2100-2104, 1994

A:Title: Cytoplasmic dynein is involved in nuclear migration in Aspergillus nidulans.
A:Reference number: A53489; MUID:94181539; PMID:8134356

A:Accession: A53489

A:Molecule type: DNA

A:Residues: 1-4344 <XIA>

A:Cross-references: UNIPROT:P45444; GB:U03904; NID:g451538; PID:AAA18338.1; PID:g451539

C:Superfamily: dynein heavy chain, cytosolic

C:Keywords: ATP; heterotrimer; hydrolase; microtubule binding; nucleotide binding; P-1

F:1933-1940/Region: nucleotide-binding motif A (P-loop)

F:2228-2235/Region: nucleotide-binding motif A (P-loop)

F:2592-2599/Region: nucleotide-binding motif A (P-loop)

F:2932-2939/Region: nucleotide-binding motif A (P-loop)

F:1939/Binding site: ATP (Lys) #status predicted

F:2234/Binding site: ATP (Lys) #status predicted

F:2598/Binding site: ATP (Lys) #status predicted
F:2938/Binding site: ATP (Lys) #status predicted

Query Match 67.2%; Score 39; DB 1; Length 4344;
Best Local Similarity 75.0%; Pred. No. 4.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 WDSLSLEFL 10
|||:|
Db 446 WDDNLSKEFL 453

RESULT 24

G84751

hypothetical protein At2g34050 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C:Accession: G84751

R:Liu, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanKien, S.E.; Umayam, L.; Tallon, L.

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617157

A:Accession: G84751

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-210 <STO>

A:Cross-references: UNIPROT:O22958; GB:AE002093; NID:g2342725; PID:AA67623.1; GSPDB:GN

C:Genetics:
A:Gene: At2g34050

A:Map position: 2

Query Match 65.5%; Score 38; DB 2; Length 210;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 WDSLSLEFL 11
|||:|
Db 99 WDDVLSKFL 107

RESULT 25

T18622
hypothetical protein AH6.7 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T18622

R:Berk, M.

submitted to the EMBL Data Library, January 1995

A:Reference number: Z18998

A:Accession: T18622

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-329 <WTL>

A:Cross-references: UNIPROT:Q09205; EMBL:Z48009; PID:CAA68086.1; GSPDB:GN00020; CESP:AH

A:Experimental source: clone AH6

C:Genetics:
A:Gene: CESP:AH6.7

A:Map position: 2

A:introns: 217/2; 279/3

C:Superfamily: Caenorhabditis elegans hypothetical protein AH6.4

Query Match 65.5%; Score 38; DB 2; Length 329;
Best Local Similarity 75.0%; Pred. No. 37;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 WDSLSLEFL 10
|||:|
Db 164 WDDPLSLEY 171

RESULT 26

S41289
Hypothetical protein ORF-S - Chlamydomonas reinhardtii
C/Species: Chlamydomonas reinhardtii
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C/Accession: S41289
R/Sivan, S.; Michaels, A.
submitted to the EMBL Data Library, December 1993
A/Reference number: S41289
A/Accession: S41289
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-423 <STV>
A/Cross-references: UNIPROT:P36495; EMBL:X76934; NID:G440398; PID:G440399
C/Keywords: chloroplast

Query Match 65.5%; Score 38; DB 2; Length 423;
Best Local Similarity 54.5%; Pred. No. 49;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAMDLSSEFL 11
| | | | |
DB 9 AGWDESLRKFV 19

RESULT 27
T30619
probable serine/threonine-specific protein kinase 17L - Molluscum contagiosum virus 1
N/Alternate names: MCO17L
C/Species: Molluscum contagiosum virus 1
C/Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 27-Oct-2003
R/Senkevich, T.G.; Bugert, J.J.; Staler, J.R.; Koonin, E.V.; Darai, G.; Moss, B.
Science 273, 813-816, 1996
A/Title: Genome sequence of a human tumorigenic poxvirus: Prediction of specific host re
A/Reference number: Z20876; MUID:96325459; PMID:8670425
A/Accession: T30619
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-443 <SEN>
A/Cross-references: EMBL:U60315; NID:G1491943; PIDN:AAC55145.1; PID:G1491960
C/Genetics: MCO17L
A/Note: MCO17L
C/Superfamily: Ser/Thr protein kinase, poxviridae type
C/Keywords: serine/threonine-specific protein kinase

Query Match 65.5%; Score 38; DB 2; Length 443;
Best Local Similarity 63.6%; Pred. No. 52;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAMDLSSEFL 11
| | | | |
DB 390 AAMSKALSEFL 400

RESULT 28
B55853
outer membrane usher protein aggc precursor - Escherichia coli
C/Species: Escherichia coli
C/Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 09-Jul-2004
C/Accession: B55853
R/Savarino, S.J.; Fox, P.; Vilkang, D.; Nataro, J.P.
J. Bacteriol. 176, 4949-4957, 1994
A/Title: Identification and characterization of a gene cluster mediating enteroaggregati
A/Reference number: A55853; MUID:94327462; PMID:7914189
A/Accession: B55853
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-842 <SAV>
A/Cross-references: UNIPROT:P46005; GB:U12894; NID:G531396; PIDN:AAA57452.1; PID:G531396
C/Genetics: aggc
A/Gene: aggc
C/Superfamily: outer membrane usher protein fimb
C/Keywords: membrane protein

Query Match 65.5%; Score 38; DB 2; Length 842;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 WDDSLSEFL 11
| | | | |
DB 161 WDDGISAFV 169

RESULT 29
XMBY2L
ribonucleoside-diphosphate reductase (EC 1.17.4.1) 3 large chain - Yeast (Saccharomyces
N/Alternate names: protein YIL066c; ribonucleotide reductase regulatory chain 3
C/Species: Saccharomyces cerevisiae
C/Date: 30-Sep-1991 #sequence_revision 19-Jul-1996 #text_change 21-Jul-2000
C/Accession: S48413; S12066; B35845; A35930
R/Smith, V.
submitted to the EMBL Data Library, September 1994
A/Reference number: S48407
A/Accession: S48413
A/Molecule type: DNA
A/Residues: 1-885 <SMI>
A/Cross-references: EMBL:Z38060; NID:G557796; PIDN:CAAB6157.1; PID:G557803; GSPDB:GN0000
R/Yagle, K.; McNetee, K.
Mol. Cell. Biol. 10, 5553-5557, 1990
A/Title: The DNA damage-inducible gene DIN1 of Saccharomyces cerevisiae encodes a regula
A/Reference number: A35930; MUID:90377250; PMID:2204819
A/Accession: S12066
A/Molecule type: DNA
A/Residues: 17-142, 'TRY', 147-227, 'L', 229-262, 'VLS', 267-302, 'TRVTRD', 315, 'V', 317, 'S', 319
A/Cross-references: EMBL:M58012; NID:G171398; PIDN:AAA34569.1; PID:G171399
R/Elledge, S.J.; Davis, R.W.
Genes Dev. 4, 740-751, 1990
A/Title: Two genes differentially regulated in the cell cycle and by DNA-damaging agents
A/Reference number: A35845; MUID:90337312; PMID:2199320
A/Accession: B35845
A/Status: nucleic acid sequence not shown; not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 17-36, 'VL', 39-52, 'F', 54-73, 'T', 75-84, 'H', 86-98, 'T', 100-117, 'TGR', 668-691, 'L'
C/Genetics: SGD:RMN3; DIN1; MIPS:YIL066c
A/Gene: SGD:RMN3; DIN1; MIPS:YIL066c
A/Cross-references: SGD:S0001328; MIPS:YIL066c
A/Map position: 9L
C/Superfamily: herpesvirus ribonucleoside-diphosphate reductase large chain
C/Keywords: deoxyribonucleotide biosynthesis; heterotetramer; oxidoreductase; redox-acti
F/234-459,880-883/Distillate bonds: redox-active #status predicted
F/442,446/Active site: Asn, Glu #status predicted
F/444/Active site: Cys (cysteine thiol radical intermediate) #status predicted

Query Match 65.5%; Score 38; DB 1; Length 885;
Best Local Similarity 55.6%; Pred. No. 1.1e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 WDDSLSEFL 11
| | | | |
DB 671 WDDSKQYV 679

RESULT 30
C83366
Hypothetical protein PA2226 [imported] - Pseudomonas aeruginosa (strain PA01)
C/Species: Pseudomonas aeruginosa
C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C/Accession: C83366
R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kaab, A.; Larbig, K.; Lam,
.; Lohy, S.; Olson, M.V.
Nature 406, 959-964, 2000
A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A/Reference number: A82950; MUID:20437337; PMID:10984043
A/Accession: C83366
A/Status: preliminary

A;Molecule type: DNA
A;Residues: 1-166 <STO>
A;Cross-references: UNIPROT:Q911P3; GB:AE004649; GB:AE004091; NID:93948246; PIDD:AA0561
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA2226

Query Match	64.7%	Score 37.5;	DB 2;	Length 166;
Best Local Similarity	50.0%	Pred. No. 22;		
Matches	8;	Conservative	3;	Mismatches 0;
				Indels 5;
				Gaps 1
QY	1	AAMD-----DSISREI	11	
			:: :	
Db	107	AAMDASVAMDNISFV	122	

RESULT 31
T40104
conserved hypothetical protein SPBC2D10.01c - fission yeast (*Schizosaccharomyces pombe*)
C|Species: Schizosaccharomyces pombe
C|Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C|Accession: T40104
R|Wood, V.; Rajandream, M.A.; Barrell, B.G.; Taylor, K.; Harris, D.
submitted to the EMBL Data Library, September 1998
A|Reference number: Z11906
A|Accession: T40104
A|Status: preliminary; translated from GB/EMBL/DBJ
A|Molecule type: DNA
A|Residues: 1-259 <MOO>
A|Cross-references: UNIPROT:Q9UMJ3; EMBL:AL031788; PIDD:CAA21159.1; GSPDB:GN00067; SPDB:
A|Experimental source: strain 972h-, cosmid C2D10
C|Genetics:
A|Gene: SPDB:SPBC2D10.01c
A|Map position: 2

Query Match	63.8%	Score 37	DB 2	Length 259
Best Local Similarity	66.7%	Pred. No. 43		
Matches	6	Conservative	1	Mismatches 2
				Indels 0
				Gaps 0
Qy	3	WDDSLSEFL	11	.
db	9	WDDSLKEFI	17	

RESULT 32
AH0147
outer membrane protein C2 ompC2 [imported] - *Yersinia pestis* (strain CO92)
C:Species: *Yersinia pestis*
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C:Accession: AH0147
R:Perkhill, J.; Wren, B.W.; Thomson, N.R.; Tlhalali, R.W.; Holden, M.T.G.; Prentice, M.B.
delo-Tarazaga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
Hill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett,
Nature 413, 523-527, 2001
A:Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AH0147
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 15371 <KUR>
A:CROSS-references: UNIPROT:Q8ZGS6; GB:AL590842; PTDN:CAC90043.1; PTD:G15979264; GSPDB:G:
C:Genetics:
A:Gene: ompC2
A:Superfamily: outer membrane protein phoB

	63.8%;	Score 37;	DB 2;	Length 377;
Query Match	Similarity	Pred.	No. 64;	
Best Local	70.0%;			
Matches	7;	Conservative	0;	Mismatches
			3;	Indels
				Gaps
				0; 0;
QY	1 AAWDDSLSEP	10		
Db	124 AAWDTMLPEF	133		

RESULT 33
 T40102
 conserved hypothetical protein SPBC2A9.11c - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 J:Accession: T40102
 R:Barrell, B.G.; Rajandream, M.A.; Lyne, M.; Skelton, J.; Churcher, C.
 submitted to the EMBL Data Library, March 1999
 A:Reference number: Z21905
 A:Accession: T40102
 A:Status: preliminary; translated from GB/EMBL/DBD
 A:Molecule type: DNA
 A:Residues: 1-395 <BAR>
 A:Cross-references: UNIPROT:Q9UUM3; EMBL:AL049495; PIDD:CAAB39853.1; GSPDB:GN00066; SPDB:
 A:Experimental source: strain 972h-, cosmid c2A9_3p
 C:Genetics:
 A:Gene: SPDB:SPBC2A9.11c
 A:Map position: 1
 A:introns: 216/3; 260/1

[illegible]

```

RESULT 34
H84228      thiamin biosynthesis protein [imported] - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C:Date: 02-Feb-2001 #sequence, revision 02-Feb-2001 #text, change 09-Jul-2004
C/NG: W.V.; Kennedy, S.P.; Mahairs, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.
C/Accession: H84228
J:Leithner, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablon
Jung, K.H.; Alam, M.; Freltas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; Li
A>Title: Genome sequence of Halobacterium species NRC-1.
A:Reference number: A84160; MUID:20504483; PMID:11016950
A:Accession: H84228
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1476 <STO>
C:Cross-references: UNIPROT:Q9HRG2; GB:AE004437; NID:g10580294; PIDN:AAG19196.1; GSPDB:G
C/Genetics:
A:Gene: thic
C/Superfamily: thiamin biosynthesis protein thic

Query Match      63.8%; Score 37; DB 2; Length 476;
Best Local Similarity 85.7%; Pred. NO. 84;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY      3 MDDSLSE 9
      |||:||||
db      363 MDDALSH 369

```

	Query Match	63.8%;	Score 37;	DB 2;	Length 476;
	Best Local Similarity	85.7%;	Pred. No. 84;		
	Matches	6;	Conservative	1;	Mismatches
				0;	Indels
					Gaps
OY	3 WDDSLSE	9			
Db	363 WDDELSS	369			

RESULT 35
 P84698
 Probable chitin biosynthesis protein [imported] - Arabidopsis thaliana
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #ext_change 09-Jul-2004
 C/Accession: F84698
 R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Bentle, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffatt, K.S.; Cronin, L.A.; Shen, M.; Vanden, S.E.; Umayam, L.; Tallon, L.;
 euse, D.; Nieman, W.C.; White, O.; Eissen, J.A.; Salberg, S.L.; Frazer, C.M.; Venter, J.
 Nature 402:761-768, 1999
 A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 R/Reference number: AB4420; MOID:20083487; PMID:10617197

A:Accession: F84698
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-644 <SNO>
A:Cross-references: UNIPROT:O82392; GB:AE002093; NID:93582335; PIDN:AA035232.1; GSPDB:GN
C:Genetics:
A:Gene: At2g29630
A:Map position: 2
C:Superfamily: thiamin biosynthesis protein thic

Query Match 63.8%; Score 37; DB 2; Length 644;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AWDLSSEF 9
Db 524 AWDALSK 531

RESULT 36

A70931
Probable PRB protein - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis

C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004

C:Accession: A70931

R:Conor, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
Rajandream, M.A.; Rogers, R.; Devlin, K.; Felwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Nature 393, 537-544, 1998

A:Authors: Sgarbes, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A>Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: A70931

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-655 <COL>

A:Cross-references: UNIPROT:O53949; GB:AL022021; GB:AL123456; NID:93250699; PIDN:CAA1772

A:Experimental source: strain H37RV

C:Genetics:

A:Gene: PRB

Query Match 63.8%; Score 37; DB 2; Length 655;
Best Local Similarity 77.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAWDSLSEF 9
Db 31 AAWDDLASE 39

RESULT 37

B69798
Hypothetical protein yecA - Bacillus subtilis

C:Species: Bacillus subtilis

C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

C:Accession: B69798

R:Kunst, F.; Ogasawara, N.; Moser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Beret
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emerson, P.T.; Ehtlan, K.D.; Erttington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funai, S.; Gallizi, A.; Gall
lech, J.; Harwood, C.R.; Heman, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.

Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauei
Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, B.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,
A:Authors: Schleich, S.; Schoeter, R.; Scofield, F.; Sekiguchi, J.; Sekowska, A.; Serot
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Tempere, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasunoto, K.; Yata, K.; Yoshida, K.

A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.

A>Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A:Reference number: A69580; MUID:98044033; PMID:9384377

A:Accession: B69798

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-857 <KUN>

A:Cross-references: UNIPROT:O31530; GB:Z99107; GB:AL009126; NID:92632866; PIDN:CAB12528.

A:Experimental source: strain 168

C:Genetics:

A:Gene: yecA

C:Superfamily: Bacillus subtilis hypothetical protein yecA

Query Match 63.8%; Score 37; DB 2; Length 857;
Best Local Similarity 75.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WDDSLSEF 10
Db 733 WDDSLSEF 740

RESULT 38

S23756
CFTR protein - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C>Date: 05-Mar-1994 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004

C:Accession: S23756

R:Tucker, S.J.; Tannahill, D.; Higgins, C.F.

Hum. Mol. Genet. 1, 77-82, 1992

A>Title: Identification and developmental expression of the Xenopus laevis cystic fibrosis

A:Reference number: S23756; MUID:93244789; PMID:1284470

A:Accession: S23756

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1485 <TUC>

A:Cross-references: UNIPROT:P26363; EMBL:X65256; NID:964622; PIDN:CAA6348.1; PID:964623

C:Superfamily: cystic fibrosis transmembrane conductance regulator; ATP-binding cassette

C:Keywords: ATP; nucleotide binding; P-loop; transmembrane protein

F:442-623/Domain: ATP-binding cassette homology <ABC1>

F:459-466/Region: nucleotide-binding motif A (P-loop)

F:1230-1422/Domain: ATP-binding cassette homology <ABC2>

F:1247-1254/Region: nucleotide-binding motif A (P-loop)

Qy 1 AAWDSLSEF 10
Db 400 ASWDEGISEF 409

RESULT 39

LYH0A1
Interferon alpha-I-1 precursor - horse

N:Alternate names: EqlFN-alpha-I-1; type I interferon

C:Species: Equus caballus (domestic horse)

C>Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004

C:Accession: A24912

R:Himler, A.; Hauptmann, R.; Adolf, G.R.; Snelly, P.

DNA 5, 345-356, 1986

A>Title: Molecular cloning and expression in Escherichia coli of equine type I interfero

A:Reference number: A90956; MUID:87053170; PMID:3022999

A:Accession: A24912

A:Molecule type: DNA

A:Residues: 1-184 <HIM>

A:Cross-references: UNIPROT:P05003; GB:M14540; NID:9164226; PIDN:AAA0953.1; PID:9164227

C:Superfamily: Interferon alpha

C:Keywords: antiviral

F:1-23/Domain: signal sequence #status predicted <SIG>

F:24-184/Product: interferon alpha-I-1 #status predicted <MAT>

F:124-122,52-162/Disulfide bonds: #status predicted

Query Match 62.1%; Score 36; DB 1; Length 184;
Best Local Similarity 63.6%; Pred. No. 45;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 AAWDSISEFL 11
 |||:|:|
 Db 98 AAWDESLDKL 108

RESULT 40

IVHOA2
 Interferon alpha-1-2 precursor - horse
 N/Alternate names: EqIFN-alpha-1-2; type I interferon
 C/Species: Equus caballus (domestic horse)
 C/Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
 C/Accession: B24912
 R/Himmler, A.; Hauptmann, R.; Adolf, G.R.; Sweetly, P.
 DNA 5, 345-356, 1986
 A/Title: Molecular cloning and expression in Escherichia coli of equine type I interferon
 A/Reference number: A50956; MUID:87053170; PMID:3022999
 A/Accession: B24912
 A/Molecule type: DNA
 A/Residues: 1-184 <HIM>
 A/Cross-references: UNIPROT:P05004; GB:M14541; NID:G164218; PIDN:AAA30950.1; PID:G164221
 C/Superfamily: Interferon alpha
 C/Keywords: antiviral
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-184/Product: interferon alpha-1-2 #status predicted <MAT>
 F:24-122,52-162/Disulfide bonds: #status predicted

Query Match 62.1%; Score 36; DB 1; Length 184;
 Best Local Similarity 63.6%; Pred. No. 45;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 AAWDSISEFL 11
 |||:|:|
 Db 98 AAWDESLDKL 108

Search completed: March 31, 2005, 12:11:17
 Job time : 15.6406 secs


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EX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marnett L., Farmer A.A., Rubin G.M., Hong L.,
RA Stopleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buetefield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marz M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RC SEQUENCE FROM N.A.
RP TISSUE=Lung;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC030984; AAH30984.1; -
DR HSSP; P01703; 7PAB.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003806; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; CI-sect; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KM Hypothetical protein.
SQ SEQUENCE 236 AA; 25024 MW; 1703B77942630E08 CRC64;

Query Match 74.1%; Score 43; DB 2; Length 236;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAMDSDL 8
Db 109 AAMDSDL 116

RESULT 3
ID Q6CLT9 PRELIMINARY; PRT; 628 AA.
AC Q6CLT9;
DT 25-OCT-2004 (TREMblrel. 28. Created)
DT 25-OCT-2004 (TREMblrel. 28. Last sequence update)
DT 25-OCT-2004 (TREMblrel. 28. Last annotation update)
DE Similar to sp|Q9HFC6|Yarrowia lipolytica Calnexin.
GN ORFNames=K1LA0F004629;
OS Kluyveromyces lactis NRRL Y-1140.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX NCBI_TaxId=284590;
RN [1]
RS SEQUENCE FROM N.A.
RC STRAIN=NRRL Y-1140;
RG Genolevures;
RA Lelonde B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barney S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boissiere A., Boyer J., Carcolico L., Confalonieri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantreay F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Kozul R., Lemaire M., Lesur I., Ma L., Muller H.,

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RA Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellens S., Potter S., Richard G.F., Straub M.L., Suleau A.,
RA Swenne D., Tekla F., Mesolowski-Louvel M., Westhof E., Wirth B.,
RA Zenlou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts."
RL Nature 430:35-44(2004).
[2]
RC SEQUENCE FROM N.A.
RP STRAIN=NRRL Y-1140;
RA Genoscope;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR382126; CAG97807.1; -
DR GO; GO:0005514; F:calcium ion storage activity; IBA.
DR InterPro; IPR001580; Calret/calnex.
DR InterPro; IPR008985; Cona-like_lig.
DR Pfam; PF00262; Calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calret/calnex; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 1.
SQ SEQUENCE 628 AA; 70981 MW; B0D8A6D1A64644EE CRC64;

Query Match 74.1%; Score 43; DB 2; Length 628;
Best Local Similarity 66.7%; Pred. No. 32;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 WDSLSFLL 11
Db 309 WDSLSFLL 317

RESULT 4
ID LV1H HUMAN STANDARD; PRT; 112 AA.
AC P06887;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig lambda chain V-I region MEM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RS SEQUENCE.
RA MEDLINE=85257662; PubMed=2410269;
RA Minaesaco E., Roy J.P., Congy N., Peran-Rivat L., Minaesaco C.;
RT "The amino acid sequence of a lambda light chain presenting abnormal
RL physicochemical and antigenic features."
RL Eur. J. Biochem. 150:349-357(1985).
CC -1- MISCELLANEOUS: Residues 33-36 and some of the sequenced peptides
CC were positioned by homology.
CC -1- MISCELLANEOUS: The C region of this chain has the Mcg+ and Kern+
CC markers.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSSP; P01703; 7PAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KM Direct protein sequencing; Immunoglobulin V region;
KM Monoclonal antibody; Pyridoxine carboxylic acid.
FT MOD_RES 1 106 Ig-1like.
FT DISULFID 22 90 Pyridoxine carboxylic acid.
FT NON_TER 112 112 By similarity.

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SO SEQUENCE 112 AA; 11789 MW; 748124F079CFBBA CRC64;
 Query Match 70.7%; Score 41; DB 1; Length 112;
 Best Local Similarity 63.6%; Pred. No. 12;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAMDLSLSEFL 11
 |||||
 :
 Db 91 AAMDLSLDGYV 101

RESULT 5
 Q6DHM4 PRELIMINARY; PRT; 237 AA.
 AC Q6DHM4;
 DT 25-OCT-2004 (TRENBLREL. 28, Created)
 DT 25-OCT-2004 (TRENBLREL. 28, Last sequence update)
 DT 25-OCT-2004 (TRENBLREL. 28, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RX NCBI_TaxID=9606;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shmolen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Dichtenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stopleverson M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millay S.J.,
 RA Bosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
 RA Krzywinski M., Skalski U., Smalls D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RA Strausberg R.L.
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC075843; AAH75843.1; -.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG-Cl.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF07654; C1-secl; 1.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00407; IG1; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
 KW Hypothetical protein.
 SQ SEQUENCE 237 AA; 25108 MW; 6814170F7E784825 CRC64;

Query Match 70.7%; Score 41; DB 2; Length 237;
 Best Local Similarity 87.5%; Pred. No. 26;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAMDLSL 8

Db 109 AAMDLSMS 116
 |||||
 :
 ID LVIF HUMAN STANDARD; PRT; 109 AA.
 AC P04208;
 DT 20-MAR-1987 (Rel. 04, Created)
 DT 20-MAR-1987 (Rel. 04, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig lambda chain V-I region WH.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RX NCBI_TaxID=9606;
 RP SEQUENCE.
 RC MEDLINE=8322161; PubMed=6407018;
 RA Takahashi Y., Takahashi N., Teraert D., Putnam F.W.;
 RT "Complete covalent structure of a human immunoglobulin D: sequence of
 RT the lambda light chain.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:3686-3690(1983).
 DR PIR; A01967; LIGHWA.
 DR HSP; P01703; 7FAB.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; P:antigen binding; NAS.
 DR GO; GO:0005955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 KW Direct protein sequencing; Immunoglobulin V region.
 FT DOMAIN 1 97
 FT DISULFID 98 109
 FT DISULFID 22 89
 FT NON TER 109 109
 SQ SEQUENCE 109 AA; 11725 MW; B17785F6ADP9BAC CRC64;

Query Match 69.0%; Score 40; DB 1; Length 109;
 Best Local Similarity 80.0%; Pred. No. 18;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAMDLSLSEFL 10
 |||||
 :
 Db 90 AAMDLSLWVF 99

RESULT 7
 Q9A925 PRELIMINARY; PRT; 355 AA.
 ID Q9A925;
 AC Q9A925;
 DT 01-JUN-2001 (TRENBLREL. 17, Created)
 DT 01-JUN-2001 (TRENBLREL. 17, Last sequence update)
 DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
 DE Hypothetical protein CC1169.
 OS OrderedlocusNames=CC1169;
 GN Caulobacter crescentus.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
 OC Caulobacteraceae; Caulobacter.
 NCBI_TaxID=155892;
 RX NCBI_TaxID=155892;
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 19089 / CB15;
 RC MEDLINE=21173698; PubMed=11259647; DOI=10.1073/pnas.061029298;
 RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
 RA Eisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
 RA Debora I., Nelson W.C., Newton A.S., Stephens C., Phadt D.H.,
 RA Deboy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
 RA Kolony J.F., Smit J., Craven M.B., Knout H.M., Shetty J.,
 RA Berry K.J., Uetebach T.R., Tran K., Wolf A.M., Vamathevan J.J.,
 RA Ermolaeva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,

RA Fraser C.M.;
 RT "Complete genome sequence of *Caulobacter crescentus*.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141 (2001).
 DR EMBL; AE005795; AK23153.1; -.
 DR PIR; E87394; E87394.
 DR TIGR; CC1169; -.
 DR InterPro; IPR011251; Luciferase_Like.
 DR Pfam; PF00296; Bac_Luciferase_I.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 355 AA; 38552 MW; 3C4AEF42825E5567 CRC64;

Query Match 69.0%; Score 40; DB 2; Length 355;
 Best Local Similarity 87.5%; Pred. No. 63;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAMDLS 8
 DB 138 SAMDLS 145

RESULT 8
 CE2_RAT STANDARD; PRT; 376 AA.
 AC Q9UK15;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Centaurin alpha 2.
 GN Name=Cent2;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxId=10116;
 RN [1]
 SEQUENCE FROM N.A., INTERACTION WITH PTDINS(4,5)P2, PTDINS(3,4,5)P3
 RP AND INS(1,3,4,5)P4, TISSUE SPECIFICITY, AND MUTAGENESIS OF ARG-151 AND
 ARG-275.
 RC TISSUE=Adipocyte;
 RA MEDLINE=22012451; PubMed=12018390;
 RA Whitley P., Gibbard A.M., Koumanov F., Oldfield S., Kilgour E.E.,
 RA Prestwich G.D., Holman G.D.;
 RT "Identification of centaurin-alpha2: a phosphatidylinositol-binding
 RT protein present in fat, heart and skeletal muscle.";
 RL Eur. J. Cell Biol. 81:222-230(2002).

-1- FUNCTION: GTPase-activating protein for the ADP ribosylation
 factor family (Potential).
 -1- SUBUNIT: Binds phosphatidylinositol 4,5-bisphosphate,
 phosphatidylinositol 3,4,5-trisphosphate (PtdInsP3) and inositol
 1,3,4,5-tetrakisphosphate (InsP4). Binding of phosphatidylinositol
 3,5-bisphosphate and phosphatidylinositol 3,4-bisphosphate occurs
 at a much lower affinity. Possesses a stoichiometry of two binding
 sites for InsP4 with identical affinity (By similarity).
 -1- SUBCELLULAR LOCATION: Cytoplasmic. Constitutively associated with
 the plasma membrane. Excluded from the nucleus (By similarity).
 -1- TISSUE SPECIFICITY: Expressed in many tissues, with highest levels
 in fat, heart and skeletal muscle. Also detected in kidney, liver
 and lung.
 -1- SIMILARITY: Contains 1 Arf-GAP domain.
 -1- SIMILARITY: Contains 2 PH domains.

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 EMBL; AJ238993; CAB88403.1; -.
 DR RGD; 708487; LOC66826.
 DR InterPro; IPR001164; hrp1p_like.
 DR InterPro; IPR001849; PH.
 DR InterPro; IPR011036; PH_related.

DR Pfam; PF01412; ArfGAP; 1.
 DR Pfam; PF00169; PH; 2.
 DR PRINTS; PR00405; REVINTRACTNG.
 DR SMART; SM00105; ArfGAP; 1.
 DR SMART; SM00233; PH; 2.
 DR PROSITE; PS50115; ARFGAP; 1.
 DR PROSITE; PS50003; PH_DOMAIN; 2.
 KW GTPase activation; Metal-binding; Repeat; Zinc; Zinc-finger.
 FT DOMAIN 9 130 Arf-GAP.
 FT ZN_FING 25 48 C4-type.
 FT DOMAIN 131 232 PH 1.
 FT DOMAIN 254 360 PH 2.
 FT MUTAGEN 151 151 R->C: Almost complete loss of InsP4
 binding.
 FT MUTAGEN 275 275 R->C: No loss of InsP4 binding. Almost
 complete loss of InsP4 binding; when
 associated with C-151.
 SQ SEQUENCE 376 AA; 43524 MW; E357392F38F0166 CRC64;

Query Match 69.0%; Score 40; DB 1; Length 376;
 Best Local Similarity 66.7%; Pred. No. 67;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 WDDSLSEFL 11
 DB 69 WDDSNVEFPM 77

RESULT 9
 CE2_HUMAN STANDARD; PRT; 381 AA.
 AC Q9NPF8; Q9N406; Q96SD5;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Centaurin alpha 2.
 GN Name=CENT2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 SEQUENCE FROM N.A. (ISOFORM 1).
 RP MEDLINE=22012451; PubMed=12018390;
 RA Whitley P., Gibbard A.M., Koumanov F., Oldfield S., Kilgour E.E.,
 RA Prestwich G.D., Holman G.D.;
 RT "Identification of centaurin-alpha2: a phosphatidylinositol-binding
 RT protein present in fat, heart and skeletal muscle.";
 RL Eur. J. Cell Biol. 81:222-230(2002).

[2]
 SEQUENCE FROM N.A. (ISOFORM 1).
 RP MEDLINE=20304757; PubMed=10843809; DOI=10.1006/geno.2000.6179;
 RA Jenne D.E., Tinschert S., Stegmann E., Reilmann H., Nurnberg P.,
 RA Horn D., Naumann I., Buske A., Thiel G.;
 RT "A common set of at least 11 functional genes is lost in the majority
 RT of NFI patients with gross deletions.";
 RL Genomics 66:93-97(2000).

[3]
 SEQUENCE FROM N.A. (ISOFORM 1).
 RP Bertsch U., Illies C., Mayr G.W.;
 RL Submitted (May-1999) to the EMBL/GenBank/DBJ databases.
 RN [4]
 SEQUENCE FROM N.A. (ISOFORM 2).
 RP TISSUE=Leukocyte;
 RC MEDLINE=22388257; PubMed=12477933; DOI=10.1073/pnas.242603899;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Sherman C.W., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Butow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stedleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Tothiyako S., Carninci P., Prange C.J.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Adamson R.D., Mullany S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gamaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney J., Helton B., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences".
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP INTERACTION WITH PTDINS(3,4,5)P3 AND INS(1,3,4,5)P4, TISSUE
 RP SPECIFICITY, AND SUBCELLULAR LOCATION.
 RX PubMed=14690521;
 RA Hanck T., Stricker R., Sedehizade F., Reiser G.,
 RT "Identification of gene structure and subcellular localization of
 RT human centaurin alpha 2, and p42IP4, a family of two highly
 RT homologous, Ins 1,3,4,5-P4-/Ptdins 3,4,5-P3-binding, adapter
 RT proteins".
 RT J. Neurochem. 88:326-336(2004).
 RL J. Neurochem. 88:326-336(2004).
 CC -1- FUNCTION: GTPase-activating protein for the ADP ribosylation
 CC factor family (Potential).
 CC -1- SUBUNIT: Binds phosphatidylinositol 3,4,5-trisphosphate (PtdinsP3)
 CC and inositol 1,3,4,5-tetrakisphosphate (InsP4). Possesses a
 CC stoichiometry of two binding sites for InsP4 with identical
 CC affinity.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic. Constitutively associated with
 CC the plasma membrane. Excluded from the nucleus.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q9NPP8-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q9NPP8-2; Sequence=VSP_011180;
 CC Note=May be due to a competing acceptor splice site. No
 CC experimental confirmation available;
 CC -1- TISSUE SPECIFICITY: Highly expressed in placenta, spleen, kidney,
 CC skeletal muscle and adrenal gland. Weakly expressed in thyroid,
 CC liver, heart, lung, small intestine, peripheral blood leukocytes.
 CC Not detected in spinal cord, brain, stomach, trachea, colon, lymph
 CC node and bone marrow.
 CC -1- SIMILARITY: Contains 1 Arf-GAP domain.
 CC -1- SIMILARITY: Contains 2 PH domains.
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 CC -----
 DR EMBL; AJ238994; CAB88383.1; -
 DR EMBL; AJ272195; CAB77266.1; -
 DR EMBL; AJ242782; CAC40651.1; -
 DR EMBL; BC033758; CAC33758.1; -
 DR Genew; HGNC:16487; CEN1A2.
 DR H-InvDB; HIX0013699; -
 DR MIM; 608635; -
 DR InterPro; IPR001164; hrip_like.
 DR InterPro; IPR001849; PH.
 DR InterPro; IPR01036; PH_related.
 DR Pfam; PF00169; PH; 2.
 DR Pfam; PF01412; ArfGAP; 1.
 DR PRINTS; PR00405; REVINTRACTNG.
 DR SMART; SM00105; ArfGAP; 1.
 DR SMART; SM00233; PH; 2.
 DR PROSITE; PS50115; ARRGAP; 1.
 DR PROSITE; PS50003; PH_DOMAIN; 2.
 KW Alternative splicing; GTPase activation; Metal-binding; Repeat; Zinc;
 KW Zinc-finger.

FT DOMAIN 9 131 Arf-GAP.
 FT ZN FING 25 48 C4-type.
 FT DOMAIN 132 233 PH 1.
 FT DOMAIN 255 361 PH 2.
 FT VARSPLIC 269 269 Missing (in isoform 2).
 FT FTID=VSP_011180.
 FT L -> P (in Ref. 3).
 SQ SEQUENCE 381 AA; 44348 MW; 4FAE208072A92C01 CRC64;
 Query Match 69.0%; Score 40; DB 1; Length 381;
 Best Local Similarity 66.7%; Pred. No. 68;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Qy 3 WDDSLSEFL 11
 Db 69 WDDSLSEFL 77
 RESULT 10
 CE22_MOUSE STANDARD; PRT; 381 AA.
 AC OBR2V5;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Centaurin alpha 2.
 GN Name=Cent2;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N. A.
 RC STRAIN=FVB/N; TISSUE=Breast tumor;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marinina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carinini P., Prange C.,
 RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gamaratne P.H.,
 RA Bosak S.A., Muzny K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Richards S., Morley K.C., McKernan K.J., Lu X., Gibbs R.A.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney J., Helton B., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences".
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RL J. Neurochem. 88:326-336(2004).
 CC -1- FUNCTION: GTPase-activating protein for the ADP ribosylation
 CC factor family (Potential).
 CC -1- SUBUNIT: Binds phosphatidylinositol 3,4,5-trisphosphate (PtdinsP3)
 CC and inositol 1,3,4,5-tetrakisphosphate (InsP4). Possesses a
 CC stoichiometry of two binding sites for InsP4 with identical
 CC affinity (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic. Constitutively associated with
 CC the plasma membrane. Excluded from the nucleus (By similarity).
 CC -1- SIMILARITY: Contains 1 Arf-GAP domain.
 CC -1- SIMILARITY: Contains 2 PH domains.
 CC -----
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CC -----
CC EMBL: BC027165; AAH27165.1; -
CC MGD; MGI:2663075; Centa2.
CC InterPro; IPR001164; hrip_1ike.
CC InterPro; IPR001849; PH.
CC InterPro; IPR01036; PH related.
CC Pfam; PF01412; ArfGAP; 1.
CC Pfam; PF00169; PH; 2.
CC PRINTS; PR00405; REVINTACTING.
CC SMART; SM00105; ArfGAP; 1.
CC SMART; SM00233; PH; 2.
CC PROSITE; PS50115; ARFGAP; 1.
CC PROSITE; PS50003; PH DOMAIN; 2.
CC GTPase activation; Metal-binding; Repeat; zinc; zinc-finger.
CC DOMAIN 9 132
CC ZN_FING 25 48
CC FT DOMAIN 132 233
CC FT DOMAIN 255 361
CC FT PH 2.
CC SEQUENCE 381 AA; 43989 MW; 28504CEFOACD84D5 CRC64;

Query Match 69.0%; Score 40; DB 1; Length 381;
Best Local Similarity 66.7%; Pred. No. 68;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 3 WDDSLSEFL 11
Db 69 WDDSMVEFM 77

RESULT 11
GLPK_RHIME STANDARD; PRT; 497 AA.
ID GLPK_RHIME
AC 086033;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE GlyceroL kinase (EC 2.7.1.30) (ATP:glycerol 3-phosphotransferase)
DE (Glycerokinase) (GK).
GN Name=glpk; OrderedLocustNames=RH135; ORFNames=SMB21009;
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Plasmid pSymB (megaplasmid 2).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396508; PubMed=11481431; DOI=10.1073/pnas.161294698;
RA Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P.,
RA Vorholter F.J., Hernandez-Lucas I., Becker A., Gouzy J.,
RA Golding B., Pecher A.,
RT "The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-
RT fixing endosymbiont Sinorhizobium meliloti."
RT Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
RL [2]
RN SEQUENCE OF 1-59 FROM N.A.
RP STRAIN=SU47 / 1021;
RC MEDLINE=99121023; PubMed=9922248;
RA Aneja P., Charles T.C.;
RT "Poly-3-hydroxybutyrate degradation in Rhizobium (Sinorhizobium)
RT meliloti: isolation and characterization of a gene encoding 3-
RT hydroxybutyrate dehydrogenase."
RT J. Bacteriol. 181:849-857(1999).
CC -1- FUNCTION: Key enzyme in the regulation of glycerol uptake and
CC metabolism.
CC -1- CATALYTIC ACTIVITY: ATP + glycerol = ADP + sn-glycerol 3-
CC phosphate.
CC -1- PATHWAY: Glycerol utilization; rate-limiting step.
CC -1- SIMILARITY: Belongs to the fucokinase / glucokinase /
CC glycerokinase / xylokinase family.
CC -----
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CC -----
CC EMBL: AL591985; CAC49535.1; -
CC EMBL: AF080548; AAD12735.1; -.
CC PIR; G95983; G95983.
CC HSSP; P08859; 1GLC.
CC DR HAMAP; MF_00186; -.
CC DR InterPro; IPR000577; FGXY_kin.
CC InterPro; IPR005929; Glycerol_kin.
CC Pfam; PF02782; FGXY_C; 1.
CC Pfam; PF00370; FGXY_N; 1.
CC TIGRFAMs; TIGR01311; glycerol_kin; 1.
CC DR PROSITE; PS00933; FGXY_KINASES_1; FALSE_NEG.
CC DR PROSITE; PS00445; FGXY_KINASES_2; 1.
CC KM ATP-binding; Complete proteome; Glycerol metabolism; Kinase; Plasmid;
CC Transferase.
CC NP_BIND 153 165
CC SEQUENCE 497 AA; 54419 MW; 42D342835ACC2B7 CRC64;

Query Match 69.0%; Score 40; DB 1; Length 497;
Best Local Similarity 70.0%; Pred. No. 90;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 2 AMDSLSEFL 11
Db 197 AMDDELTEVL 206

RESULT 12
Q48904 PRELIMINARY; PRT; 502 AA.
ID Q48904
AC Q48904;
DT 01-NOV-1996 (TRENDEL 01, Created)
DT 01-NOV-1996 (TRENDEL 01, Last sequence update)
DT 01-MAR-2004 (TRENDEL 26, Last annotation update)
DE ORP2.
DE Microcystis aeruginosa.
OC Bacteria; Cyanobacteria; Chroococcales; Microcystis.
OX NCBI_TaxID=1126;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HUB 5-2-4;
RA Juerchott K., Boerner T.;
RT Submitted (NCV-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z28337; CA882191.1; -.
DR PIR; S49113; S49113.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR007936; VIRE.
DR Pfam; PF05272; VIRE; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
SQ SEQUENCE 502 AA; 58859 MW; 98E61D5C214520B6 CRC64;

Query Match 69.0%; Score 40; DB 2; Length 502;
Best Local Similarity 60.0%; Pred. No. 91;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 2 AMDSLSEFL 11
Db 434 SWEDELAFL 443

RESULT 13
YP93 CAEBL STANDARD; PRT; 1714 AA.
ID YP93 CAEBL
AC Q09475;
DT 01-NOV-1995 (Rel. 32, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Putative helicase C28H6.3 (EC 3.6.1.-).

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GN ORFNames=C28H8.3;
OC Caenorhabditis elegans.
OC Eukaryota; Metazoa; Chromadorea; Rhabditida; Rhabditoidea;
OC Chabditidae; Peloderinae; Caenorhabditis.
OC NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
   investigating biology."
RL Science 282:2012-2018(1998).
RN [2]
RP REVISIONS.
RA Waterston R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -1- SIMILARITY: Belongs to the helicase family. SKI2 subfamily.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL, U20861; AAA62291.2; -.
DR WormBase; WBGene00016194; C28H8.3.
DR WormPeP; C28H8.3; CE29195.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR001650; Helicase_C.
DR Pfam; PF00270; DEAD, 1.
DR Pfam; PF00271; Helicase_C, 1.
DR SMART; SM00487; HELIC_C, 1.
DR SMART; SM00490; HELIC_C, 1.
DR TIGFAMS; TIGR01870; cas TM1810; 2.
KW ATP-binding; Helicase; Hydrolase; Hypothetical protein;
KW Nuclear protein.
FT NP_BIND 607 614 ATP (Potential).
FT NP_BIND 806 813 ATP (Potential).
FT SITE 913 916 DEVH box.
SQ SEQUENCE 1714 AA; 194095 MW; 0936764D27C7EFAD CRC64;
-----
Query Match 69.0%; Score 40; DB 1; Length 1714;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
-----
QY 1 AAMDLSSE 9
DB 5 AAMDSDSE 13
-----
RESULT 14
ID_DYHC_NEUCR STANDARD; PRT; 4367 AA.
AC P45443; Q7RVH1;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Dynein heavy chain, cytosolic (DYHC).
GN Name=ro-1; ORFNames=NCU06976.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=74-OR23-1A / FGSC 987;
RX MEDLINE=95014704; PubMed=7929559; DOI=10.1083/jcb.127.1.139;
RA Plamann M., Minko P.F., Timley J.H., Bruno K.S.;
RA "Cytoplasmic dynein and actin-related protein Arp1 are required for

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RT normal nuclear distribution in filamentous fungi.",
RL J. Cell Biol. 127:139-149(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=74-OR23-1A / FGSC 987;
RX PubMed=12712197; DOI=10.1038/nature01554;
RA Galagan J.E., Calvo S.E., Borokovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Renhan B.,
RA Elkins T., Engle R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Bell-Pedersen D., Nelson M.A.,
RA Werner-Washburne M., Selitrenikoff C.P., Kinsey J.A., Braun E.L.,
RA Zelter A., Schulte U., Kothe G.O., Jedd G., Mewes H.-W., Staben C.,
RA Marcotte E., Greenberg D., Roy A., Foley K., Naylor J.,
RA Stange-Thomann N., Barrett R., Gnerre S., Kamal M., Kamyszelis M.,
RA Manceil E., Bielke C., Rudd S., Frisman D., Kravtsova S.,
RA Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S., Cogoni C.,
RA Macino G., Catchside D., Li M., Pratt R.J., Omani S.A.,
RA Desouza C.P., Glass L., Orbach M.J., Berglund J.A., Voelker R.,
RA Yarden O., Plamann M., Seltzer S., Dunlap J., Radford A., Aramayo R.,
RA Nativ D.O., Alex L.A., Mannheim G., Eboile D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.;
RA "The genome sequence of the filamentous fungus Neurospora crassa."
RL Nature 422:859-868(2003).
CC -1- FUNCTION: Cytoplasmic dynein acts as a motor for the intracellular
CC retrograde motility of vesicles and organelles along microtubules.
CC Dynein has ATPase activity; the force-producing power stroke is
CC thought to occur on release of ADP. Required to maintain uniform
CC nuclear distribution in hyphae.
CC -1- SUBUNIT: Consists of at least two heavy chains and a number of
CC intermediate and light chains.
CC -1- DOMAIN: Dynein heavy chains probably consist of an N-terminal stem
CC (which binds cargo and interacts with other dynein components),
CC and the head or motor domain. The motor contains six tandemly-
CC linked AAA domains in the head, which form a ring. A stalk-like
CC structure (formed by two of the coiled coil domains) protrudes
CC between AAA 4 and AAA 5 and terminates in a microtubule-binding
CC site. A seventh domain may also contribute to this ring; it is not
CC clear whether the N-terminus or the C-terminus forms this extra
CC domain. There are four well-conserved and two non-conserved ATPase
CC sites, one per AAA domain. Probably only one of these (within AAA
CC 1) actually hydrolyzes ATP, the others may serve a regulatory
CC function.
CC -1- SIMILARITY: Belongs to the dynein heavy chain family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
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CC -----
DR EMBL, L31504; AAA64908.1; -.
DR EMBL, AABX01000204; EAA33380.1; -.
DR PIR; B54802; B54802.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR004273; Dynein_heavy.
DR Pfam; PF03028; Dynein_heavy, 1.
DR SMART; SM00382; AAA, 3.
KW ATP-binding; Coiled coil; Dynein; Microtubule; Motor protein; Repeat.
FT DOMAIN 1 1904 AAA 1 (By similarity).
FT DOMAIN 2 2130 Stem (By similarity).
FT DOMAIN 3 2202 AAA 2 (By similarity).
FT DOMAIN 4 2460 AAA 3 (By similarity).
FT DOMAIN 5 2566 AAA 4 (By similarity).
FT DOMAIN 6 2909 AAA 5 (By similarity).
FT DOMAIN 7 3193 AAA 6 (By similarity).
FT DOMAIN 8 3481 Stalk (By similarity).
FT DOMAIN 9 3565 AAA 5 (By similarity).
FT DOMAIN 10 3794 AAA 5 (By similarity).
FT DOMAIN 11 4003 AAA 6 (By similarity).
FT DOMAIN 12 4215 AAA 6 (By similarity).
FT DOMAIN 13 4376 Coiled coil (Potential).
FT DOMAIN 14 1176 Coiled coil (Potential).
FT DOMAIN 15 1357 Coiled coil (Potential).
FT DOMAIN 16 1557 Coiled coil (Potential).

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FT DOMAIN 1637 1668 Coiled coil (Potential)
FT DOMAIN 2195 2228 Coiled coil (Potential)
FT DOMAIN 3193 3236 Coiled coil (Potential)
FT DOMAIN 3423 3481 Coiled coil (Potential)
FT DOMAIN 3778 3809 Coiled coil (Potential)
FT NP_BIND 1943 1950 ATP (Potential)
FT NP_BIND 2240 2247 ATP (Potential)
FT NP_BIND 2605 2612 ATP (Potential)
FT NP_BIND 2947 2954 ATP (Potential)
SQ SEQUENCE 4367 AA; 495568 MW; 1E10F3E2D170D6DF CRC64;

Query Match
Best Local Similarity 69.0%; Score 40; DB 1; Length 4367;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 AAMDLSLEP 10
DB 455 AMDSIEKEF 463

RESULT 15
O87GV3 PRELIMINARY; PRT; 182 AA.
AC O87GV3;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Hypothetical protein VPA1212.
GN OrderedLocusNames=VPA1212;
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrrio.
CX NCBI_TaxID=670;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RIMD 2210633 / Serotype O3:K6;
RX MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Nishijima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yaenunga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT distinct from that of V. cholerae.";
RL Lancet 361:743-749(2003).
KM EMBL; AP005088; BAC62555.1; -
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 182 AA; 21333 MW; 2559B8C9FD78332 CRC64;

Query Match
Best Local Similarity 67.2%; Score 39; DB 2; Length 182;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAMDLSLEP 10
DB 27 SSMDDNLTOF 36

RESULT 16
O6GMV7 PRELIMINARY; PRT; 236 AA.
AC O6GMV7;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

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RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buelow K.H., Scheeler C.F., Bat N.K.,
RA Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strauberg R.;
RL Submitted (JUN-2004) to the EMBL/Genbank/DBJ databases.
DE EMBL; BC073795; AAH73795.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG-MHC.
DR InterPro; IPR003596; IG-V.
DR Pfam; PF07654; CI-bet; I.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG-LIKE; 2.
DR PROSITE; PS00290; IG-MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 24950 MW; 3B0477247847E930 CRC64;

Query Match
Best Local Similarity 67.2%; Score 39; DB 2; Length 236;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAMDLSL 7
DB 109 AAMDLSL 115

RESULT 17
KAPI_BOVIN STANDARD; PRT; 397 AA.
ID KAPI_BOVIN
AC P24256;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE CAMP-dependent protein kinase, beta-2-catalytic subunit (EC 2.7.1.37)
DE (PKA C-beta-2).
GN Name=PRKCB2;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
CX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=91161607; PubMed=2002051;
RA Wiemann S., Kinzel V., Pyerin W.;
RT "Isoform C beta 2, an unusual form of the bovine catalytic subunit of
RT CAMP-dependent protein kinase.";
RL J. Biol. Chem. 266:5140-5146(1991).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.

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CC -1- ENZYME REGULATION: Activated by cAMP.
CC -1- SUBUNIT: A number of inactive tetrameric holoenzymes are produced
CC by the combination of homo- or heterodimers of the different
CC regulatory subunits associated with two catalytic subunits. cAMP
CC causes the dissociation of the inactive holoenzyme into a dimer of
CC regulatory subunits bound to four cAMP and two free monomeric
CC catalytic subunits.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=N-terminal differences in alternatively spliced products
CC could be involved in regulation such as alternative targeting;
CC Name=2; Synonyms=Beta-2;
CC IsoId=P24256-1; Sequence=Displayed;
CC Name=1; Synonyms=Beta-1;
CC IsoId=P05131-1; Sequence=External;
CC Note=No experimental confirmation available;
CC -1- TISSUE SPECIFICITY: Mainly expressed in heart and brain tissue.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family. cAMP
CC subfamily.
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DR EMBL, M60482; AAA30424.1; -.
DR PIR, A23716; OKBOB2.
DR HSSP, P36887; ICTP.
DR InterPro, IPR011009; Kinase like.
DR InterPro, IPR000961; Kinase C.
DR InterPro, IPR000719; Prot_kinase.
DR InterPro, IPR008271; Ser_thr_kin_AS.
DR InterPro, IPR002290; Ser_thr_kinase.
DR Pfam, PF00069; Kinase; 1.
DR Pfam, PF00433; Kinase C; 1.
DR ProDom, PD000001; Prot_kinase; 1.
DR SMART, SM00133; S_TK_X; 1.
DR SMART, SM00220; S_TK; 1.
DR PROSITE, PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE, PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE, PS00108; PROTEIN_KINASE_ST; 1.
KW Alternative splicing; ATP-binding; cAMP; Multigene family;
KW Phosphorylation; Serine/threonine-protein kinase; Transferase.
FT DOMAIN 90 344 Protein kinase.
FT NP_BIND 96 104 ATP (By similarity).
FT BINDING 119 119 ATP (By similarity).
FT ACT_SITE 213 213 Proton acceptor (By similarity).
FT MOD_RES 244 244 Phosphothreonine (By similarity).
FT MOD_RES 385 385 Phosphoserine (By similarity).
SQ SEQUENCE 397 AA; 46108 MW; 7F87EF506C32FE29 CRC64;

Query Match 67.2%; Score 39; DB 1; Length 397;
Best Local Similarity 63.6%; Pred. No. 1.1e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Salivary gland;
RG The German cDNA Consortium;
RA Mamut R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Salivary gland;
RG The German cDNA Consortium;
RA Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA Han M., Wiemann S.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC EMBL, BX537705; CAD97818.1; -.
CC HSSP, BX641026; CAB46017.1; -.
DR GO, GO:0005524; F:ATP binding; IEA.
DR GO, GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO, GO:0016740; F:transferase activity; IEA.
DR GO, GO:0004688; P:protein amino acid phosphorylation; IEA.
DR InterPro, IPR011009; Kinase like.
DR InterPro, IPR000719; Prot_kinase.
DR InterPro, IPR008271; Ser_thr_kin_AS.
DR Pfam, PF00069; Kinase; 1.
DR ProDom, PD000001; Prot_kinase; 1.
DR PROSITE, PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE, PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE, PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Hypothetical protein; Kinase;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 398 AA; 46236 MW; 49EFAF3E426468FC CRC64;

Query Match 67.2%; Score 39; DB 2; Length 398;
Best Local Similarity 63.6%; Pred. No. 1.1e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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Oy 1 AAADSLSEFL 11
Db .56 ALMDRSMEFL 66

RESULT 18
O7Z3M1 PRELIMINARY; PRT; 398 AA.
AC 07Z3M1;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Hypothetical protein DKFZp668H10244 (Hypothetical protein
DE DKFZp668K18247).
GN Name=DKFZp668H10244; Synonyms=DKFZp668K18247;

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O8W0B5 PRELIMINARY; PRT; 578 AA.
AC 08W0B5;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Putative cytochrome P-450LXX1A1 (CYP71A1) family.
GN Name=P0452P10.8;
OS Oryza sativa (Japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhacoidae; Oryzaceae; Oryza.
OX NCBI_TaxId=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC Pubmed=12447438; DOI=10.1038/nature01184;
RA Sasaki T., Matsunoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
RA Wu J., Nilmura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
RA Hijiishi S., Honda M., Ichikawa Y., Iiduma A., Iijima M., Ikeda M.,
RA Ikono M., Itoh S., Itoh T., Itoh Y., Iwabuchi A., Kamiya K.,
RA Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,

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RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,
 RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
 RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshinara R., Yokawa K.,
 RA Zhong H., Iwana H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
 RA Yan M., Jiang J., Gajdosi T.,
 RT "The genome sequence and structure of rice chromosome 1,"
 CC Nature 420:312-316(2002).
 DR EMBL: AP003434; BAB78671.1; -.
 DR HSSP: P77901; IH5Z.
 DR Gramene; Q8W0B5; -.
 DR GO: GO:0004497; F:monooxygenase activity; IEA.
 DR GO: GO:0006118; P:electron transport; IEA.
 DR Pfam: PF00067; p450: 1.
 DR PRINTS: PR00463; EP4501.
 DR PROSITE: PS00086; CYTOCHROME_P450; UNKNOWN_1.
 DR Heme; Monooxygenase; Oxidoreductase.
 SQ SEQUENCE 578 AA; 62437 MW; 11FEF35AD3D1FB5 CRC64;

Query Match 67.2%; Score 39; DB 2; Length 578;
 Best Local Similarity 63.6%; Pred. No. 1.6e+02;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 AAMDLSSEFL 11
 DB 466 AAMGDSAEFFV 476

RESULT 20
 ID 06C021 PRELIMINARY; PRT; 751 AA.
 AC 06C021;
 DT 25-OCT-2004 (TRENBLrel. 28, Created)
 DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
 DE Similarity.
 GN ORFNames=YAL10F20614g;
 OS Yarrowia lipolytica CLIB99.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Dipodascaceae; Yarrowia.
 OX NCBI_TaxID=284591;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CLIB99;
 RG Genolevures;
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
 RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla B.,
 RA Goffard N., Fraigneul L., Aigle M., Anthouard V., Babour A., Barbe V.,
 RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykaeten C.,
 RA Boissarie A., Boyer J., Catolico L., Comandollet F., de Daruvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dunazet H., Groppi A.,
 RA Hantreya F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Niccaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
 RA Pellens S., Potier S., Richard G.F., Straub M.L., Suleau A.,
 RA Swenene D., Tekai F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zeniou-Meyer M., Zivanovic I., Bojotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J.,
 RA Wincker P., Souciet J.L.;
 RT "Genome evolution in yeasts";
 RL Nature 430:35-44(2004).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CLIB99;
 RA Genoscope;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: CR382132; CAC78480.1; -.
 DR InterPro: IPR001623; DnaJ_N.
 DR Pfam: PF00226; DnaJ.1.
 DR SMART: SMO0271; DnaJ.1.
 DR PROSITE: PS50076; DnaJ.2; 1.
 SQ SEQUENCE 751 AA; 85290 MW; 0A9E620ECB01102E CRC64;

Query Match 67.2%; Score 39; DB 2; Length 751;
 Best Local Similarity 75.0%; Pred. No. 2.2e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 WDDSLSEF 10
 DB 87 WDDSFSDP 94

RESULT 21
 ID 074B13 PRELIMINARY; PRT; 894 AA.
 AC 074B13;
 DT 05-JUL-2004 (TRENBLrel. 27, Created)
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
 DE 2-oxoglutarate dehydrogenase, E1 component (EC 1.2.4.2).
 GN Name=SucA; OrderedLocustNames=GSU2449;
 OS Geobacter sulfurreducens.
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
 OC Geobacteraceae; Geobacter.
 OX NCBI_TaxID=35554;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PCA / ATCC 51573;
 RX PubMed=14671304; DOI=10.1126/science.1088727;
 RA Melhe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C.,
 RA Heidelberg J.F., Wu D., Wu M., Ward N.L., Beaman M.J., Dodson R.J.,
 RA Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
 RA Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengue J.,
 RA Davidson T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,
 RA Weidman J.F., Khouri H.M., Feldblyum T.V., Ueberback T.R.,
 RA Van Aken S.E., Lovley D.R., Fraser C.M.;
 RT "Genome of Geobacter sulfurreducens: metal reduction in subsurface
 environments";
 RL Science 302:1967-1969(2003).
 DR EMBL: AE017180; AAR35822.1; -.
 DR TIGR: GSU2449; -.
 DR GO: GO:0016491; F:oxidoreductase activity; IEA.
 DR GO: GO:0004591; F:oxoglutarate dehydrogenase (succinyl-transf. .); IEA.
 DR GO: GO:0008152; P:metabolism; IEA.
 DR InterPro: IPR001017; Dehydrogenase_E1.
 DR InterPro: IPR005475; Transketolase_CR.
 DR Pfam: PF00676; E1_dh; 1.
 DR Pfam: PF02779; Transket. pyr; 1.
 KW Complete proteome; Oxidoreductase.
 SQ SEQUENCE 894 AA; 99395 MW; C33888A0C8EFOA66 CRC64;

Query Match 67.2%; Score 39; DB 2; Length 894;
 Best Local Similarity 77.8%; Pred. No. 2.6e+02;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 AWDLSSEF 10
 DB 620 AWDLSSEF 628

RESULT 22
 ID 07RY83 PRELIMINARY; PRT; 969 AA.
 AC 07RY83;
 DT 01-MAR-2004 (TRENBLrel. 26, Created)
 DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Predicted protein.
 GN Name=NCU00022.1;
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
 OX NCBI_TaxID=5141;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engle R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Inakiev P., Pedersen D., Nelson M., Washburne M.,
RA Seitzman K.C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal K., Kamysseilis M., Mauceli E., Bielke C., Rudd S., Frisman D.,
RA Krysiofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Omani S.A.,
RA Desouza C.C., Glass L., Ordach M.J., Berglund J., Voelker R.,
RA Varden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Navvig D.O., Alex L.A., Mannheim G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.,
RA "The Genome Sequence of the Filamentous Fungus Neurospora crassa."
RL Nature 0:0-0(2003).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC DR EMBL: AABX01000729; EAA27773.1; -
SQ SEQUENCE 969 AA; 10665 MW; 869181A24C9DB1D1 CRC64;

Query Match 67.2%; Score 39; DB 2; Length 969;
Best Local Similarity 66.7%; Pred. No. 2.8e+02;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 WDDSLSEFL 11
Db 667 WDDALSEW 675

RESULT 23
Q98TR8 PRELIMINARY; PRT; 1466 AA.
AC Q98TR8;
DT 01-JUN-2001 (TRENBLREL. 17, Created)
DT 01-JUN-2001 (TRENBLREL. 17, Last sequence update)
DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
DE Cyclic fibrosis transmembrane conductance regulator.
GN Name=CFTF;
OS Buto bufo (European toad).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Bufonidae; Bufo.
CX NCBI_Taxid=8384;
RX [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Belly skin;
RA Amstrup J., Hvid Larsen E.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL: AY026761; AAK07685.1; -
DR HSP; Q00555; ICKX.
DR GO: GO:0016021; C:Integral to membrane; IEA.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0042626; F:ATPase activity; coupled to transmembrane m. . .; IEA.
DR GO: GO:0005254; F:chloride channel activity; IEA.
DR GO: GO:0006166; F:nucleotide binding; IEA.
DR GO: GO:0006811; P:ion transport; IEA.
DR InterPro: IPR003593; AAA ATPase.
DR InterPro: IPR011527; ABC membrane 1.
DR InterPro: IPR003439; ABC TM transp.
DR InterPro: IPR005291; CMF_c1_channel.
DR InterPro: IPR009147; CyfB1b_conduc.
DR Pfam: PF00664; ABC_trans. 2.
DR PRINTS: PRO0005; ABC_tran. 2.
DR PRODOM: PD000006; ABC_transporter; 2.
DR SMART: SM00382; AAA; 3.
DR TIGRPFAM: TIGR00953; 3a01202; 1.
DR TIGRPFAM: TIGR01271; CFTF_protein; 1.
DR PROSITE: PS50929; ABC_TM1F; 2.

DR PROSITE: PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE: PS50893; ABC_TRANSPORTER_2; 2.
CX ATP-binding; Transmembrane.
SQ SEQUENCE 1466 AA; 16596 MW; EB692EC3C611C169 CRC64;

Query Match 67.2%; Score 39; DB 2; Length 1466;
Best Local Similarity 54.5%; Pred. No. 4.4e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAMDLSSEFL 11
Db 395 ASWDGFEFL 405

RESULT 24
YCX7 CHLRE STANDARD; PRT; 1995 AA.
AC P36495; Q37303;
DT 01-JUN-1994 (Rel. 29, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 232.2 kDa protein (ORF1995) (ORF-S) (ORFA).
OS Chlamydomonas reinhardtii.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
CX NCBI_Taxid=3055;
RX [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97218038; PubMed=9065699; DOI=10.1007/s004380050368;
RA Boudreau E., Turmel M., Goldschmidt-Clermont M., Rochaix J.-D.,
RA Sivan S., Michaels A., Leu S.;
RT "A large open reading frame (orf1995) in the chloroplast DNA of
RT Chlamydomonas reinhardtii encodes an essential protein."
RL Mol. Gen. Genet. 253:649-653 (1997).
RN [2]
RP SEQUENCE OF 1573-1995 FROM N.A.
RC STRAIN=cw15;
RA Sivan S., Michaels A.;
RL Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 1897-1995 FROM N.A.
RX MEDLINE=87031585; PubMed=2876928; DOI=10.1016/0378-1119(86)90038-7;
RA Woessner J.P., Gilham N.W., Boynton J.E.;
RT "The sequence of the chloroplast atpB gene and its flanking regions in
RT Chlamydomonas reinhardtii."
RL Gene 44:17-28(1986).
RN [4]
RP PARTIAL SEQUENCE FROM N.A.
RX MEDLINE=94207185; PubMed=8155879;
RA Boudreau E., Otis C., Turmel M.;
RT "Conserved gene clusters in the highly rearranged chloroplast genomes
RT of Chlamydomonas moewusii and Chlamydomonas reinhardtii."
RL Plant Mol. Biol. 24:585-602(1994).
RN [5]
RP COMPLETE PLASTID GENOME.
RX MEDLINE=22305394; PubMed=12417694;
RA Maul J.E., Lilly J.W., Cui L., dePamphilis C.W., Miller W.,
RA Harris E.H., Stern D.B.;
RT "The Chlamydomonas reinhardtii plastid chromosome: islands of genes in
RT a sea of repeats."
RL Plant Cell 14:2659-2679(2002).
CC -1- FUNCTION: Essential for cell growth. May be involved in binding
CC chloroplast DNA to either the chloroplast envelope or the
CC thylakoid membrane.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (potential).
CC -1- SIMILARITY: To C.vulgaris ORF819.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----

DR EMBL; X92726; CAA63385.1; -

DR EMBL; X76934; CAA54257.1; -

DR EMBL; M13704; AAA84144.1; ALT_INIT.

DR EMBL; BK000554; DAA00959.1; -

DR PIR; S41289; S41289.

DR PIR; T08186; T08186.

DR InterPro; IPR008934; AcPase_VanParase.

DR InterPro; IPR001123; Lyse_

KW Chloroplast; Thylakoid; Transmembrane.

FT TRANSMEM 31 51 Potential.

FT TRANSMEM 53 73 Potential.

FT TRANSMEM 106 126 Potential.

FT TRANSMEM 157 177 Potential.

FT TRANSMEM 212 232 Potential.

FT TRANSMEM 254 274 Potential.

FT TRANSMEM 307 327 Potential.

FT CONFLICT 1588 1588 K -> R (in Ref. 2).

SO SEQUENCE 1995 AA; 232194 MW; 55A3F167EAF5FC8A CRC64;

Query Match 67.2%; Score 39; DB 1; Length 1995;
Best Local Similarity 54.5%; Pred. No. 6.2e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAMDLSLSEFL 11
Db 1581 AGWDESLKFKV 1591

RESULT 25
DTHC_EMENTI STANDARD; PRT; 4344 AA.

AC P45444;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Dynein heavy chain, cytosolic (DYHC).
GN Name=NDU4;
OS Emericella nidulans (Aspergillus nidulans).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; Emericella.
OX NCBI_TaxID=162425;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94181539; PubMed=8134356;
RA Xiang X., Beckwith S.M., Morris R.N.;
RT "Cytoplasmic dynein is involved in nuclear migration in Aspergillus nidulans.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:2100-2104(1994).
CC -1- FUNCTION: Cytoplasmic dynein acts as a motor for the intracellular retrograde motility of vesicles and organelles along microtubules. Dynein has ATPase activity; the force-producing power stroke is thought to occur on release of ADP. Required to maintain uniform nuclear distribution in hyphae.
CC -1- SUBUNIT: Consists of at least two heavy chains and a number of intermediate and light chains.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- DOMAIN: Dynein heavy chains probably consist of an N-terminal stem (which binds cargo and interacts with other dynein components), and the head or motor domain. The motor contains six tandemly-linked AAA domains in the head, which form a ring. A stalk-like structure (formed by two of the coiled coil domains) protrudes between AAA 4 and AAA 5 and terminates in a microtubule-binding site. A seventh domain may also contribute to this ring; it is not clear whether the N-terminus or the C-terminus forms this extra domain. There are four well-conserved and two non-conserved ATPase sites, one per AAA domain. Probably only one of these (within AAA 1) actually hydrolyzes ATP, the others may serve a regulatory function.
CC -1- SIMILARITY: Belongs to the dynein heavy chain family.

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CC -----

DR EMBL; U03904; AAA18338.1; -

DR PIR; A53489; A53489.

DR InterPro; IPR003593; AAA ATPase.

DR InterPro; IPR004273; Dynein_heavy.

DR Pfam; PF03028; Dynein_heavy; 1.

DR SMART; SM00382; AAA; 3.

KW ATP-binding; Coiled coil; Dynein; Microtubule; Motor protein; Repeat.

FT DOMAIN 1 1894 AAA 1 (By similarity).

FT DOMAIN 1895 2120 AAA 2 (By similarity).

FT DOMAIN 2190 2448 AAA 3 (By similarity).

FT DOMAIN 2553 2800 AAA 4 (By similarity).

FT DOMAIN 2894 3163 AAA 5 (By similarity).

FT DOMAIN 3179 3463 Stalk (By similarity).

FT DOMAIN 3549 3780 AAA 6 (By similarity).

FT DOMAIN 3994 4206 AAA 6 (By similarity).

FT DOMAIN 667 687 Coiled coil (Potential).

FT DOMAIN 913 933 Coiled coil (Potential).

FT DOMAIN 1321 1341 Coiled coil (Potential).

FT DOMAIN 1548 1564 Coiled coil (Potential).

FT DOMAIN 1627 1656 Coiled coil (Potential).

FT DOMAIN 3179 3270 Coiled coil (Potential).

FT DOMAIN 3407 3463 Coiled coil (Potential).

FT DOMAIN 3700 3798 Coiled coil (Potential).

FT NP_BIND 1933 1940 ATP (Potential).

FT NP_BIND 2223 2230 ATP (Potential).

FT NP_BIND 2592 2599 ATP (Potential).

FT NP_BIND 2932 2939 ATP (Potential).

SO SEQUENCE 4344 AA; 492470 MW; 302A586C4F8BD019 CRC64;

Query Match 67.2%; Score 39; DB 1; Length 4344;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WDDSLSEF 10
Db 446 WDDNLKEF 453

RESULT 26
Q73YE0 PRELIMINARY; PRT; 170 AA.

AC Q73YE0;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=MAP2016;
OS Mycobacterium paratuberculosis.
OC Bacteria; Actinobacteria; Actinomycetales;
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1770;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=k10;
RA Li L., Bannantine J., Zhang O., Amonsin A., Alt D., Kapur V.;
RL Submitted (SRP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017234; AAS04333.1; -
KW Complete proteome.
SO SEQUENCE 170 AA; 19523 MW; 3A0C9E48C606E3B2 CRC64;

Query Match 65.5%; Score 38; DB 2; Length 170;
Best Local Similarity 77.8%; Pred. No. 67;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAMDLSLSEF 10

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Db      20  AAMDVLSTF 28

RESULT 27
Q67NP3  PRELIMINARY; PRT; 215 AA.
ID Q67NP3;
AC Q67NP3;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN ORFNames=STH1715;
OS Symbiobacterium thermophilum.
OC Bacteria; Actinobacteria; Symbiobacterium.
OX NCBI_TaxId=2734;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IAM14863;
RA Ueda K., Yamashita A., Ishikawa J., Shimada M., Watsuji T.,
RA Morimura K., Ikeda H., Hattori M., Beppu T.;
RT "Complete genome sequence of an uncultured bacterium Symbiobacterium
RT thermophilum."
RL Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP006840; BAD40700.1; -.
DR InterPro; IPR003817; PS_Decarboxylase.
DR InterPro; IPR004428; PS_Decarb_rel.
DR Pfam; PF02666; PS_Decarboxylase; 1.
DR TIGRFAMs; TIGR00164; PS_decarb_rel; 1.
KW Hypothetical protein.
SQ SEQUENCE 215 AA; 23743 MW; C502881B59E6D8E9 CRC64;

Query Match      65.5%; Score 38; DB 2; Length 215;
Best Local Similarity 66.7%; Pred. No. 86;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1  AAMDLSLSE 9
Db      122  AAMDPTVGE 130

RESULT 28
Q31358  PRELIMINARY; PRT; 244 AA.
ID Q31358;
AC Q31358;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Major histocompatibility class II protein.
GN Name=mhc2deb; Synonyms=MHC Brre-DEB;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxId=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=95130065; PubMed=7829056;
RA Sultman H., Mayer W.E., Figueroa F., O'Huigin C., Klein J.;
RT "Organization of Mhc class II B genes in the zebrafish (Brachydanio
RT rerio)."
RN Genomics 23:1-14(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC Submitted (Apr-1994) to the EMBL/GenBank/DBJ databases.
RA EMBL; U08874; AAA87895.1; -.
DR HSSP; Q3135; IES0.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0045012; P: MHC class II receptor activity; IEA.
DR GO; GO:0018884; P: antigen presentation, exogenous antigen; IEA.
DR GO; GO:0018886; P: antigen processing, exogenous antigen via M. .; IEA.
DR GO; GO:0006955; P: immune response; IEA.

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DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF00969; MHC_II_beta; 1.
DR Prodom; PD000328; MHC_II_beta; 1.
DR SMART; SM00407; Igc1; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Glycoprotein; MHC II; Transmembrane.
SQ SEQUENCE 244 AA; 28014 MW; 6A84C5AD721CE8F8 CRC64;

Query Match      65.5%; Score 38; DB 2; Length 244;
Best Local Similarity 87.5%; Pred. No. 99;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2  AAMDLSLSE 9
Db      201  AAMDLSLSE 208

RESULT 29
Q631V6  PRELIMINARY; PRT; 252 AA.
ID Q631V6;
AC Q631V6;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Probable transcriptional regulator.
GN ORFNames=BTZK4740;
OS Bacillus cereus ZK.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxId=288681;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ZK;
RA Bretin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Rice H.;
RT "Complete genome sequence of Bacillus cereus ZK."
RL Submitted (Jul-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CP000001; AAU15537.1; -.
SQ SEQUENCE 252 AA; 29184 MW; 208B07DE890A1DB2 CRC64;

Query Match      65.5%; Score 38; DB 2; Length 252;
Best Local Similarity 54.5%; Pred. No. 1e+02;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy      1  AAMDLSLSEFL 11
Db      129  SAMNDTLEVL 139

RESULT 30
Q72Y69  PRELIMINARY; PRT; 252 AA.
ID Q72Y69;
AC Q72Y69;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedCusNames=BCB5152;
OS Bacillus cereus (strain ATCC 10987).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxId=222523;
RN [1]
RP SEQUENCE FROM N.A.
RC PubMed=14960714; DOI=10.1093/nar/gkh258;
RA Rasko D.A., Ravel J., Oksford O.A., Helgason B., Cer R.Z., Jiang L.,
RA Shores K.A., Fouts D.E., Tourasse N.J., Anguino J.S.V., Kolonay J.F.,
RA Nelson W.C., Koileva A.B., Fraser C.M., Reed T.D.;
RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
RT adaptations and a large plasmid related to Bacillus anthracis pXO1."
RL Nucleic Acids Res. 32:977-988(2004).

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DR EMBL: AE017280; AAS44053.1; -.
DR TIGR: BCE5152; -.
DR InterPro: IPR002831; TrmB_Trans_reg.
DR InterPro: IPR009058; Wng_hlx_DNA_bnd.
DR InterPro: IPR011571; Wng_hlx_trns_reg.
DR Pfam: PF01978; TrmB; 1.
DR ProDom: PD006327; Wng_hlx_tran_reg; 1.
KW Complete proteome.
SQ
SEQUENCE 252 AA; 29139 MW; DDCFBEDA0CA40DED CRC64;

Query Match
Best Local Similarity 65.5%; Score 38; DB 2; Length 252;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAMDLSSEFL 11
Db 129 SAMMDTLEFL 139

RESULT 31
Q815W5 PRELIMINARY; PRT; 252 AA.
AC Q815W5;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Transcriptional regulator.
GN OrderedLocustNames=BC5010;
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=226900;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
RA Kapatsrel V., Bhattacharya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goldman E., Larsen N., D'Souza M., Malunas T.,
RA Grechkin Y., Pusch G., Haselkorn R., Fomstein M., Ehrlich S.D.,
RA Overbeek R., Kyrides N.C.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
RT Bacillus anthracis."
RL Nature 423:87-91(2003).
DR EMBL: AE017014; AAP11882.1; -.
DR InterPro: IPR002831; TrmB_Trans_reg.
DR InterPro: IPR009058; Wng_hlx_DNA_bnd.
DR InterPro: IPR011571; Wng_hlx_trns_reg.
DR Pfam: PF01978; TrmB; 1.
DR ProDom: PD006327; Wng_hlx_tran_reg; 1.
KW Complete proteome.
SQ
SEQUENCE 252 AA; 29164 MW; 3C08334F2B14A5C8C CRC64;

Query Match
Best Local Similarity 65.5%; Score 38; DB 2; Length 252;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAMDLSSEFL 11
Db 129 SAMMDTLEFL 139

RESULT 32
Q81X10 PRELIMINARY; PRT; 252 AA.
AC Q81X10; Q6HRB3; Q6KRN0;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=BA5257; BAA54883; GBA5257;
OS Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1392;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=Ames / Isolate Porton;
RX MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
RA Read T.D., Peterson S.N., Tourasse N.J., Ballile L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapple E.K., Okstad O.A., Helgason E., Rittstone J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
RA Debey R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Bentley J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nieman W.C.,
RA Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,
RA Salzberg S.L., Thomson B., Friedlander A.M., Koehler T.M.,
RA Hanna P.C., Kolstoe A.B., Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria."
RL Nature 423:81-86(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Ames / Isolate 0581;
RA Ravel J., Raeko D.A., Shumway M.F., Jiang L., Cer R.Z., Fedorova N.B.,
RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
RA Fraser C.M.;
RT "Bacillus anthracis comparative genomics."
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Stearns;
RA Bretin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AE017040; AAP28922.1; -.
DR EMBL: AE017334; AAT94388.1; -.
DR EMBL: AE017225; AAT57175.1; -.
DR TIGR: BAA5257; -.
DR TIGR: BAA5257; -.
DR InterPro: IPR002831; TrmB_Trans_reg.
DR InterPro: IPR009058; Wng_hlx_DNA_bnd.
DR InterPro: IPR011571; Wng_hlx_trns_reg.
DR Pfam: PF01978; TrmB; 1.
DR ProDom: PD006327; Wng_hlx_tran_reg; 1.
KW Complete proteome; Hypothetical protein.
SQ
SEQUENCE 252 AA; 29185 MW; 282127D06704FD5C CRC64;

Query Match
Best Local Similarity 65.5%; Score 38; DB 2; Length 252;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAMDLSSEFL 11
Db 129 SAMMDTLEFL 139

RESULT 33
Q6HBPI PRELIMINARY; PRT; 252 AA.
AC Q6HBPI;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Probable transcriptional regulator.
GN OrderedLocustNames=BR9727_4725;
OS Bacillus thuringiensis (subsp. konkukian).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=180856;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97-27;
RA Bretin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RL "Complete genome sequence of Bacillus thuringiensis 97-27."

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RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017355; AAT62564.1; -.
DR InterPro; IPR002831; Trmb_trans_reg.
DR InterPro; IPR009058; Wng_hlx_DNA_bnd.
DR InterPro; IPR011571; Wng_hlx_trns_reg.
DR Pfam; PF01978; Trmb; 1.
DR ProDom; PD006327; Wng_hlx_tran_reg; 1.
KW Complete proteome.
SQ SEQUENCE 252 AA; 29185 MW; 282127D06704F5DC CRC64;

Query Match
Best Local Similarity 65.5%; Score 38; DB 2; Length 252;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAMDLSLEFL 11
Db 129 SAMDTLLEFL 139

RESULT 34
ID 074E50 PRELIMINARY; PRT; 299 AA.
AC 074E50;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE TPR domain protein.
GN OrderedLocustNames=GSU1114;
OS Geobacter sulfurreducens.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
OC Geobacteraceae; Geobacter.
OX NCBI_TaxId=35554;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PCA / ATCC 51573;
RX PubMed=14671304; DOI=10.1126/science.1088727;
RA Methe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C.,
RA Heidelberg J.F., Wu D., Wu M., Ward N.L., Beaman M.J., Dodson R.J.,
RA Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
RA Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,
RA Davidson T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,
RA Weltsman J.F., Khouri H.M., Feldblyum T.V., Uterback T.R.,
RA Van Aken S.E., Lovley D.R., Frazer C.M.;
RA "Genome of Geobacter sulfurreducens: metal reduction in subsurface
RT environments."
RT Science 302:1967-1969(2003).
DR EMBL; AE017180; AAR34440.1; -.
DR TIGR; GSU114; -.
DR InterPro; IPR008940; Prenyl_trans.
DR InterPro; IPR001440; TPR.
DR Pfam; PR00515; TPR; 1; 4.
DR SMART; SM00028; TPR; 5.
DR PROSITE; PS50005; TPR; 5.
DR PROSITE; PS00293; TPR_REGION; 1.
KW Complete proteome; Repeat; TPR repeat.
SQ SEQUENCE 299 AA; 33461 MW; AB863B1549C7342E CRC64;

Query Match
Best Local Similarity 65.5%; Score 38; DB 2; Length 299;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 WDDSLSEFL 10
Db 164 WDDALSEFL 171

RESULT 35
ID DAPA_XANAC STANDARD; PRT; 302 AA.
AC 06PLN5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 41, Last annotation update)

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DE Dihydrodipicolinate synthase (EC 4.2.1.52) (DHDDS).
GN Name=dapa; OrderedLocustNames=XAC1760;
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxId=92829;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=306 / ATCC 13902 / XV 101;
RX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Parah C.S., Furian L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A.,
RA Camarotte G., Cammaran F., Cardozo J., Chamargo F., Ciapina L.P.,
RA Ciccarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos B.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rosel N.M.,
RA Martins E.C., Melandris J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinoia L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitejima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities."
RT Nature 417:459-463(2002).
CC -1- CATALYTIC ACTIVITY: L-aspartate 4-semialdehyde + pyruvate =
CC dihydrodipicolinate + 2 H(2)O.
CC -1- PATHWAY: Biosynthesis of diaminopimelate and lysine from aspartate
CC semialdehyde; first step.
CC -1- SUBUNIT: Homotetramer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the DHDS family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL; AE011807; AAM36624.1; -.
DR HSSP; P05640; IDHP.
DR HAMAP; MF_00418; -, 1.
DR InterPro; IPR005263; Dapa_synth.
DR InterPro; IPR002220; DHDS.
DR Pfam; PR00701; DHDS; 1.
DR PRINTS; PR00146; DHPICNTHASE.
DR ProDom; PD001859; DHDS; 1.
DR TIGRPFAM; TIGR00674; dapa; 1.
DR PROSITE; PS00665; DHDS_1; 1.
DR PROSITE; PS00666; DHDS_2; 1.
KW Complete proteome; Diaminopimelate biosynthesis; Lyase;
KW lysine biosynthesis.
FT ACT_SITE 162 162 By similarity.
SQ SEQUENCE 302 AA; 31018 MW; 884C08BD13DC299 CRC64;

Query Match
Best Local Similarity 70.0%; Score 38; DB 1; Length 302;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAMDLSLEFL 10
Db 231 AAMDALSEFL 240

RESULT 36
ID SRA3_CAEEL STANDARD; PRT; 329 AA.
AC 009205;

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DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
GN Serpentine receptor class alpha 3 (Sra-3 protein).
DE Name=sra-3; ORFNames=AH6.7;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
KW (1)
RN SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology.";
RL Science 282:2012-2018(1998).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: Belongs to the C.elegans receptor-like protein sra
family.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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CC EMBL, 248009; CAA8086.1; -.
CC PIR, T18622; T18622.
CC WormBase, WBGene00005029; sra-3.
CC WormPeP, AH6.7; CE01461.
CC InterPro, IPR000344; Sra_chemrecept.
CC Pfam, PF02117; Sra_1.
CC PRINTS, PR00697; TMPTREINRA.
CC MultiGene family; Transmembrane.
KW TRANSMEM 25 45 Potential.
FT TRANSMEM 104 124 Potential.
FT TRANSMEM 144 164 Potential.
FT TRANSMEM 187 207 Potential.
FT TRANSMEM 238 258 Potential.
FT TRANSMEM 273 293 Potential.
SQ SEQUENCE 329 AA; 38548 MW; 5AC3FB73B996287 CRC64;

Query Match 65.5%; Score 38; DB 1; Length 329;
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 WDDSLSEF 10
DB 164 WDDPLSEY 171

RESULT 37
Q9F6D9 PRELIMINARY; PRT; 348 AA.
AC Q9F6D9;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Acyl transferase.
GN Name=znuC;
OS Streptomyces sp. R1128.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=140437;
RN (1)
RN SEQUENCE FROM N.A.
RC STRAIN=R1128;
RX MEDLINE=20517899; PubMed=10931852; DOI=10.1074/jbc.M006766200;
RA Marti T., Hu Z., Pohl N.L., Shah A.N., Khoja C.,
RT "Cloning, nucleotide sequence, and heterologous expression of the

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RT biosynthetic gene cluster for R1128, a non-steroidal estrogen receptor
antagonist. Insights into an unusual priming mechanism.";
RL J. Biol. Chem. 275:33443-33448(2000).
DE EMBL, AF293442; AAC30190.1; -.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro, IPR01227; Ac_transferase.
DR Pfam, PF00698; Acyl_transf_1; 1.
KW Transferase.
SQ SEQUENCE 348 AA; 36543 MW; D83E2D0C855A660 CRC64;

Query Match 65.5%; Score 38; DB 2; Length 348;
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAMDLSLE 9
DB 322 AAMDPLAE 329

RESULT 38
Q6R8A6 PRELIMINARY; PRT; 395 AA.
ID Q6R8A6;
AC Q6R8A6;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Prgh.
GN Name=prgh;
OS Sodalis glossinidius.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Sodalis.
OX NCBI_TaxID=63612;
RN (1)
RN SEQUENCE FROM N.A.
RP Dale C., Jones T., Pontes M.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL, AY508229; AAS66870.1; -.
SQ SEQUENCE 395 AA; 43940 MW; 3D2FA4BA8CA6696 CRC64;

Query Match 65.5%; Score 38; DB 2; Length 395;
Best Local Similarity 60.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAMDLSLEF 10
DB 119 AAMDITLNF 128

RESULT 39
Q76S23 PRELIMINARY; PRT; 443 AA.
ID Q76S23;
AC Q76S23;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE MCO17L (B-M,N,L,7 protein).
GN Name=MCO17L; Synonyms=B-M,N,L,7;
OS Molluscum contagiosum virus subtype 1 (MCOV1).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Molluscipoxvirus.
OX NCBI_TaxID=10280;
RN (1)
RN SEQUENCE FROM N.A.
RX MEDLINE=96325459; PubMed=8670425;
RA Senkevitch T.G., Bugert J.D., Sisler J.R., Koonin E.V., Darai G.,
RA Moss B.;
RT "Genome sequence of a human tumorigenic poxvirus: prediction of
RT specific host response-evasion genes.";
RL Science 273:813-816(1996).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=97093414; PubMed=8938976;

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RA Martin-Gallardo A., Moratilla M., Funes J.M., Agromayor M., Nunez A.,
 RA Varas A.J., Collado M., Valencia A., Lopez-Estebaranz J.L.,
 RA Estebaranz M.;
 RT "Sequence analysis of a Molluscum contagiosum virus DNA region which
 RT includes the gene encoding protein kinase 2 and other genes with
 RT unique organization.";
 RL Virus genes 13:19-29(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97352177; PubMed=9208457; DOI=10.1023/A:1007991508159;
 RA Moratilla M., Agromayor M., Nunez A., Funes J.M., Varas A.J.,
 RA Lopez-Estebaranz J.L., Estebaranz M., Martin-Gallardo A.;
 RT "A random DNA sequencing, computer-based approach for the generation
 RT of a gene map of molluscum contagiosum virus.";
 RL Virus genes 14:73-80(1997).
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL, U60315; AAC55145.1; -.
 DR EMBL, U86894; AAB57937.1; -.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR011009; Kinase_like.
 DR InterPro; IPR008790; Pox_ser_thr_kin.
 DR InterPro; IPR00719; Prot_kinase.
 DR InterPro; IPR001854; Ribosomal_L29.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR Pfam; PF05445; Pox_ser_thr_kin_1.
 DR PIRSF; PIRSF015695; STPK_F10L; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS00579; RIBOSOMAL_L29; UNKNOWN 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 443 AA; 52077 MW; 6EE91137BA113CEA CRC64;

Query Match 65.5%; Score 38; DB 2; Length 443;
 Best Local Similarity 63.6%; Pred. No. 1.9e+02;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Cx 1 AAWDSLSEFL 11
 Db 390 AAWSKALGEFL 400

RESULT 40
 083155 PRELIMINARY; PRT; 443 AA.
 AC 083155; O12529; O12603; O12818; O12884;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Protein kinase 2 homolog (CK2 protein).
 GN Name=Lil; Synonyms=CK2;
 OS Molluscum contagiosum virus.
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Molluscipoxvirus.
 OX NCBI_TaxID=10279;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Martin-Gallardo A., Moratilla M., Funes J.M., Agromayor M., Nunez A.,
 RA Varas A.J., Collado M., Valencia A., Lopez-Estebaranz J.L.,
 RA Estebaranz M.;
 RT "Sequence analysis of a Molluscum contagiosum virus DNA region which
 RT includes the gene encoding protein kinase 2 and other genes with
 RT unique organization.";
 RL Virus genes 0:0-0(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MCV 1;
 RX MEDLINE=97152522; PubMed=9000105;
 RA Douglas N.J., Blake N.W., Cream J.J., Soteriou B.A., Zhang H.Y.,
 RA Theodoridou A., Archard L.C.;
 RT "Similarity in genome organization between Molluscum contagiosum virus

RT (MCV) and vaccinia virus (VV): identification of MCV homologues of the
 RT VV genes for protein kinase 2, structural protein VP8, RNA polymerase
 RT 35 kDa subunit and beta-hydroxysteroid dehydrogenase.";
 RL J. Gen. Virol. 77:3113-3120(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MCV 1;
 RA Douglas N., Blake N., Archard L.;
 RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL, U52849; AAB59658.1; -.
 DR EMBL, U32423; AAB59658.1; -.
 DR PIR; T30619; T30619.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR011009; Kinase_like.
 DR InterPro; IPR008790; Pox_ser_thr_kin.
 DR InterPro; IPR00719; Prot_kinase.
 DR InterPro; IPR001854; Ribosomal_L29.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR Pfam; PF05445; Pox_ser_thr_kin_1.
 DR PIRSF; PIRSF015695; STPK_F10L; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS00579; RIBOSOMAL_L29; UNKNOWN 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 443 AA; 52077 MW; 6EE91137BA113CEA CRC64;

Query Match 65.5%; Score 38; DB 2; Length 443;
 Best Local Similarity 63.6%; Pred. No. 1.9e+02;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Cx 1 AAWDSLSEFL 11
 Db 390 AAWSKALGEFL 400

Search completed: March 31, 2005, 12:09:47
 Job time : 75.2135 secs

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